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(54) Title: **NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED TOLERANCE TO ENVIRONMENTAL STRESS**

(57) Abstract: This invention relates generally to nucleic acid sequences encoding proteins that are associated with abiotic stress responses and abiotic stress tolerance in plants. This invention further relates to transformed plant cells with altered metabolic activity compared to a corresponding non-transformed wild type plant cell, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.

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**NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH
ABIOTIC STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH
INCREASED TOLERANCE TO ENVIRONMENTAL STRESS**

5 **0001.0.1** This invention relates generally to nucleic acid sequences encoding proteins that are associated with abiotic stress responses and abiotic stress tolerance in plants.

0002.0.1 This invention further relates to transformed plant cells with altered metabolic activity compared to a corresponding non transformed wild type plant cell,
10 wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.

0003.0.1 In particular, this invention relates to nucleic acid sequences encoding
15 proteins that confer drought, heat, cold, and/or salt tolerance and/or resistance to plants, especially by altering the metabolic activity leading to drought, heat, cold, and/or salt tolerance and/or resistance to plants. The invention also deals with methods of producing, screening for and breeding such plant cells or plants and method of detecting stress in plants cells or plants.

20 **0004.0.1** Abiotic environmental stresses such as drought stress, salinity stress, heat stress and cold stress, are major limiting factors of plant growth and productivity (Boyer, 1982, *Science* 218, 443-448). Crop losses and crop yield losses of major crops such as rice, maize (corn) and wheat caused by these stresses represent a significant economic and political factor and contribute to food shortages in many underdeveloped
25 countries.

0005.0.1 Plants are typically exposed during their life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions of low water or desiccation (drought). However, if the severity and duration of the drought conditions are too great, the effects on plant
30 development, growth and yield of most crop plants are profound. Continuous exposure to drought causes major alterations in the plant metabolism. These great changes in metabolism ultimately lead to cell death and consequently yield losses.

0006.0.1 Developing stress-tolerant plants is a strategy that has the potential to solve or mediate at least some of these problems (McKersie and Leshem, 1994, *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers). However,
35 traditional plant breeding strategies to develop new lines of plants that exhibit resistance (tolerance) to these types of stresses are relatively slow and require specific resistant lines for crossing with the desired line. Limited germplasm resources for

stress tolerance and incompatibility in crosses between distantly related plant species represent significant problems encountered in conventional breeding. Additionally, the cellular processes leading to drought, cold and salt tolerance are complex in nature and involve multiple mechanisms of cellular adaptation and numerous metabolic pathways (McKersie and Leshem, 1994. *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers). This multi-component nature of stress tolerance has not only made breeding for tolerance largely unsuccessful, but has also limited the ability to genetically engineer stress tolerance plants using biotechnological methods.

0007.0.1 Drought, heat, cold and salt stresses have a common theme important for plant growth and that is water availability. Plants are exposed during their entire life cycle to conditions of reduced environmental water content. Most plants have evolved strategies to protect themselves against these conditions. However, if the severity and duration of the drought conditions are too great, the effects on plant development, growth and yield of most crop plants are profound. Since high salt content in some soils result in less available water for cell intake, its effect is similar to those observed under drought conditions. Additionally, under freezing temperatures, plant cells lose water as a result of ice formation that starts in the apoplast and withdraws water from the symplast (McKersie and Leshem, 1994. *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers). Commonly, a plant's molecular response mechanisms to each of these stress conditions are similar.

0008.0.1 The results of current research indicate that drought tolerance is a complex quantitative trait and that no real diagnostic marker is available yet. High salt concentrations or dehydration may cause damage at the cellular level during drought stress but the precise injury is not entirely clear (Bray, 1997. *Trends Plant Sci.* 2, 48–54). This lack of a mechanistic understanding makes it difficult to design a transgenic approach to improve drought tolerance. However, an important consequence of damage may be the production of reactive oxygen radicals that cause cellular injury, such as lipid peroxidation or protein and nucleic acid modification. Details of oxygen free radical chemistry and their reaction with cellular components such as cell membranes have been described (McKersie and Leshem, 1994. *Stress and Stress Coping in Cultivated Plants*, Kluwer Academic Publishers).

0009.0.1 It is the object of this invention to identify new, unique genes capable of conferring stress tolerance to plants upon expression or over-expression.

0010.0.1 It is further object of this invention to identify, produce and breed new, unique stress tolerant and/or resistant plant cells or plants and methods of inducing and detecting stress tolerance and/or resistance in plants or plant cells. It is a further object to identify new methods to detect stress tolerance and/or

resistance in plants or plant cells. It is also the object of this invention to identify new, unique genes capable of conferring stress tolerance to plants upon expression or over-expression.

5 0011.0.1 The present invention provides a transformed plant cell with altered metabolic activity compared to a corresponding non transformed wild type plant cell, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.

10 0012.0.2 The present invention provides a transgenic plant cell transformed by Stress-Related Protein (SRP) coding nucleic acid, selected from the group consisting of:

- 15 a) nucleic acid molecule encoding one of the polypeptides shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an an altered metabolic activity in an organism or a part thereof;
- b) nucleic acid molecule comprising one of the nucleic acid molecule shown in Fig. 1a, 1b or 1c;
- 20 c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;
- d) nucleic acid molecule which encodes a polypeptide which has at least 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;
- 25 e) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers as shown in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- 30 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- 35

- h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig. 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring an altered metabolic activity in an organism or a part thereof.

or comprising a sequence which is complementary thereto.

0013.0.1 As used herein, the term "metabolite" refers to intermediate substances, preferably such of low molecular weight, which occur during anabolism and catabolism in a cell or plant, in other words a substance produced or consumed by metabolism.

0014.0.1 The term "altered metabolic activity" refers to the change (increase or decrease) of the amount, concentration or activity (meaning here the effective concentration for the purposes of chemical reactions and other mass action) of a metabolite in a specific volume relative to a corresponding volume (e.g. in an organism, a tissue, a cell or a cell compartment) of a control, reference or wild type, including the de novo creation of the activity or expression, measured for example by one of the methods described herein below, which is changed (increased or decreased) as compared to a corresponding non transformed wild type plant cell.

0015.0.2 The terms "increased", "rised", "extended", "enhanced", "improved" or "amplified" relate to a corresponding change of a property in an organism, a part of an organism such as a tissue, seed, root, leave, flower etc. or in a cell and are interchangeable. Preferably, the overall activity in the volume is increased or enhanced in cases if the increase or enhancement is related to the increase or enhancement of an activity of a gene product, independent whether the amount of gene product or the specific activity of the gene product or both is increased or enhanced or whether the amount, stability or translation efficacy of the nucleic acid sequence or gene encoding for the gene product is increased or enhanced. The terms "reduction", "decrease" or "deletion" relate to a corresponding change of a property in an organism, a part of an organism such as a tissue, seed, root, leave, flower etc. or in a cell. Preferably, the overall activity in the volume is reduced, decreased or deleted in cases if the reduction, decrease or deletion is related to the reduction, decrease or deletion of an activity of a gene product, independent whether the amount of gene product or the specific activity of the gene product or both is reduced, decreased or

deleted or whether the amount, stability or translation efficacy of the nucleic acid sequence or gene encoding for the gene product is reduced, decreased or deleted.

0016.0.2 The terms "increase" or "decrease" relate to a corresponding change of a property in an organism or in a part of an organism, such as a tissue, seed, root, leave, flower etc. or in a cell. Preferably, the overall activity in the volume is increased in cases the increase relates to the increase of an activity of a gene product, independent whether the amount of gene product or the specific activity of the gene product or both is increased or generated or whether the amount, stability or translation efficacy of the nucleic acid sequence or gene encoding for the gene product is increased.

0017.0.2 Under "change of a property" it is understood that the activity, expression level or amount of a gene product or the metabolite content is changed in a specific volume relative to a corresponding volume of a control, reference or wild type, including the de novo creation of the activity or expression.

0018.0.2 The terms "increase" or "decrease" include the change of said property in only parts of the subject of the present invention, for example, the modification can be found in compartment of a cell, like a organelle, or in a part of a plant, like tissue, seed, root, leave, flower etc. but is not detectable if the overall subject, i.e. complete cell or plant, is tested. Preferably, the increase or decrease is found cellular, thus the term "increase of an activity" or "increase of a metabolite content" relates to the cellular increase compared to the wild typ cell.

0019.0.2 Accordingly, the term "increase" or "decrease" means that the specific activity of an enzyme as well as the amount of a compound or metabolite, e.g. of a polypeptide, a nucleic acid molecule or of the fine chemical of the invention or an encoding mRNA or DNA, can be increased or decreased in a volume.

0020.0.2 The terms "wild type", "control" or "reference" are exchangeable and can be a cell or a part of organisms such as an organelle or a tissue, or an organism, in particular a microorganism or a plant, which was not modified or treated according to the herein described process according to the invention. Accordingly, the cell or a part of organisms such as an organelle or a tissue, or an organism, in particular a microorganism or a plant used as wild typ, control or reference corresponds to the cell, organism or part thereof as much as possible and is in any other property but in the result of the process of the invention as identical to the subject matter of the invention as possible. Thus, the wild type, control or reference is treated identically or as identical as possible, saying that only conditions or properties might be different which do not influence the quality of the tested property.

0021.0.2 Preferably, any comparison is carried out under analogous conditions. The term "analogous conditions" means that all conditions such as, for example, culture or growing conditions, assay conditions (such as buffer composition, temperature, substrates, pathogen strain, concentrations and the like) are kept identical between the experiments to be compared.

0022.0.2 The "reference", "control", or "wild type" is preferably a subject, e.g. an organelle, a cell, a tissue, an organism, in particular a plant or a microorganism, which was not modified or treated according to the herein described process of the invention and is in any other property as similar to the subject matter of the invention as possible.

The reference, control or wild type is in its genome, transcriptome, proteome or metabolome as similar as possible to the subject of the present invention. Preferably, the term "reference-" "control-" or "wild type-"organelle, -cell, -tissue or -organism, in particular plant or microorganism, relates to an organelle, cell, tissue or organism, in particular plant or microorganism, which is nearly genetically identical to the organelle, cell, tissue or organism, in particular microorganism or plant, of the present invention or a part thereof preferably 95%, more preferred are 98%, even more preferred are 99,00%, in particular 99,10%, 99,30%, 99,50%, 99,70%, 99,90%, 99,99%, 99, 999% or more. Most preferable the "reference", "control", or "wild type" is a subject, e.g. an organelle, a cell, a tissue, an organism, which is genetically identical to the organism, cell or organelle used according to the process of the invention except that the responsible or activity conferring nucleic acid molecules or the gene product encoded by them are amended, manipulated, exchanged or introduced according to the inventive process.

0023.0.2 Preferably, the reference, control or wild type differs from the subject of the present invention only in the cellular activity of the polypeptide of the invention, e.g. as result of an increase in the level of the nucleic acid molecule of the present invention or an increase of the specific activity of the polypeptide of the invention, e.g. by or in the expression level or activity of an protein having the activity of an Stress-Related Protein (SRP) or its homologs, its biochemical or genetical causes and the altered metabolic activity.

0024.0.2 In case, a control, reference or wild type differing from the subject of the present invention only by not being subject of the process of the invention can not be provided, a control, reference or wild type can be an organism in which the cause for the modulation of an activity conferring the altered metabolic activity or expression of the nucleic acid molecule of the invention as described herein has been switched back or off, e.g. by knocking out the expression of responsible gene product, e.g. by antisense inhibition, by inactivation of an activator or agonist, by activation of an

inhibitor or antagonist, by inhibition through adding inhibitory antibodies, by adding active compounds as e.g. hormones, by introducing negative dominant mutants, etc. A gene production can for example be knocked out by introducing inactivating point mutations, which lead to an enzymatic activity inhibition or a destabilization or an inhibition of the ability to bind to cofactors etc.

0025.0.2 Accordingly, preferred reference subject is the starting subject of the present process of the invention. Preferably, the reference and the subject matter of the invention are compared after standardization and normalization, e.g. to the amount of total RNA, DNA, or protein or activity or expression of reference genes, like housekeeping genes, such as ubiquitin, actin or ribosomal proteins.

0026.0.2 A series of mechanisms exists via which a modification of the a protein, e.g. the polypeptide of the invention can directly or indirectly affect the yield, production and/or production efficiency of the amino acid.

0027.0.2 For example, the molecule number or the specific activity of the polypeptide or the nucleic acid molecule may be increased. Larger amounts of the fine chemical can be produced if the polypeptide or the nucleic acid of the invention is expressed *de novo* in an organism lacking the activity of said protein. However, it is also possible to increase the expression of the gene which is naturally present in the organisms, for example by modifying the regulation of the gene, or by increasing the stability of the corresponding mRNA or of the corresponding gene product encoded by the nucleic acid molecule of the invention, or by introducing homologous genes from other organisms which are differently regulated, e.g. not feedback sensitive.

0028.0.2 This also applies analogously to the combined increased expression of the nucleic acid molecule of the present invention or its gene product with that of further enzymes of the amino acid biosynthesis pathways, e.g. which are useful for the synthesis of the fine chemicals.

0029.0.2 The increase, decrease or modulation according to this invention can be constitutive, e.g. due to a stable permanent transgenic expression or to a stable mutation in the corresponding endogenous gene encoding the nucleic acid molecule of the invention or to a modulation of the expression or of the behaviour of a gene conferring the expression of the polypeptide of the invention, or transient, e.g. due to an transient transformation or temporary addition of a modulator such as a agonist or antagonist or inducible, e.g. after transformation with a inducible construct carrying the nucleic acid molecule of the invention under control of a inducible promoter and adding the inducer, e.g. tetracycline or as described herein below.

0030.0.2 The increase in activity of the polypeptide amounts in a cell, a tissue, a organelle, an organ or an organism or a part thereof preferably to at least 5%,

preferably to at least 20% or at to least 50%, especially preferably to at least 70%, 80%, 90% or more, very especially preferably are to at least 200%, most preferably are to at least 500% or more in comparison to the control, reference or wild type.

0031.0.2 The specific activity of a polypeptide encoded by a nucleic acid molecule of the present invention or of the polypeptide of the present invention can be tested as described in the examples. In particular, the expression of a protein in question in a cell, e.g. a plant cell or a microorganism and the detection of an increase the fine chemical level in comparison to a control is an easy test and can be performed as described in the state of the art.

0032.0.2 The term "increase" includes, that a compound or an activity is introduced into a cell *de novo* or that the compound or the activity has not been detectable before, in other words it is "generated".

0033.0.2 Accordingly, in the following, the term "increasing" also comprises the term "generating" or "stimulating". The increased activity manifests itself in an increase of the fine chemical.

0034.0.1 The transformed plant cells are compared to the corresponding non-transformed wild type of the same genus and species under otherwise identical conditions (such as, for example, culture conditions, age of the plants and the like). In this context, a change in metabolic activity of at least 10%, advantageously of at least 20%, preferably at least 30%, especially preferably of at least 40%, 50% or 60%, very especially preferably of at least 70%, 80%, 90%, 95% or even 100% or more, in comparison with the non-transformed organism is advantageous.

0035.0.1 Preferably the change in metabolite concentration of the transformed plant cells is the changed compared to the corresponding non-transformed wild type. Preferably the change in metabolite concentration is measured by HPLC and calculated by dividing the peak height or peak area of each analyte (metabolite) through the peak area of the respective internal standards. Data is normalised using the individual sample fresh weight. The resulting values are divided by the mean values found for wild type plants grown under control conditions and analysed in the same sequence, resulting in the so-called ratios, which represent values independent of the analytical sequence. These ratios indicate the behavior of the metabolite concentration of the transformed plants in comparison to the concentration in the wild type control plants.

0036.0.1 According to this method, the change in at least one metabolite concentration of the transformed plant cells compared to the corresponding non-transformed wild type is at least 10%, advantageously of at least 20%, preferably at

least 40%, 60% or 80%, especially preferably of at least 90%, 100% or 200%, very especially preferably of at least 700%, 800%, 900% 1000% or more.

0037.0.1 Data significance can be determined by all statistical methods known by a person skilled in the art, preferably by a t-test, more preferably by the student t-test.

0038.0.1 Altered metabolic activity also refers to metabolites that, compared to a corresponding non transformed wild type plant cell, are not produced after transformation or are only produced after transformation.

0039.0.1 Preferred metabolites of the invention are 2,3-dimethyl-5-phytylquinol or 2-hydroxy-palmitic acid or 3,4-dihydroxyphenylalanine (= dopa) or 3-hydroxy-palmitic acid or 5-oxoprolin or alanine or alpha linolenic acid (c18:3 (c9, c12, c15)) or alpha-tocopherol or aminoadipic acid or anhydroglucose or arginine or aspartic acid or beta-apo-8' carotenal or beta-carotene or beta-sitosterol or beta-tocopherol or (delta-7-cis,10-cis)-hexadecadienic acid or hexadecatrienic acid or margoric acid or delta-15-cis-tetracosenic acid or ferulic acid or campesterol or cerotic acid (c26:0) or citrulline or cryptoxanthine or eicosenoic acid (20:1) or fructose or fumarate or galactose or gamma-aminobutyric acid or gamma-tocopherol or gluconic acid or glucose or glutamic acid or glutamine or glycerate or glyceraldehyd or glycerol or glycerol-3-phosphate or glycine or homoserine or inositol or isoleucine or iso-maltose or isopentenyl pyrophosphate or leucine or lignoceric acid (c24:0) or linoleic acid (c18:2 (c9, c12)) or luteine or lycopene or malate or mannose or methionine or methylgalactofuranoside or methylgalactopyranoside or methylgalactopyranoside or palmitic acid (c16:0) or phenylalanine or phosphate or proline or putrescine or pyruvat or raffinose or ribonic acid or serine or shikimate or sinapine acid or stearic acid (c18:0) or succinate or sucrose or threonine or triacontanoic acid or tryptophane or tyrosine or ubiquinone or udp-glucose or valine or zeaxanthine.

0040.0.1 Metabolic activity may also be altered concerning one or more derivatives of one or more of the above metabolites.

0041.0.1 Preferably metabolic activity is altered concerning one or more metabolites selected from the group consisting of all of the above metabolites.

0042.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of mannose, inositol, phosphate, aspartic acid, isoleucine, leucine, gamma-aminobutyric acid, glyceraldehyd, sucrose, campesterol, valine, beta-tocopherol, ubiquinone, palmitic acid (c16:0), 2-hydroxy-palmitic acid, 2,3-dimethyl-5-phytylquinol, beta-carotene, alpha-linolenic acid (c18:3 (c9, c12, c15)), lycopene.

0043.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of methylgalactofuranoside, beta-sitosterol, delta-15-cis-tetracosenic acid (c24:1 me), margaric acid (c17:0 me), stearic acid (c18:0), methylgalactopyranoside, gamma-tocopherol, linoleic acid (c18:2 (c9, c12)), hexadecatrienic acid (c16:3 me), shikimate, raffinose, glutamic acid, glutamine, 5 udp-glucose, proline, threonine, isopentenyl pyrophosphate, 5-oxoproline, ferulic acid, sinapine acid.

0044.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of tryptophane, citrulline, serine, alanine, glycerate, arginine, 3-hydroxy-palmitic acid, putrescine, 3,4-dihydroxyphenylalanine (=dopa), alpha-tocopherol, aminoadipic acid, anhydroglucose, beta-apo-B' carotenol, delta-7-cis,10-cis-hexadecadienic acid (c16:2 me), cerotic acid (c26:0), cryptoxanthine, eicosenoic acid (20:1), fructose, fumarate.

0045.0.1 Alternatively metabolic activity may be altered concerning one or more metabolites selected from the group consisting of galactose, gluconic acid, glucose, glycerol, glycerol-3-phosphate, glycine, homoserine, iso-maltose, lignoceric acid (c24:0), luteine, malate, triscontanoic acid, methionine, phenylalanine, pyruvate, ribonic acid, succinate, tyrosine, zeaxanthine.

0046.0.1 The present invention provides a transgenic plant cell, wherein expression of said nucleic acid sequence in the plant cell results altered metabolic activity leading to increased tolerance and/or resistance to environmental stress as compared to a corresponding non-transformed wild type plant cell. One preferred wild type plant cell is a non-transformed *Arabidopsis* plant cell. An example here is the *Arabidopsis* wild type C24 (Nottingham *Arabidopsis* Stock Centre, UK; NASC Stock N806).

0047.0.1 Other preferred wild type plant cells are a non-transformed from plants selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass and forage crops.

0048.0.1 More preferred wild type plant cells are a non-transformed *Linum* plant cell, preferably *Linum usitatissimum*, more preferably the variety Brigitta, Golda, Gold Merchant, Helle, Juliet, Olpina, Livla, Marlin, Maedgold, Sporpion, Serenade, Linus, Taunus, Lifax or Livola, a non-transformed *Hellantus* plant cell, preferably *Hellantus annuus*, more preferably the variety Aurasol, Capella, Flavia, Flores, Jazzy, Palulo, Pegasol, PIR64A54, Rigasol, Sariuca, Sideral, Sunny, Alenka, Candisol or Floyd, or a

non-transformed Brassica plant cell, preferably Brassica napus, more preferably the variety Dorothy, Evita, Heros, Hyola, Kimbar, Lambada, Licolly, Liconira, Licosmos, Lisonne, Mistral, Passat, Serator, Siapula, Sponsor, Star, Caviar, Hybridol, Baical, Olga, Lara, Doublol, Karola, Falcon, Spirit, Olymp, Zeus, Libero, Kyola, Licord, Lion, 5 Lirajet, Lisbeth, Magnum, Maja, Mendel, Mica, Mohican, Olpop, Ontario, Panthar, Prince, Pronio, Susanna, Talani, Titan, Transfer, Wiking, Woltan, Zeniah, Artus, Contact or Smart.

0049.0.1 The expression of said nucleic acid sequence in the plant cell may directly or indirectly influence the metabolic activity of the transformed plant cells.

10 **Preferably they influence the activity of the above metabolites.**

0050.0.1 Preferably metabolic activity may be altered by transformation with one or more Stress-Related Protein (SRP) coding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1cb homologs of the afore mentioned sequences.

15 **0051.0.1** It is within the scope of the invention to identify the genes encoded by a nucleic acid sequence selected from the group consisting of the nucleic acid of Fig. 1a, 1b or 1c and/or homologs thereof in target plants, especially crop plants, and then express the corresponding gene to achieve the altered metabolic activity resulting in increased tolerance and/or resistance to environmental stress. Consequently the 20 invention is not limited to a specific plant.

0052.0.2 A protein having an activity conferring an altered metabolic activity preferably has the structure of the polypeptide described herein, in particular of the polypeptides comprising the consensus sequence shown in Fig. 2 or of the polypeptide as shown in Fig. 1a, 1b or 1c or the functional homologues thereof as described herein, 25 or is encoded by the nucleic acid molecule characterized herein or the nucleic acid molecule according to the invention, for example by the nucleic acid molecule as shown in Fig. 1a, 1b or 1c or its herein described functional homologues and has the herein mentioned activity.

0053.0.1 It is further possible to detect environmental stress in plant cells or plants 30 by screening the plant cells for altered metabolic activity as compared to non-stress conditions. This allows for monitoring of stress levels in plants, even when no symptoms are visible. Therefore counter action can be taken earlier and e.g. crop losses minimized by timely watering.

0054.0.1 It is also within the scope of the invention to screen plant cells or plants 35 for increased tolerance and/or resistance to environmental stress by screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions. This allows selection of plants with increased tolerance and/or

resistance to environmental stress without the identification of genes or visual symptoms.

0055.0.1 With the invention it is further possible to breed plant cells or plants towards increased tolerance and/or resistance to environmental stress by screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions and selecting those with increased tolerance and/or resistance to environmental stress. The screening for metabolite activity is faster and easier than e.g. screening for genes.

0056.0.1 Screening is well known to those skilled in the art and generally refers to the search for a particular attribute or trait. In the invention this trait in a plant or plant cell is preferably the concentration of a metabolite, especially preferred the concentration of the above metabolites. The methods and devices for screening are familiar to those skilled in the art and include GC (gas chromatography), LC (liquid chromatography), HPLC (high performance (pressure) liquid chromatography), MS (mass spectrometry), NMR (nuclear magnetic resonance) spectroscopy, IR (infra red) spectroscopy, photometric methods etc and combinations of these methods.

0057.0.1 Breeding is also customary knowledge for those skilled in the art. It is understood as the directed and stable incorporation of a particular attribute or trait into a plant or plant cell.

0058.0.1 The various breeding steps are characterized by well-defined human intervention such as selecting the lines to be crossed, directing pollination of the parental lines, or selecting appropriate progeny plants. Different breeding measures can be taken, depending on the desired properties. All the techniques are well known by a person skilled in the art and include for example, but are not limited to hybridization, inbreeding, backcross breeding, multiline breeding, variety blend, interspecific hybridization, aneuploid techniques, etc. Hybridization techniques also can include the sterilization of plants to yield male or female sterile plants by mechanical, chemical, or biochemical means. Cross pollination of a male sterile plant with pollen of a different line assures that the genome of the male sterile but female fertile plant will uniformly obtain properties of both of the parental lines. The transgenic seeds and plants according to the invention can therefore be used for the breeding of improved plant lines, which can increase the effectiveness of conventional methods such as herbicide or pesticide treatment or which allow one to dispense with said methods due to their modified genetic properties. Alternatively new crops with improved stress tolerance, preferably drought and temperature, can be obtained, which, due to their optimized genetic "equipment", yield harvested product of better quality than products that were not able to tolerate comparable adverse developmental conditions.

0059.0.1 The invention provides that the environmental stress can be salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof, preferably drought and/or temperature.

5 **0060.0.1** The object of the invention is a transgenic plant cell, wherein the SRP (=stress related protein) is selected preferably from yeast, preferably *Saccharomyces cerevisiae*, or *E. coli* or a plant, preferably *Brassica napus*, *Glycine max*, or *Oryza sativa*.

10 **0061.0.1** Object of the invention is also a transgenic plant cell, wherein the SRP coding nucleic acid is at least about 50 % homologous to one of the nucleic acid of Fig. 1a, 1b or 1c.

0062.0.1 In the transgenic plant cell of the invention, the expression of said nucleic acid results in increased tolerance to an environmental stress, which is preferably achieved by altering metabolic activity, as compared to a corresponding non-transformed wild type plant cell. Herein, the environmental stress is selected from
15 the group consisting of salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof, preferably drought and/or temperature.

0063.0.2 The term "expression" refers to the transcription and/or translation of a coding gene segment or gene. As a rule, the resulting product is an mRNA or a protein. However, expression products can also include functional RNAs such as, for
20 example, antisense, nucleic acids, tRNAs, snRNAs, rRNAs, RNAi, siRNA, ribozymes etc. Expression may be systemic, local or temporal, for example limited to certain cell types, tissue, organs or time periods.

0064.0.2 Unless otherwise specified, the terms "polynucleotides", "nucleic acid" and "nucleic acid molecule" are interchangeably in the present context. Unless
25 otherwise specified, the terms "peptide", "polypeptide" and "protein" are interchangeably in the present context. The term "sequence" may relate to polynucleotides, nucleic acids, nucleic acid molecules, peptides, polypeptides and proteins, depending on the context in which the term "sequences" is used. The terms "gene(s)", "polynucleotide", "nucleic acid sequence", "nucleotide sequence", or "nucleic
30 acid molecule(s)" as used herein refers to a polymeric form of nucleotides of any length, either ribonucleotides or deoxyribonucleotides. The terms refer only to the primary structure of the molecule.

0065.0.2 Thus, the terms "gene(s)", "polynucleotide", "nucleic acid sequence", "nucleotide sequence", or "nucleic acid molecule(s)" as used herein include double-
35 and single-stranded DNA and RNA. They also include known types of modifications, for example, methylation, "caps", substitutions of one or more of the naturally occurring

nucleotides with an analog. Preferably, the DNA or RNA sequence of the invention comprises a coding sequence encoding the herein defined polypeptide.

0066.0.2 A "coding sequence" is a nucleotide sequence, which is transcribed into mRNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the 5'-terminus and a translation stop codon at the 3'-terminus. A coding sequence can include, but is not limited to mRNA, cDNA, recombinant nucleotide sequences or genomic DNA, while introns may be present as well under certain circumstances.

0067.0.2 For the purposes of the invention, as a rule the plural is intended to encompass the singular and vice versa.

0068.0.1 Further, the transgenic plant cell is derived from a monocotyledonous plant. Alternatively, the transgenic plant cell is derived from a dicotyledonous plant. Preferably, the transgenic plant cell is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, popper, sunflower, flax, borage, sunflower, linseed, primrose, rapeseed, tump rape, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, Vicia species, pea, alfalfa, coffee, cacao, tea, Salix species, oil palm, coconut, perennial grass, forage crops and Arabidopsis thaliana. Moreover, the transgenic plant cell of the present invention can be derived from a gymnosperm plant. Preferably, the plant is selected from the group of spruce, pine and fir.

0069.0.1 The invention further provides a seed produced by a transgenic plant transformed by a SRP coding nucleic acid, wherein the plant is true breeding for increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant cell. The transgenic plant might be a monocot, a dicot or a gymnosperm plant. The invention further provides a seed produced by a transgenic plant expressing an SRP wherein the plant is true breeding for increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant cell. The invention pertains to a seed produced by a transgenic plant, wherein the seed is genetically homozygous for a transgene conferring an increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant.

0070.0.1 The invention further provides an agricultural product produced by any of the below-described transgenic plants, plant parts such as leaves, petal, anther, roots, tubers, stems, buds, flowers or seeds. The invention further provides a isolated recombinant expression vector comprising a SRP encoding nucleic acid.

0071.0.1 The invention further provides a method of producing a transgenic plant with a SRP coding nucleic acid, wherein expression of the nucleic acid in the plant results in increased tolerance and/or resistance to an environmental stress, which is preferably achieved by altering metabolic activity, as compared to a corresponding non-transformed wild type plant cell, comprising

- a) transforming a plant cell with an expression vector including a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs or parts thereof and
- b) generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant.

0072.0.1 With regard to invention described here, "transformed or transgene" means all those plants or parts thereof which have been brought about by genetic manipulation methods and in which either

- c) one or more genes, preferably encoded by one or more nucleic acid sequences as depicted in Fig. 1a, 1b or 1c and/or a homolog thereof, or
- d) a genetic regulatory element, for example a promoter, which is functionally linked e.g. to the nucleic acid sequence as depicted in Fig. 1a, 1b or 1c and/or a homolog thereof, or
- e) (a) and (b)

is/are not present in its/their natural genetic environment or has/have been modified by means of genetic manipulation methods, it being possible for the modification to be, by way of example, a substitution, addition, deletion, inversion or insertion of one or more nucleotide radicals.

0073.0.1 "Natural genetic environment" means the natural chromosomal locus in the organism of origin or the presence in a genomic library. In the case of a genomic library, the natural, genetic environment of the nucleic acid sequence is preferably at least partially still preserved. The environment flanks the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, particularly preferably at least 1000 bp, very particularly preferably at least 5000 bp.

0074.0.1 In said method for producing a transgenic plant comprising an SRP, the SRP coding nucleic acid is selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences. Further, the SRP coding nucleic acid used in the said method is at least about 50% homologous to one of the nucleic acid of Fig. 1a, 1b or 1c.

0075.0.1 A plant or plant cell is considered "true breeding" for a particular trait if it is genetically homozygous for that trait to the extent that, when the true-breeding plant is self-pollinated, a significant amount of independent segregation of the trait among the progeny is not observed. In the present invention, the trait arises from the transgenic expression of one or more DNA sequences introduced into a plant cell or plant.

0076.0.1 The present invention also provides methods of modifying stress tolerance of a plant comprising, modifying the level of expression of a SRP nucleic acid in the plant. The invention provides one method of producing a transgenic plant with a synthetic, novel or modified transcription factor that acts by increasing the transcription of a SRP gene. Theoretically it is also possible to obtain a decrease in expression of the gene.

0077.0.1 A method of detecting environmental stress in plant cells or plants comprising screening the plant cells for altered metabolic activity as compared to non-stress conditions is also in the scope of the invention.

0078.0.1 Further a method of screening plant cells or plants for increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions is encompassed in the invention.

0079.0.1 The present invention also encompasses a method of breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions and selecting those with increased tolerance and/or resistance to environmental stress.

0080.0.1 In these methods metabolite activity is preferably altered concerning the above metabolites and groups of metabolites.

0081.0.1 The present invention also encompasses the use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for selection of plants or plant cells with increased tolerance to environmental stress.

0082.0.1 The present invention further encompasses the use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for detection of stress in plants or plant cells.

0083.0.1 The present invention also provides methods of modifying stress tolerance of a crop plant comprising utilizing a SRP coding nucleic acid sequence to

identify individual plants in populations segregating for either increased or decreased environmental stress tolerance (DNA marker).

0084.0.1 In the said method of modifying stress tolerance of a plant the SRP encoding nucleic acid may be selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences. Further the SRP coding nucleic acid used therein may at least about 50% homologous to one of the nucleic acid of Fig. 1a, 1b or 1c. Also an expression vector as described in the present invention might be used in the said method.

0085.0.1 In a variant method of said method of modifying stress tolerance, the plant is transformed with an inducible promoter that directs expression of the SRP. For example, the promoter is tissue specific. In a variant method, the used promoter is developmentally regulated.

0086.0.2 In a further embodiment, the method of modifying stress tolerance comprises one or more of the following steps:

- a) stabilizing a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or of the polypeptide of the invention having the herein-mentioned activity of altering the metabolic activity;
- b) stabilizing a mRNA conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or its homologs or of a mRNA encoding the polypeptide of the present invention having the herein-mentioned activity of altering the metabolic activity;
- c) increasing the specific activity of a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or of the polypeptide of the present invention or decreasing the inhibitory regulation of the polypeptide of the invention;
- d) generating or increasing the expression of an endogenous or artificial transcription factor mediating the expression of a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the invention or of the polypeptide of the invention having the herein-mentioned activity of altering the metabolic activity;
- e) stimulating activity of a protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the present invention or a polypeptide of the present invention having the herein-mentioned activity of altering the metabolic activity by adding one or more exogenous inducing factors to the organismus or parts thereof;

- f) expressing a transgenic gene encoding a protein conferring the increased expression of a polypeptide encoded by the nucleic acid molecule of the present invention or a polypeptide of the present invention, having the herein-mentioned activity of altering the metabolic activity; and/or
- 5 g) increasing the copy number of a gene conferring the increased expression of a nucleic acid molecule encoding a polypeptide encoded by the nucleic acid molecule of the invention or the polypeptide of the invention having the herein-mentioned activity of altering the metabolic activity;
- h) increasing the expression of the endogenous gene encoding the polypeptide of the invention or its homologs by adding positive expression or removing negative expression elements, e.g. homologous recombination can be used to either introduce positive regulatory elements like for plants the 35S enhancer into the promoter or to remove repressor elements from regulatory regions. Further gene conversion methods can be used to disrupt repressor elements or to enhance to activity of positive elements- positive elements can be randomly introduced in plants by T-DNA or transposon mutagenesis and lines can be identified in which the positive elements have been integrated near to a gene of the invention, the expression of which is thereby enhanced;
- 10 and/or
- i) modulating growth conditions of the plant in such a manner, that the expression or activity of the gene encoding the protein of the invention or the protein itself is enhanced;
- j) selecting of organisms with especially high activity of the proteins of the invention from natural or from mutagenized resources and breeding them into the target organisms, eg the elite crops.
- 15 20 25

0087.0.2 Preferably, said mRNA is the nucleic acid molecule of the present invention and/or the protein conferring the increased expression of a protein encoded by the nucleic acid molecule of the present invention or the polypeptide having the herein mentioned activity is the polypeptide of the present invention, e.g. conferring increased tolerance to environmental stress by altering the metabolic activity.

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0088.0.2 In general, the amount of mRNA, polynucleotide or nucleic acid molecule in a cell or a compartment of an organism correlates with the amount of encoded protein and thus with the overall activity of the encoded protein in said volume. Said correlation is not always linear, the activity in the volume is dependent on the stability of the molecules, the degradation of the molecules or the presence of

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activating or inhibiting co-factors. Further, product and educt inhibitions of enzymes are well known, e.g. Zinser et al. "Enzyminhibitoren / Enzyme inhibitors".

0089.0.2 The activity of the abovementioned proteins and/or polypeptide encoded by the nucleic acid molecule of the present invention can be increased in various ways.

- 5 For example, the activity in an organism or in a part thereof, like a cell, is increased via increasing the gene product number, e.g. by increasing the expression rate, like introducing a stronger promoter, or by increasing the stability of the mRNA expressed, thus increasing the translation rate, and/or increasing the stability of the gene product, thus reducing the proteins decayed. Further, the activity or turnover of enzymes can be
- 10 influenced in such a way that a reduction or increase of the reaction rate or a modification (reduction or increase) of the affinity to the substrate results, is reached. A mutation in the catalytic centre of a polypeptide of the invention, e.g. as enzyme, can modulate the turn over rate of the enzyme, e.g. a knock out of an essential amino acid can lead to a reduced or completely knock out activity of the enzyme, or the deletion or
- 15 mutation of regulator binding sites can reduce a negative regulation like a feedback inhibition (or a substrate inhibition, if the substrate level is also increased). The specific activity of an enzyme of the present invention can be increased such that the turn over rate is increased or the binding of a co-factor is improved. Improving the stability of the encoding mRNA or the protein can also increase the activity of a gene product. The
- 20 stimulation of the activity is also under the scope of the term "increased activity".

- 0090.0.2** Moreover, the regulation of the abovementioned nucleic acid sequences may be modified so that gene expression is increased. This can be achieved advantageously by means of heterologous regulatory sequences or by modifying, for example mutating, the natural regulatory sequences which are present. The
- 25 advantageous methods may also be combined with each other.

- 0091.0.2** In general, an activity of a gene product in an organism or part thereof, in particular in a plant cell, a plant, or a plant tissue or a part thereof or in a microorganism can be increased by increasing the amount of the specific encoding mRNA or the corresponding protein in said organism or part thereof. "Amount of protein
- 30 or mRNA" is understood as meaning the molecule number of polypeptides or mRNA molecules in an organism, a tissue, a cell or a cell compartment. "Increase" in the amount of a protein means the quantitative increase of the molecule number of said protein in an organism, a tissue, a cell or a cell compartment or part thereof - for example by one of the methods described herein below - in comparison to a wild type, control or reference.
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0092.0.2 The increase in molecule number amounts preferably to at least 1%, preferably to more than 10%, more preferably to 30% or more, especially preferably to

50%, 70% or more, very especially preferably to 100%, most preferably to 500% or more. However, a de novo expression is also regarded as subject of the present invention.

5 **0093.0.2** A modification, i.e. an increase or decrease, can be caused by endogenous or exogenous factors. For example, an increase in activity in an organism or a part thereof can be caused by adding a gene product or a precursor or an activator or an agonist to the media or nutrition or can be caused by introducing said subjects into a organism, transient or stable.

10 **0094.0.2** In one embodiment the increase or decrease in metabolic activity in the plant or a part thereof, e.g. in a cell, a tissue, a organ, an organelle etc., is achieved by increasing the endogenous level of the polypeptide of the invention. Accordingly, in an embodiment of the present invention, the present invention relates to a process wherein the gene copy number of a gene encoding the polynucleotide or nucleic acid molecule of the invention is increased. Further, the endogenous level of the
15 polypeptide of the invention can for example be increased by modifying the transcriptional or translational regulation of the polypeptide.

0095.0.2 In one embodiment the metabolic activity in the plant or part thereof can be altered by targeted or random mutagenesis of the endogenous genes of the invention. For example homologous recombination can be used to either introduce
20 positive regulatory elements like for plants the 35S enhancer into the promoter or to remove repressor elements from regulatory regions. In addition gene conversion like methods described by Kochevenko and Willmitzer (Plant Physiol. 2003 May;132(1):174-84) and citations therein can be used to disrupt repressor elements or to enhance to activity of positive regulatory elements.
25 Furthermore positive elements can be randomly introduced in (plant) genomes by T-DNA or transposon mutagenesis and lines can be screened for, in which the positive elements has be integrated near to a gene of the invention, the expression of which is thereby enhanced. The activation of plant genes by random integrations of enhancer elements has been described by Hayashi et al., 1992 (Science 258:1350-1353) or
30 Weigel et al., 2000 (Plant Physiol. 122, 1003-1013) and others cited therein.

0096.0.2 Reverse genetic strategies to identify insertions (which eventually carrying the activation elements) near in genes of interest have been described for various cases eg. Krysan et al., 1999 (Plant Cell 1999, 11, 2263-2290); Sessions et al., 2002 (Plant Cell 2002, 14, 2985-2994); Young et al., 2001, (Plant Physiol. 2001, 125, 513-518); Koprek et al., 2000 (Plant J. 2000, 24, 253-263) ; Jeon et al., 2000 (Plant J. 2000, 22, 561-570) ; Tissier et al., 1999 (Plant Cell 1999, 11, 1841-1852); Speulmann et al., 1999 (Plant Cell 1999 ,11 , 1853-1866). Briefly material from all plants of a large

T-DNA or transposon mutagenized plant population is harvested and genomic DNA prepared. Then the genomic DNA is pooled following specific architectures as described for example in Krysan et al., 1999 (Plant Cell 1999, 11, 2283-2290). Pools of genomic DNAs are then screened by specific multiplex PCR reactions detecting the combination of the Insertional mutagen (eg T-DNA or Transposon) and the gene of interest. Therefore PCR reactions are run on the DNA pools with specific combinations of T-DNA or transposon border primers and gene specific primers. General rules for primer design can again be taken from Krysan et al., 1999 (Plant Cell 1999, 11, 2283-2290). Rescreening of lower levels DNA pools lead to the identification of individual plants in which the gene of interest is activated by the insertional mutagen.

0097.0.2 The enhancement of positive regulatory elements or the disruption or working of negative regulatory elements can also be achieved through common mutagenesis techniques: The production of chemically or radiation mutated populations is a common technique and known to the skilled worker. Methods for plants are described by Koomeef et al. 1982 and the citations therein and by Lightner and Caspar In "Methods in Molecular Biology" Vol 82. These techniques usually induce pointmutations that can be identified in any known gene using methods such as TILLING (Colbert et al. 2001).

0098.0.2 Accordingly, the expression level can be increased if the endogenous genes encoding a polypeptide conferring an increased expression of the polypeptide of the present invention, in particular genes comprising the nucleic acid molecule of the present invention, are modified via homologous recombination, Tilling approaches or gene conversion

0099.0.2 Regulatory sequences can be operatively linked to the coding region of an endogenous protein and control its transcription and translation or the stability or decay of the encoding mRNA or the expressed protein. In order to modify and control the expression, promoter, UTRs, splicing sites, processing signals, polyadenylation sites, terminators, enhancers, repressors, post transcriptional or posttranslational modification sites can be changed, added or amended. For example, the activation of plant genes by random integrations of enhancer elements has been described by Hayashi et al., 1992 (Science 258:1350-1353) or Weigel et al., 2000 (Plant Physiol. 122, 1003-1013) and others cited therein. For example, the expression level of the endogenous protein can be modulated by replacing the endogenous promoter with a stronger transgenic promoter or by replacing the endogenous 3'UTR with a 3'UTR, which provides more stability without amending the coding region. Further, the transcriptional regulation can be modulated by introduction of a artificial transcription

factor as described in the examples. Alternative promoters, terminators and UTRs are described below.

0100.0.2 The activation of an endogenous polypeptide having above-mentioned activity, e.g. conferring an increased tolerance to environmental stress after altering the metabolic activity can also be increased by introducing a synthetic transcription factor, which binds close to the coding region of the protein of the invention encoding gene and activates its transcription. A chimeric zinc finger protein can be construed, which comprises a specific DNA-binding domain and an activation domain as e.g. the VP16 domain of Herpes Simplex virus. The specific binding domain can bind to the regulatory region of the protein coding region. The expression of the chimeric transcription factor in a plant leads to a specific expression of the protein of the invention, see e.g. in WO01/52820, Oriz, Proc. Natl. Acad. Sci. USA, 2002, Vol. 99, 13290 or Guan, Proc. Natl. Acad. Sci. USA, 2002, Vol. 99, 13296.

0101.0.2 In one further embodiment of the method according to the invention, plants are used in which one of the abovementioned genes, or one of the abovementioned nucleic acids, is mutated in a way that the activity of the encoded gene products is less influenced by cellular factors, , or not at all, in comparison with the unmutated proteins. For example, well known regulation mechanism of enzymic activity are substrate inhibition or feed back regulation mechanisms. Ways and techniques for the introduction of substitutions, deletions and additions of one or more bases, nucleotides or amino acids of a corresponding sequence are described herein below in the corresponding paragraphs and the references listed there, e.g. in Sambrook et al., Molecular Cloning, Cold Spring Harbour, NY, 1989. The person skilled in the art will be able to identify regulation domains and binding sites of regulators by comparing the sequence of the nucleic acid molecule of the present invention or the expression product thereof with the state of the art by computer software means which comprise algorithms for the identifying of binding sites and regulation domains or by introducing into a nucleic acid molecule or in a protein systematically mutations and assaying for those mutations which will lead to an increased specific activity or an increased activity per volume, in particular per cell.

0102.0.2 It is therefore advantageously to express in a plant a nucleic acid molecule of the invention or a polypeptide of the invention derived from a evolutionary distantly related organism, as e.g. using a prokaryotic gene in a eukaryotic host, as in these cases the regulation mechanism of the host cell may not weaken the activity (cellular or specific) of the gene or its expression product

0103.0.2 The mutation is introduced in such a way that the production of the amino acids is not adversely affected.

0104.0.2 Less influence on the regulation of a gene or its gene product is understood as meaning a reduced regulation of the enzymatic activity leading to an increased specific or cellular activity of the gene or its product. An increase of the enzymatic activity is understood as meaning an enzymatic activity, which is increased by at least 10%, advantageously at least 20, 30 or 40%, especially advantageously by at least 50, 60 or 70% in comparison with the starting organism.

0105.0.1 The invention provides that the above methods can be performed such that the stress tolerance is increased. It is also possible to obtain a decrease in stress tolerance.

0106.0.1 The invention is not limited to specific nucleic acids, specific polypeptides, specific cell types, specific host cells, specific conditions or specific methods etc. as such, but may vary and numerous modifications and variations therein will be apparent to those skilled in the art. It is also to be understood that the terminology used herein is for the purpose of describing specific embodiments only and is not intended to be limiting.

0107.0.1 The present invention also relates to isolated Stress Related Proteins (SRP) which are selected from the group comprising the proteins of Fig. 1a, 1b or 1c and/or homologs thereof. Preferably, the isolated Stress Related Proteins (SRP) of the present invention are selected from yeast or *E. coli*. Further, the present invention is related to isolated Stress Related Protein (SRP) encoding nucleic acids selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs thereof. Here, preferably, an isolated Stress Related Protein (SRP) encoding nucleic acid encodes an SRP which is selected from yeast or *E. coli*.

0108.0.1 The present invention provides stress related gene sequences selected from the group consisting of the the nucleic acid of Fig. 1a, 1b or 1c of yeast, preferably from *Saccharomyces cerevisiae* or *E. coli*.

0109.0.1 Homologs of the aforementioned sequences can be isolated advantageously from yeast, fungi, viruses, algae, bacteria, such as *Acetobacter* (subgen. *Acetobacter*) *aceti*; *Acidithiobacillus ferrooxidans*; *Acinetobacter* sp.; *Actinobacillus* sp; *Aeromonas salmonicida*; *Agrobacterium tumefaciens*; *Aquifex aeolicus*; *Arcanobacterium pyogenes*; *Aster yellows phytoplasma*; *Bacillus* sp.; *Bifidobacterium* sp.; *Borrelia burgdorferi*; *Brevibacterium linens*; *Brucella melitensis*; *Buchnera* sp.; *Butyrivibrio fibrisolvens*; *Campylobacter jejuni*; *Caulobacter crescentus*; *Chlamydia* sp.; *Chlamydomypha* sp.; *Chlorobium limicola*; *Citrobacter rodentium*; *Clostridium* sp.; *Comamonas testosteroni*; *Corynebacterium* sp.; *Coxiella burnetii*; *Deinococcus radiodurans*; *Dichelobacter nodosus*; *Edwardsiella ictaluri*; *Enterobacter* sp.; *Erysipelothrix rhusiopathiae*; *Escherichia coli*; *Flavobacterium* sp.; *Francisella*

tularensis; *Frankia* sp. Cpl1; *Fusobacterium nucleatum*; *Geobacillus stearothermophilus*; *Gluconobacter oxydans*; *Haemophilus* sp.; *Helicobacter pylori*; *Klebsiella pneumoniae*; *Lactobacillus* sp.; *Lactococcus lactis*; *Listeria* sp.; *Mannheimia haemolytica*; *Mesorhizobium loti*; *Methylophaga thalassica*; *Microcystis aeruginosa*;
5 *Microscilla* sp. PRE1; *Moraxella* sp. TA144; *Mycobacterium* sp.; *Mycoplasma* sp.; *Neisseria* sp.; *Nitrosomonas* sp.; *Nostoc* sp. PCC 7120; *Novosphingobium aromaticivorans*; *Oenococcus oeni*; *Pantoea citrea*; *Pasteurella multocida*; *Pediococcus pentosaceus*; *Phormidium foveolarum*; *Phytoplasma* sp.; *Plectonoma boryanum*; *Prevotella ruminicola*; *Propionibacterium* sp.; *Proteus vulgaris*;
10 *Pseudomonas* sp.; *Ralstonia* sp.; *Rhizobium* sp.; *Rhodococcus equi*; *Rhodothermus marinus*; *Rickettsia* sp.; *Riemerella anatipestifer*; *Ruminococcus flavefaciens*; *Salmonella* sp.; *Selenomonas ruminantium*; *Serratia entomophila*; *Shigella* sp.; *Sinorhizobium meliloti*; *Staphylococcus* sp.; *Streptococcus* sp.; *Streptomyces* sp.; *Synechococcus* sp.; *Synechocystis* sp. PCC 6803; *Thermotoga maritima*; *Treponema* sp.;
15 *Ureaplasma urealyticum*; *Vibrio cholerae*; *Vibrio parahaemolyticus*; *Xylella fastidiosa*; *Yersinia* sp.; *Zymomonas mobilis*, preferably *Salmonella* sp. or *Escherichia coli* or plants, preferably from yeasts such as from the genera *Saccharomyces*, *Pichia*, *Candida*, *Hansenula*, *Torulopsis* or *Schizosaccharomyces* or plants such as *Arabidopsis thaliana*, maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut,
20 cotton, borage, sunflower, linseed, primrose, rapeseed, canola and turnip rape, manihot, pepper, sunflower, tagetes, solanaceous plant such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa, bushy plants such as coffee, cacao, tea, *Salix* species, trees such as oil palm, coconut, perennial grass, such as ryegrass and fescue, and forage crops, such as alfalfa and clover and from spruce, pine or fir for
25 example. More preferably homologs of aforementioned sequences can be isolated from *Saccharomyces cerevisiae*, *E. coli* or plants, preferably *Brassica napus*, *Glycine max*, or *Oryza sativa*.

0110.0.1 The stress related proteins of the present invention are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule
30 encoding the protein is cloned into an expression vector, for example in to a binary vector, the expression vector is introduced into a host cell, for example the *Arabidopsis thaliana* wild type NASC N906 or any other plant cell as described in the examples see below, and the stress related protein is expressed in said host cell. Examples for binary vectors are pBIN19, pBI101, pBinAR, pGPTV, pCAMBIA, pBIE-HYG, pBecks,
35 pGreen or pPZP (Hajukiewicz, P. et al., 1994, Plant Mol. Biol., 25: 989-994 and Hellens et al, Trends in Plant Science (2000) 5, 446-451.).

0111.0.1 Advantageously, the nucleic acid sequences according to the invention or the gene construct together with at least one reporter gene are cloned into an expression cassette, which is introduced into the organism via a vector or directly into the genome. This reporter gene should allow easy detection via a growth, fluorescence, chemical, bioluminescence or resistance assay or via a photometric measurement. Examples of reporter genes which may be mentioned are antibiotic- or herbicide-resistance genes, hydrolase genes, fluorescence protein genes, bioluminescence genes, sugar or nucleotide metabolic genes or biosynthesis genes such as the Ura3 gene, the Ilv2 gene, the luciferase gene, the β -galactosidase gene, the gfp gene, the 2-deoxyglucose-8-phosphate phosphatase gene, the β -glucuronidase gene, β -lactamase gene, the neomycin phosphotransferase gene, the hygromycin phosphotransferase gene or the BASTA (= glufosinate-resistance) gene. These genes permit easy measurement and quantification of the transcription activity and hence of the expression of the genes. In this way genome positions may be identified which exhibit differing productivity.

0112.0.1 In a preferred embodiment a nucleic acid construct, for example an expression cassette, comprises upstream, i.e. at the 5' end of the encoding sequence, a promoter and downstream, i.e. at the 3' end, a polyadenylation signal and optionally other regulatory elements which are operably linked to the intervening encoding sequence with the nucleic acid of Fig. 1a, 1b or 1c. By an operable linkage is meant the sequential arrangement of promoter, encoding sequence, terminator and optionally other regulatory elements in such a way that each of the regulatory elements can fulfill its function in the expression of the encoding sequence in due manner. The sequences preferred for operable linkage are targeting sequences for ensuring subcellular localization in plastids. However, targeting sequences for ensuring subcellular localization in the mitochondrion, in the endoplasmic reticulum (= ER), in the nucleus, in oil corpuscles or other compartments may also be employed as well as translation promoters such as the 5' lead sequence in tobacco mosaic virus (Gallie et al., Nucl. Acids Res. 15 (1987), 8693 -8711).

0113.0.1 A nucleic acid construct, for example an expression cassette may, for example, contain a constitutive promoter or a tissue-specific promoter (preferably the USP or napin promoter) the gene to be expressed and the ER retention signal. For the ER retention signal the KDEL amino acid sequence (lysine, aspartic acid, glutamic acid, leucine) or the KKX amino acid sequence (lysine-lysine-X-stop, wherein X means every other known amino acid) is preferably employed.

0114.0.1 For expression in a prokaryotic or eukaryotic host organism, for example a microorganism such as a fungus or a plant the expression cassette is

advantageously inserted into a vector such as by way of example a plasmid, a phage or other DNA which allows optimum expression of the genes in the host organism. Examples of suitable plasmids are: in *E. coli* pLG338, pACYC184, pBR series such as e.g. pBR322, pUC series such as pUC18 or pUC19, M13mp series, pKC30, pRep4, pHS1, pHS2, pPIC236, pMBL24, pLG200, pUR290, pIN-III¹¹³-B1, λ gt11 or pBdCl; in *Streptomyces* pIJ101, pIJ364, pIJ702 or pIJ361; in *Bacillus* pUB110, pC194 or pBD214; in *Corynebacterium* pSA77 or pAJ667; in fungi pALS1, pIL2 or pBB118; other advantageous fungal vectors are described by Romanos, M.A. et al., [(1992) „Foreign gene expression in yeast: a review“, *Yeast* 8: 423-488] and by van den Hondel, C.A.M.J.J. et al. [(1991) „Heterologous gene expression in filamentous fungi“ as well as in *More Gene Manipulations in Fungi* (J.W. Bennet & L.L. Lasure, eds., pp. 398-428: Academic Press: San Diego] and in „Gene transfer systems and vector development for filamentous fungi“ [van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) in: *Applied Molecular Genetics of Fungi*, Peberdy, J.F. et al., eds., pp. 1-28, Cambridge University Press: Cambridge]. Examples of advantageous yeast promoters are 2 μ M, pAG-1, YE6, YEp13 or pEMBLYe23. Examples of algal or plant promoters are pLGV23, pGHlac⁺, pBIN18, pAK2004, pVKH or pDH51 (see Schmidt, R. and Willmitzer, L., 1986). The vectors identified above or derivatives of the vectors identified above are a small selection of the possible plasmids. Further plasmids are well known to those skilled in the art and may be found, for example, in the book *Cloning Vectors* (Eds. Pouwels P.H. et al. Elsevier, Amsterdam-New York-Oxford, 1985, ISBN 0 444 904018). Suitable plant vectors are described inter alia in „*Methods in Plant Molecular Biology and Biotechnology*“ (CRC Press), Ch. 6/7, pp. 71-119. Advantageous vectors are known as shuttle vectors or binary vectors which replicate in *E. coli* and *Agrobacterium*.

0115.0.1 By vectors is meant with the exception of plasmids all other vectors known to those skilled in the art such as by way of example phages, viruses such as SV40, CMV, baculovirus, adenovirus, transposons, IS elements, phasmids, phagemids, cosmids, linear or circular DNA. These vectors can be replicated autonomously in the host organism or be chromosomally replicated, chromosomal replication being preferred.

0116.0.1 In a further embodiment of the vector the expression cassette according to the invention may also advantageously be introduced into the organisms in the form of a linear DNA and be integrated into the genome of the host organism by way of heterologous or homologous recombination. This linear DNA may be composed of a linearized plasmid or only of the expression cassette as vector or the nucleic acid sequences according to the invention.

0117.0.1 In a further advantageous embodiment the nucleic acid sequence according to the invention can also be introduced into an organism on its own.

0118.0.1 If in addition to the nucleic acid sequence according to the invention further genes are to be introduced into the organism, all together with a reporter gene
5 in a single vector or each single gene with a reporter gene in a vector in each case can be introduced into the organism, whereby the different vectors can be introduced simultaneously or successively.

0119.0.1 The vector advantageously contains at least one copy of the nucleic acid sequences according to the invention and/or the expression cassette (= gene
10 construct) according to the invention.

0120.0.3 The invention further provides an isolated recombinant expression vector comprising a SRP nucleic acid as described above, wherein expression of the vector in a host cell results in increased tolerance to environmental stress as compared to a wild type variety of the host cell. As used herein, the term "vector" refers to a
15 nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid," which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are
20 introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such
25 vectors are referred to herein as "expression vectors." In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses, and adeno-associated viruses), which serve equivalent
30 functions.

0121.0.3 The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory
35 sequences, selected on the basis of the host cells to be used for expression, which is operatively linked to the nucleic acid sequence to be expressed. As used herein with respect to a recombinant expression vector, "operatively linked" is intended to mean

that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers, and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990) and Gruber and Crosby, in: Methods in Plant Molecular Biology and Biotechnology, eds. Glick and Thompson, Chapter 7, 89-108, CRC Press: Boca Raton, Florida, including the references therein. Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells and those that direct expression of the nucleotide sequence only in certain host cells or under certain conditions. It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of polypeptide desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides or peptides, including fusion polypeptides or peptides, encoded by nucleic acids as described herein (e.g., SRPs, mutant forms of SRPs, fusion polypeptides, etc.).

0122.0.3 The recombinant expression vectors of the invention can be designed for expression of SRPs in prokaryotic or eukaryotic cells. For example, SRP genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (See Romanos, M.A. et al., 1992, Foreign gene expression in yeast: a review, Yeast 8:423-438; van den Hondel, C.A.M.J.J. et al., 1991, Heterologous gene expression in filamentous fungi, in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J., 1991, Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. et al., eds., p. 1-28, Cambridge University Press: Cambridge), algae (Falcione et al., 1999, Marine Biotechnology 1(3):239-251), ciliates of the types: Holotrichia, Peritrichia, Spirotrichia, Suctoria, Tetrahymena, Paramecium, Colpidium, Glaucoma, Platyophrya, Potomacus, Pseudocohnilembus, Euplotes, Engelmanniella, and Stylonychia, especially of the genus Stylonychia lemnae with vectors following a transformation method as described in PCT Application No. WO 98/01572, and multicellular plant cells (See Schmidt, R. and Willmitzer, L., 1988, High efficiency *Agrobacterium tumefaciens*-mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants, Plant Cell Rep. 583-586; Plant Molecular Biology and

Biotechnology, G Press, Boca Raton, Florida, chapter 6/7, S.71-119 (1993); F.F. White, B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. Kung und R. Wu, 129-43, Academic Press: 1993; Potrykus, 1991, Annu. Rev. Plant Physiol. Plant Molec. Biol. 42:205-225 and references cited therein) or mammalian cells. Suitable host cells are discussed further in Goeddel, Gene Expression Technology: Methods in Enzymology 185, Academic Press: San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

- 10 **0123.0.3** Expression of polypeptides in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion polypeptides. Fusion vectors add a number of amino acids to a polypeptide encoded therein, usually to the amino terminus of the recombinant polypeptide but also to the C-terminus or fused within suitable regions in the
- 15 polypeptides. Such fusion vectors typically serve three purposes: 1) to increase expression of a recombinant polypeptide; 2) to increase the solubility of a recombinant polypeptide; and 3) to aid in the purification of a recombinant polypeptide by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant polypeptide
- 20 to enable separation of the recombinant polypeptide from the fusion moiety subsequent to purification of the fusion polypeptide. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin, and enterokinase.

- 0124.0.1** By way of example the plant expression cassette can be installed in the pRT transformation vector ((a) Toepfer et al., 1993, Methode Enzymol., 217: 66-78; (b)
- 25 Toepfer et al. 1987, Nucl. Acids. Res. 15: 5690 ff.).

0125.0.1 Alternatively, a recombinant vector (= expression vector) can also be transcribed and translated *in vitro*, e.g. by using the T7 promoter and the T7 RNA polymerase.

- 0126.0.1** Expression vectors employed in prokaryotes frequently make use of
- 30 inducible systems with and without fusion proteins or fusion oligopeptides, wherein these fusions can ensue in both N-terminal and C-terminal manner or in other useful domains of a protein. Such fusion vectors usually have the following purposes: i.) to increase the RNA expression rate; ii.) to increase the achievable protein synthesis rate; iii.) to increase the solubility of the protein; iv.) or to simplify purification by means of a binding sequence usable for affinity chromatography. Proteolytic cleavage points are
- 35 also frequently introduced via fusion proteins, which allow cleavage of a portion of the

fusion protein and purification. Such recognition sequences for proteases are recognized, e.g. factor Xa, thrombin and enterokinase.

0127.0.1 Typical advantageous fusion and expression vectors are pGEX [Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 87: 31-40], pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which contains glutathione S-transferase (GST), maltose binding protein or protein A.

0128.0.3 In one embodiment, the coding sequence of the SRP is cloned into a pGEX expression vector to create a vector encoding a fusion polypeptide comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X polypeptide. The fusion polypeptide can be purified by affinity chromatography using glutathione-agarose resin. Recombinant PKSRP unfused to GST can be recovered by cleavage of the fusion polypeptide with thrombin.

0129.0.1 Other examples of *E. coli* expression vectors are pTrc [Amann et al., (1988) *Gene* 69:301-315] and pET vectors [Studler et al., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89; Stratagene, Amsterdam, The Netherlands].

0130.0.2 Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid *trp-lac* fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 *gn10-lac* fusion promoter mediated by a co-expressed viral RNA polymerase (T7 *gn1*). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 *gn1* gene under the transcriptional control of the *lacUV5* promoter.

0131.0.2 One strategy to maximize recombinant polypeptide expression is to express the polypeptide in a host bacteria with an impaired capacity to proteolytically cleave the recombinant polypeptide (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada et al., 1992, *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

0132.0.1 Other advantageous vectors for use in yeast are pYepSec1 (Baldari, et al., (1987) *Embo J.* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY98 (Schultz et al., (1987) *Gene* 54:113-123), and pYES derivatives (Invitrogen Corporation, San Diego, CA). Vectors for use in filamentous fungi are described in; van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) „Gene transfer systems

and vector development for filamentous fungi", in: Applied Molecular Genetics of Fungi, J.F. Peberdy, et al., eds., pp. 1-28, Cambridge University Press: Cambridge.

0133.0.1 Alternatively, insect cell expression vectors can also be advantageously utilized, e.g. for expression in Sf 9 cells. These are e.g. the vectors of the pAc series
5 (Smith et al. (1983) *Mol. Cell Biol.* 3:2158-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

0134.0.1 Furthermore, plant cells or algal cells can advantageously be used for gene expression. Examples of plant expression vectors may be found in Becker, D., et al. (1992) „New plant binary vectors with selectable markers located proximal to the left
10 border", *Plant Mol. Biol.* 20: 1195-1197 or in Bevan, M.W. (1984) „Binary *Agrobacterium* vectors for plant transformation", *Nucl. Acid. Res.* 12: 8711-8721.

0135.0.1 Furthermore, the nucleic acid sequences may also be expressed in mammalian cells, advantageously in nonhuman mammalian cells. Examples of corresponding expression vectors are pCDM8 and pMT2PC referred to in: Seed, B.
15 (1987) *Nature* 329:640 or Kaufman et al. (1987) *EMBO J.* 6: 187-195). At the same time promoters preferred for use are of viral origin, such as by way of example promoters of polyoma, adenovirus 2, cytomegalovirus or simian virus 40. Other prokaryotic and eukaryotic expression systems are referred to in chapters 16 and 17 of Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring
20 Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

0136.0.3 In a preferred embodiment of the present invention, the SRPs are expressed in plants and plant cells such as unicellular plant cells (e.g. algae) (See Falcione et al., 1999, *Marine Biotechnology* 1(3):239-251 and references therein) and
25 plant cells from higher plants (e.g., the spermatophytes, such as crop plants). A SRP may be "introduced" into a plant cell by any means, including transfection, transformation or transduction, electroporation, particle bombardment, agroinfection, and the like. One transformation method known to those of skill in the art is the dipping of a flowering plant into an *Agrobacteria* solution, wherein the *Agrobacteria* contains
30 the SRP nucleic acid, followed by breeding of the transformed gametes.

0137.0.3 Other suitable methods for transforming or transfecting host cells including plant cells can be found in Sambrook, et al., *Molecular Cloning: A Laboratory Manual*, 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989, and other laboratory manuals such as *Methods in*
35 *Molecular Biology*, 1995, Vol. 44, *Agrobacterium* protocols, ed: Gartland and Davey, Humana Press, Totowa, New Jersey. As biotic and abiotic stress tolerance is a general trait wished to be inherited into a wide variety of plants like maize, wheat, rye,

oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed and canola, manihot, pepper, sunflower and tagetes, solanaceous plants like potato, tobacco, eggplant, and tomato, Vicia species, pea, alfalfa, bushy plants (coffee, cacao, tea), Salix species, trees (oil palm, coconut), perennial grasses, and forage crops, these crop plants are also preferred target plants for a genetic engineering as one further embodiment of the present invention. Forage crops include, but are not limited to, Wheatgrass, Canarygrass, Bromegrass, Wildrye Grass, Bluegrass, Orchardgrass, Alfalfa, Salfoin, Birdsfoot Trefoil, Alsike Clover, Red Clover, and Sweet Clover.

0138.0.3 In one embodiment of the present invention, transfection of a SRP into a plant is achieved by *Agrobacterium* mediated gene transfer. *Agrobacterium* mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986, Mol. Gen. Genet. 204:383-396) or LBA4404 (Clontech) *Agrobacterium tumefaciens* strain. Transformation can be performed by standard transformation and regeneration techniques (Deblacqre et al., 1994, Nucl. Acids Res. 13:4777-4788; Gelvin, Stanton B. and Schilperoort, Robert A, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht : Kluwer Academic Publ., 1995. - in Sect., Ringbuc Zentrale Signatur: BT11-P ISBN 0-7923-2731-4; Glick, Bernard R.; Thompson, John E., Methods in Plant Molecular Biology and Biotechnology, Boca Raton : CRC Press, 1993 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989, Plant Cell Report 8:238-242; De Block et al., 1989, Plant Physiol. 91:694-701). Use of antibiotics for *Agrobacterium* and plant selection depends on the binary vector and the *Agrobacterium* strain used for transformation. Rapeseed selection is normally performed using kanamycin as selectable plant marker. *Agrobacterium* mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994, Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent No. 0397 667, U.S. Patent No. 5,376,543, or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake or via the silicon carbide fiber technique. (See, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97826-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387, and a specific example of wheat transformation can be found in PCT Application No. WO 93/07256.

0139.0.3 According to the present invention, the introduced SRP may be maintained in the plant cell stably if it is incorporated into a non-chromosomal autonomous replicon or integrated into the plant chromosomes. Alternatively, the

introduced SRP may be present on an extra-chromosomal non-replicating vector and be transiently expressed or transiently active.

0140.0.3 In one embodiment, a homologous recombinant microorganism can be created wherein the SRP is integrated into a chromosome, a vector is prepared which contains at least a portion of a SRP gene into which a deletion, addition, or substitution has been introduced to thereby alter, e.g., functionally disrupt, the SRP gene. Preferably, the SRP gene is a yeast, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP gene, but it can be a homolog from a related plant or even from a mammalian or insect source. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous SRP gene is functionally disrupted (i.e., no longer encodes a functional polypeptide; also referred to as a knock-out vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous SRP gene is mutated or otherwise altered but still encodes a functional polypeptide (e.g., the upstream regulatory region can be altered to thereby alter the expression of the endogenous SRP). To create a point mutation via homologous recombination, DNA-RNA hybrids can be used in a technique known as chimeraplasmy (Cole-Strauss et al., 1989, *Nucleic Acids Research* 27(5):1323-1330 and Kmiec, 1999 *Gene therapy American Scientist*, 87(3):240-247). Homologous recombination procedures in *Physcomitrella patens* are also well known in the art and are contemplated for use herein.

0141.0.3 Whereas in the homologous recombination vector, the altered portion of the SRP gene is flanked at its 5' and 3' ends by an additional nucleic acid molecule of the SRP gene to allow for homologous recombination to occur between the exogenous SRP gene carried by the vector and an endogenous SRP gene, in a microorganism or plant. The additional flanking SRP nucleic acid molecule is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several hundreds of base pairs up to kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See, e.g., Thomas, K.R., and Capecchi, M.R., 1987, *Cell* 51:503 for a description of homologous recombination vectors or Strepp et al., 1998, *PNAS*, 95 (8):4368-4373 for cDNA based recombination in *Physcomitrella patens*. The vector is introduced into a microorganism or plant cell (e.g., via polyethylene glycol mediated DNA), and cells in which the introduced PKSRP gene has homologously recombined with the endogenous PKSRP gene are selected using art-known techniques.

0142.0.3 In another embodiment, recombinant microorganisms can be produced that contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of a SRP gene on a vector placing it under control of the

lac operon permits expression of the SRP gene only in the presence of IPTG. Such regulatory systems are well known in the art.

0143.0.3 Whether present in an extra-chromosomal non-replicating vector or a vector that is integrated into a chromosome, the SRP polynucleotide preferably resides in a plant expression cassette. A plant expression cassette preferably contains regulatory sequences capable of driving gene expression in plant cells that are operatively linked so that each sequence can fulfill its function, for example, termination of transcription by polyadenylation signals. Preferred polyadenylation signals are those originating from *Agrobacterium tumefaciens* T-DNA such as the gene 3 known as octopine synthase of the Ti-plasmid pTiACH5 (Gielen et al., 1984, EMBO J. 3:835) or functional equivalents thereof but also all other terminators functionally active in plants are suitable. As plant gene expression is very often not limited on transcriptional levels, a plant expression cassette preferably contains other operatively linked sequences like translational enhancers such as the overdrive-sequence containing the 5'-untranslated leader sequence from tobacco mosaic virus enhancing the polypeptide per RNA ratio (Gallie et al., 1987, Nucl. Acids Research 15:8693-8711). Examples of plant expression vectors include those detailed in: Becker, D. et al., 1992, New plant binary vectors with selectable markers located proximal to the left border, Plant Mol. Biol. 20: 1195-1197; and Bevan, M.W., 1984, Binary *Agrobacterium* vectors for plant transformation, Nucl. Acid. Res. 12:8711-8721; and Vectors for Gene Transfer in Higher Plants; in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds.: Kung and R. Wu, Academic Press, 1993, S. 15-38.

0144.0.1 "Transformation" is defined herein as a process for introducing heterologous DNA into a plant cell, plant tissue, or plant. It may occur under natural or artificial conditions using various methods well known in the art. Transformation may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method is selected based on the host cell being transformed and may include, but is not limited to, viral infection, electroporation, lipofection, and particle bombardment. Such "transformed" cells include stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome. They also include cells which transiently express the inserted DNA or RNA for limited periods of time. Transformed plant cells, plant tissue, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof.

0145.0.1 The terms "transformed," "transgenic," and "recombinant" refer to a host organism such as a bacterium or a plant into which a heterologous nucleic acid molecule has been introduced. The nucleic acid molecule can be stably integrated into

the genome of the host or the nucleic acid molecule can also be present as an extrachromosomal molecule. Such an extrachromosomal molecule can be auto-replicating. Transformed cells, tissues, or plants are understood to encompass not only the end product of a transformation process, but also transgenic progeny thereof. A "non-transformed," "non-transgenic," or "non-recombinant" host refers to a wild-type organism, e.g., a bacterium or plant, which does not contain the heterologous nucleic acid molecule.

0146.0.1 A "transgenic plant", as used herein, refers to a plant which contains a foreign nucleotide sequence inserted into either its nuclear genome or organellar genome. It encompasses further the offspring generations i.e. the T1-, T2- and consecutively generations or BC1-, BC2- and consecutively generation as well as crossbreeds thereof with non-transgenic or other transgenic plants.

0147.0.1 The host organism (= transgenic organism) advantageously contains at least one copy of the nucleic acid according to the invention and/or of the nucleic acid construct according to the invention.

0148.0.2 In principle all plants can be used as host organism. Preferred transgenic plants are, for example, selected from the families Aceraceae, Anacardiaceae, Apiaceae, Asteraceae, Brassicaceae, Cactaceae, Cucurbitaceae, Euphorbiaceae, Fabaceae, Malvaceae, Nymphaeaceae, Papaveraceae, Rosaceae, Salicaceae, Solanaceae, Arecaceae, Bromeliaceae, Cyperaceae, Iridaceae, Liliaceae, Orchidaceae, Gentianaceae, Labiaceae, Magnoliaceae, Ranunculaceae, Carifolaceae, Rubiaceae, Scrophulariaceae, Caryophyllaceae, Ericaceae, Polygonaceae, Violaceae, Juncaceae or Poaceae and preferably from a plant selected from the group of the families Apiaceae, Asteraceae, Brassicaceae, Cucurbitaceae, Fabaceae, Papaveraceae, Rosaceae, Solanaceae, Liliaceae or Poaceae. Preferred are crop plants such as plants advantageously selected from the group of the genus peanut, oilseed rape, canola, sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay, pumpkin/squash, linseed, soya, pistachio, borage, maize, wheat, rye, oats, sorghum and millet, triticale, rice, barley, cassava, potato, sugarbeet, egg plant, alfalfa, and perennial grasses and forage plants, oil palm, vegetables (brassicas, root vegetables, tuber vegetables, pod vegetables, fruiting vegetables, onion vegetables, leafy vegetables and stem vegetables), buckwheat, Jerusalem artichoke, broad bean, vetches, lentil, dwarf bean, lupin, clover and Lucerne for mentioning only some of them.

0149.0.2 In one preferred embodiment, the host plant is selected from the families Aceraceae, Anacardiaceae, Apiaceae, Asteraceae, Brassicaceae, Cactaceae, Cucurbitaceae, Euphorbiaceae, Fabaceae, Malvaceae, Nymphaeaceae, Papaveraceae, Rosaceae, Salicaceae, Solanaceae, Arecaceae, Bromeliaceae,

- Cyperaceae, Iridaceae, Liliaceae, Orchidaceae, Gentianaceae, Labiaceae, Magnoliaceae, Ranunculaceae, Carifolaceae, Rubiaceae, Scrophulariaceae, Caryophyllaceae, Ericaceae, Polygonaceae, Violaceae, Juncaceae or Poaceae and preferably from a plant selected from the group of the families Apiaceae, Asteraceae,
- 5 Brassicaceae, Cucurbitaceae, Fabaceae, Papaveraceae, Rosaceae, Solanaceae, Liliaceae or Poaceae. Preferred are crop plants and in particular plants mentioned herein above as host plants such as the families and genera mentioned above for example preferred the species *Anacardium occidentale*, *Calendula officinalis*, *Carthamus tinctorius*, *Cichorium intybus*, *Cynara scolymus*, *Helianthus annuus*, *Tagetes lucida*, *Tagetes erecta*, *Tagetes tenuifolia*, *Daucus carota*, *Corylus avellana*, *Corylus*
- 10 *columna*, *Borago officinalis*, *Brassica napus*, *Brassica rapa* ssp., *Sinapis arvensis*, *Brassica juncea*, *Brassica juncea* var. *juncea*, *Brassica juncea* var. *crispifolia*, *Brassica juncea* var. *foliosa*, *Brassica nigra*, *Brassica sinapioides*, *Melanosthaphis communis*, *Brassica oleracea*, *Arabidopsis thaliana*, *Anana comosus*, *Ananas ananas*, *Bromella*
- 15 *comosa*, *Carica papaya*, *Cannabis sativa*, *Ipomoea batatas*, *Ipomoea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomoea fastigiata*, *Ipomoea tiliacea*, *Ipomoea triloba*, *Convolvulus panduratus*, *Beta vulgaris*, *Beta vulgaris* var. *altissima*, *Beta vulgaris* var. *vulgaris*, *Beta maritima*, *Beta vulgaris* var. *perennis*, *Beta vulgaris* var. *conditiva*, *Beta vulgaris* var. *esculenta*, *Cucurbita maxima*, *Cucurbita mixta*,
- 20 *Cucurbita pepo*, *Cucurbita moschata*, *Olea europaea*, *Manihot utilissima*, *Janipha manihot*, *Jatropha manihot*, *Manihot aipil*, *Manihot dulcis*, *Manihot manihot*, *Manihot melanobasis*, *Manihot aeculenta*, *Ricinus communis*, *Pisum sativum*, *Pisum arvensis*, *Pisum humile*, *Medicago sativa*, *Medicago falcata*, *Medicago varia*, *Glycine max*, *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*, *Phaseolus max*, *Soja hispida*, *Soja max*,
- 25 *Cocos nucifera*, *Pelargonium grossularioides*, *Oleum coccas*, *Laurus nobilis*, *Persea americana*, *Arachis hypogaea*, *Linum usitatissimum*, *Linum humile*, *Linum austriacum*, *Linum bienne*, *Linum angustifolium*, *Linum catharticum*, *Linum flavum*, *Linum grandiflorum*, *Adenolinum grandiflorum*, *Linum lewisii*, *Linum narbonense*, *Linum perenne*, *Linum perenne* var. *lewisii*, *Linum pratense*, *Linum trigynum*, *Punica*
- 30 *granatum*, *Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium barbadense*, *Gossypium herbaceum*, *Gossypium thurberi*, *Musa nana*, *Musa acuminata*, *Musa paradisiaca*, *Musa* spp., *Elaeis guineensis*, *Papaver orientale*, *Papaver rhoeas*, *Papaver dubium*, *Sesamum indicum*, *Piper aduncum*, *Piper amalago*, *Piper angustifolium*, *Piper auitum*, *Piper betel*, *Piper cuboba*, *Piper longum*, *Piper nigrum*,
- 35 *Piper retrofractum*, *Artanthe adunca*, *Artanthe elongata*, *Peperomia elongata*, *Piper elongatum*, *Steffensia elongata*, *Hordeum vulgare*, *Hordeum jubatum*, *Hordeum murinum*, *Hordeum socalinum*, *Hordeum distichon*, *Hordeum aegiceras*, *Hordeum*

- hexastichon*, *Hordeum hexastichum*, *Hordeum irregulare*, *Hordeum sativum*, *Hordeum secalinum*, *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida*, *Sorghum bicolor*, *Sorghum halepense*, *Sorghum saccharatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum arundinaceum*, *Sorghum caffrorum*, *Sorghum oeruum*, *Sorghum dochna*, *Sorghum drummondii*, *Sorghum durra*, *Sorghum guineense*, *Sorghum lanceolatum*, *Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sorghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum millaceum* millet, *Panicum millaceum*, *Zea mays*, *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum hybernum*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare*, *Coffea* spp., *Coffea arabica*, *Coffea canephora*, *Coffea liberica*, *Capsicum annuum*, *Capsicum annuum* var. *glabriusculum*, *Capsicum frutescens*, *Capsicum annuum*, *Nicotiana tabacum*, *Solanum tuberosum*, *Solanum melongena*, *Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*, *Solanum integrifolium*, *Solanum lycopersicum* *Theobroma cacao* or *Camellia sinensis*.
- 0150.0.2 Anacardiaceae such as the genera *Pistacia*, *Mangifera*, *Anacardium* e.g. the species *Pistacia vera* [pistachios, Pistazie], *Mangifer indica* [Mango] or *Anacardium occidentale* [Cashew]; Asteraceae such as the genera *Calendula*, *Carthamus*, *Centaurea*, *Cichorium*, *Cynara*, *Helianthus*, *Lactuca*, *Locusta*, *Tagetes*, *Valeriana* e.g. the species *Calendula officinalis* [Marigold], *Carthamus tinctorius* [safflower], *Centaurea cyanus* [cornflower], *Cichorium intybus* [blue daisy], *Cynara scolymus* [Artichoke], *Helianthus annuus* [sunflower], *Lactuca sativa*, *Lactuca crispata*, *Lactuca esculenta*, *Lactuca scariola* L. ssp. *sativa*, *Lactuca scariola* L. var. *integrata*, *Lactuca scariola* L. var. *integrifolia*, *Lactuca sativa* subsp. *romana*, *Locusta communis*, *Valeriana locustia* [lettuce], *Tagetes lucida*, *Tagetes erecta* or *Tagetes tenuifolia* [Marigold]; Apiaceae such as the genera *Daucus* e.g. the species *Daucus carota* [carrot]; Betulaceae such as the genera *Corylus* e.g. the species *Corylus avellana* or *Corylus colurna* [hazelnut]; Boraginaceae such as the genera *Borago* e.g. the species *Borago officinalis* [borage]; Brassicaceae such as the genera *Brassica*, *Melanosinapis*, *Sinapis*, *Arabidopsis* e.g. the species *Brassica napus*, *Brassica rapa* ssp. [canola, oilseed rape, turnip rape], *Sinapis arvensis* *Brassica juncea*, *Brassica juncea* var. *juncea*, *Brassica juncea* var. *crispifolia*, *Brassica juncea* var. *foliosa*, *Brassica nigra*, *Brassica sinapioides*, *Melanosinapis communis* [mustard], *Brassica oleracea* [fodder beet] or *Arabidopsis thaliana*; Bromeliaceae such as the genera *Anana*, *Bromelia* e.g. the species *Anana comosus*, *Ananas ananas* or *Bromelia comosa* [pineapple]; Caricaceae such as the genera *Carica* e.g. the species *Carica papaya* [papaya]; Cannabaceae such as the genera *Cannabis* e.g. the species *Cannabis*

- sative [hemp], Convolvulaceae such as the genera *Ipomoea*, *Convolvulus* e.g. the species *Ipomoea batatas*, *Ipomoea pandurata*, *Convolvulus batatas*, *Convolvulus tiliaceus*, *Ipomoea fastigiata*, *Ipomoea tiliacea*, *Ipomoea triloba* or *Convolvulus panduratus* [sweet potato, Man of the Earth, wild potato], Chenopodiaceae such as the genera *Beta*,
5 i.e. the species *Beta vulgaris*, *Beta vulgaris* var. *altissima*, *Beta vulgaris* var. *Vulgaris*, *Beta maritima*, *Beta vulgaris* var. *perennis*, *Beta vulgaris* var. *conditiva* or *Beta vulgaris* var. *esculenta* [sugar beet]; Cucurbitaceae such as the genera *Cucurbita* e.g. the species *Cucurbita maxima*, *Cucurbita mixta*, *Cucurbita pepo* or *Cucurbita moschata* [pumpkin, squash];
10 Elaeagnaceae such as the genera *Elacagnus* e.g. the species *Olea europaea* [olive]; Ericaceae such as the genera *Kalmia* e.g. the species *Kalmia latifolia*, *Kalmia angustifolia*, *Kalmia microphylla*, *Kalmia polifolia*, *Kalmia occidentalis*, *Cistus chamaerhodendros* or *Kalmia lucida* [American laurel, broad-leaved laurel, calico bush, spoon wood, sheep laurel, alpine laurel, bog laurel, western bog-laurel, swamp-laurel];
Euphorbiaceae such as the genera *Manihot*, *Janipha*, *Jatropha*, *Ricinus* e.g. the species
15 *Manihot utilissima*, *Janipha manihot*, *Jatropha manihot*, *Manihot aipil*, *Manihot dulcis*, *Manihot manihot*, *Manihot melanobasis*, *Manihot esculenta* [manihot, arrowroot, tapioca, cassava] or *Ricinus communis* [castor bean, Castor Oil Bush, Castor Oil Plant, Palma Christi, Wonder Tree]; Fabaceae such as the genera *Pisum*, *Albizia*, *Cathornion*, *Feuillea*, *Inga*, *Pithecolobium*, *Acacia*, *Mimosa*, *Medicago*, *Glycine*, *Dolichos*,
20 *Phaseolus*, *Soja* e.g. the species *Pisum sativum*, *Pisum arvense*, *Pisum humile* [pea], *Albizia berteriana*, *Albizia julibrissin*, *Albizia lebbek*, *Acacia berteriana*, *Acacia littoralis*, *Albizia berteriana*, *Albizia berteriana*, *Cathornion berteriana*, *Feuillea berteriana*, *Inga fragrans*, *Pithecolobium berterianum*, *Pithecolobium fragrans*, *Pithecolobium berterianum*, *Pseudalbizia berteriana*, *Acacia julibrissin*, *Acacia nemu*,
25 *Albizia nemu*, *Feuillea julibrissin*, *Mimosa julibrissin*, *Mimosa speciosa*, *Sericanrda julibrissin*, *Acacia lebbek*, *Acacia macrophylla*, *Albizia lebbek*, *Feuillea lebbek*, *Mimosa lebbek*, *Mimosa speciosa* [bastard logwood, silk tree, East Indian Walnut], *Medicago sativa*, *Medicago falcata*, *Medicago varia* [alfalfa] *Glycine max* *Dolichos soja*, *Glycine gracilis*, *Glycine hispida*, *Phaseolus max*, *Soja hispida* or *Soja max*
30 [soybean]; Geraniaceae such as the genera *Pelargonium*, *Cocos*, *Oleum* e.g. the species *Cocos nucifera*, *Pelargonium grossularioides* or *Oleum cocois* [coconut]; Gramineae such as the genera *Saccharum* e.g. the species *Saccharum officinarum*; Juglandaceae such as the genera *Juglans*, *Wallia* e.g. the species *Juglans regia*, *Juglans ailanthifolia*, *Juglans sieboldiana*, *Juglans cinerea*, *Wallia cinerea*, *Juglans bixbyi*, *Juglans californica*, *Juglans hindsii*, *Juglans intermedia*, *Juglans jamaicensis*, *Juglans major*,
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- Juglans microcarpa*, *Juglans nigra* or *Walfia nigra* [walnut, black walnut, common walnut, persian walnut, white walnut, butternut, black walnut]; Lauraceae such as the genera *Persea*, *Laurus* e.g. the species *laurel* [*Laurus nobilis*] [bay, laurel, bay laurel, sweet bay], *Persea americana* [*Persea americana*, *Persea gratissima* or *Persea persea*]
- 5 [avocado]; Leguminosae such as the genera *Arachis* e.g. the species *Arachis hypogaea* [peanut]; Linaceae such as the genera *Linum*, *Adenoclinum* e.g. the species *Linum usitatissimum*, *Linum humile*, *Linum austriacum*, *Linum bienne*, *Linum angustifolium*, *Linum catharticum*, *Linum flavum*, *Linum grandiflorum*, *Adenoclinum grandiflorum*, *Linum lewisii*, *Linum narbonense*, *Linum perenne*, *Linum poronae* var. *lewisii*, *Linum*
- 10 *pratense* or *Linum trigynum* [flax, linseed]; Lythraceae such as the genera *Punica* e.g. the species *Punica granatum* [pomegranate]; Malvaceae such as the genera *Gossypium* e.g. the species *Gossypium hirsutum*, *Gossypium arboreum*, *Gossypium barbadense*, *Gossypium herbaceum* or *Gossypium thurberi* [cotton]; Musaceae such as the genera *Musa* e.g. the species *Musa nana*, *Musa acuminata*, *Musa paradisiaca*, *Musa* spp.
- 15 [banana]; Onagraceae such as the genera *Camissonia*, *Oenothera* e.g. the species *Oenothera biennis* or *Camissonia brevipes* [primrose, evening primrose]; Palmae such as the genera *Elaeis* e.g. the species *Elaeis guineensis* [oil palm]; Papaveraceae such as the genera *Papaver* e.g. the species *Papaver orientale*, *Papaver rhoeas*, *Papaver dubium* [poppy, oriental poppy, corn poppy, field poppy, shirley poppies, field poppy, long-
- 20 headed poppy, long-pod poppy]; Pedaliaceae such as the genera *Sesamum* e.g. the species *Sesamum indicum* [sesame]; Piperaceae such as the genera *Piper*, *Artanthe*, *Peperomia*, *Steffensia* e.g. the species *Piper aduncum*, *Piper amalago*, *Piper angustifolium*, *Piper auritum*, *Piper betel*, *Piper cubeba*, *Piper longum*, *Piper nigrum*, *Piper retrofractum*, *Artanthe adunca*, *Artanthe elongata*, *Peperomia elongata*, *Piper*
- 25 *elongatum*, *Steffensia elongata*. [Cayenne pepper, wild pepper]; Poaceae such as the genera *Hordeum*, *Secale*, *Avena*, *Sorghum*, *Andropogon*, *Holcus*, *Panicum*, *Oryza*, *Zea*, *Triticum* e.g. the species *Hordeum vulgare*, *Hordeum jubatum*, *Hordeum murinum*, *Hordeum secalinum*, *Hordeum distichon*, *Hordeum aegyptiacum*, *Hordeum hexastichon*, *Hordeum hexastichum*, *Hordeum irregulare*, *Hordeum sativum*, *Hordeum secalinum*
- 30 [barley, pearl barley, foxtail barley, wall barley, meadow barley], *Secale cereale* [rye], *Avena sativa*, *Avena fatua*, *Avena byzantina*, *Avena fatua* var. *sativa*, *Avena hybrida* [oat], *Sorghum bicolor*, *Sorghum halepense*, *Sorghum saccharatum*, *Sorghum vulgare*, *Andropogon drummondii*, *Holcus bicolor*, *Holcus sorghum*, *Sorghum aethiopicum*, *Sorghum arundinaceum*, *Sorghum cafferum*, *Sorghum cernuum*, *Sorghum dochna*,
- 35 *Sorghum drummondii*, *Sorghum durra*, *Sorghum guineense*, *Sorghum lanceolatum*,

- Sorghum nervosum*, *Sorghum saccharatum*, *Sorghum subglabrescens*, *Sorghum verticilliflorum*, *Sorghum vulgare*, *Holcus halepensis*, *Sorghum miliaceum* millet, *Panicum miliaceum* [*Sorghum*, millet], *Oryza sativa*, *Oryza latifolia* [rice], *Zea mays* [corn, maize] *Triticum aestivum*, *Triticum durum*, *Triticum turgidum*, *Triticum*
 5 *hybernum*, *Triticum macha*, *Triticum sativum* or *Triticum vulgare* [wheat, bread wheat, common wheat], Proteaceae such as the genera *Macadamia* e.g. the species *Macadamia integrifolia* [macadamia]; Rubiaceae such as the genera *Coffea* e.g. the species *Coffea* spp., *Coffea arabica*, *Coffea canephora* or *Coffea liberica* [coffee]; Scrophulariaceae such as the genera *Verbascum* e.g. the species *Verbascum blattaria*, *Verbascum chalcidii*,
 10 *Verbascum densiflorum*, *Verbascum lagurus*, *Verbascum longifolium*, *Verbascum lychnitis*, *Verbascum nigrum*, *Verbascum olympicum*, *Verbascum phlomoides*, *Verbascum phoenicum*, *Verbascum pulverulentum* or *Verbascum thapsus* [mullein, white moth mullein, nettle-leaved mullein, dense-flowered mullein, silver mullein, long-leaved mullein, white mullein, dark mullein, greek mullein, orange mullein, purple
 15 mullein, hoary mullein, great mullein]; Solanaceae such as the genera *Capsicum*, *Nicotiana*, *Solanum*. *Lycopersicon* e.g. the species *Capsicum annuum*, *Capsicum annuum* var. *glabriusculum*, *Capsicum frutescens* [pepper], *Capsicum annuum* [paprika], *Nicotiana tabacum*, *Nicotiana glauca*, *Nicotiana attenuata*, *Nicotiana glauca*, *Nicotiana langsdorffii*, *Nicotiana obtusifolia*, *Nicotiana quadrivalvis*, *Nicotiana*
 20 *repanda*, *Nicotiana rustica*, *Nicotiana sylvestris* [tobacco], *Solanum tuberosum* [potato], *Solanum melongena* [egg-plant] (*Lycopersicon esculentum*, *Lycopersicon lycopersicum*, *Lycopersicon pyriforme*, *Solanum integrifolium* or *Solanum lycopersicum* [tomato]; Sterculiaceae such as the genera *Theobroma* e.g. the species *Theobroma cacao* [cacao]; Theaceae such as the genera *Camellia* e.g. the species
 25 *Camellia sinensis*) [tea].

0151.0.1 The introduction of the nucleic acids according to the invention, the expression cassette or the vector into organisms, plants for example, can in principle be done by all of the methods known to those skilled in the art. The introduction of the nucleic acid sequences gives rise to recombinant or transgenic organisms.

- 30 **0152.0.1** In the case of microorganisms, those skilled in the art can find appropriate methods in the textbooks by Sambrook, J. et al. (1989) Molecular cloning: A laboratory manual, Cold Spring Harbor Laboratory Press, by F.M. Ausubel et al. (1994) Current protocols in molecular biology, John Wiley and Sons, by D.M. Glover et al., DNA Cloning Vol.1, (1995), IRL Press (ISBN 019-963476-9), by Kaiser et al. (1994)
 35 Methods in Yeast Genetics, Cold Spring Harbor Laboratory Press or Guthrie et al.

Guide to Yeast Genetics and Molecular Biology, Methods In Enzymology, 1994, Academic Press.

0153.0.1 The transfer of foreign genes into the genome of a plant is called transformation. In doing this the methods described for the transformation and regeneration of plants from plant tissues or plant cells are utilized for transient or stable transformation. Suitable methods are protoplast transformation by poly(ethylene glycol)-induced DNA uptake, the „biolistic“ method using the gene cannon – referred to as the particle bombardment method, electroporation, the incubation of dry embryos in DNA solution, microinjection and gene transfer mediated by *Agrobacterium*. Said methods are described by way of example in B. Jenes et al., Techniques for Gene Transfer, in: Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press (1993) 128-143 and in Potrykus Annu. Rev. Plant Physiol. Plant Molec. Biol. 42 (1991) 205-225). The nucleic acids or the construct to be expressed is preferably cloned into a vector which is suitable for transforming *Agrobacterium tumefaciens*, for example pBin19 (Devan et al., Nucl. Acids Res. 12 (1984) 8711). *Agrobacteria* transformed by such a vector can then be used in known manner for the transformation of plants, in particular of crop plants such as by way of example tobacco plants, for example by bathing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media. The transformation of plants by means of *Agrobacterium tumefaciens* is described, for example, by Höfgen and Willmitzer in Nucl. Acid Res. (1988) 16, 9877 or is known inter alia from F.F. White, Vectors for Gene Transfer in Higher Plants; in Transgenic Plants, Vol. 1, Engineering and Utilization, eds. S.D. Kung and R. Wu, Academic Press, 1993, pp. 15-38.

0154.0.1 *Agrobacteria* transformed by an expression vector according to the invention may likewise be used in known manner for the transformation of plants such as test plants like *Arabidopsis* or crop plants such as cereal crops, corn, oats, rye, barley, wheat, soybean, rice, cotton, sugar beet, canola, sunflower, flax, hemp, potatoes, tobacco, tomatoes, carrots, paprika, oilseed rape, tapioca, cassava, arrowroot, tagetes, alfalfa, lettuce and the various tree, nut and vine species, in particular of oil-containing crop plants such as soybean, peanut, castor oil plant, sunflower, corn, cotton, flax, oilseed rape, coconut, oil palm, safflower (*Carthamus tinctorius*) or cocoa bean, e.g. by bathing bruised leaves or chopped leaves in an agrobacterial solution and then culturing them in suitable media.

0155.0.1 The genetically modified plant cells may be regenerated by all of the methods known to those skilled in the art. Appropriate methods can be found in the publications referred to above by S.D. Kung and R. Wu, Potrykus or Höfgen and Willmitzer.

0156.0.1 Accordingly, a further aspect of the invention relates to transgenic organisms transformed by at least one nucleic acid sequence, expression cassette or vector according to the invention as well as cells, cell cultures, tissue, parts – such as, for example, leaves, roots, etc. in the case of plant organisms – or reproductive material derived from such organisms. The terms „host organism“, „host cell“, „recombinant (host) organism“ and „transgenic (host) cell“ are used here interchangeably. Of course these terms relate not only to the particular host organism or the particular target cell but also to the descendants or potential descendants of these organisms or cells. Since, due to mutation or environmental effects certain modifications may arise in successive generations, these descendants need not necessarily be identical with the parental cell but nevertheless are still encompassed by the term as used here.

0157.0.1 For the purposes of the invention „transgenic“ or „recombinant“ means with regard for example to a nucleic acid sequence, an expression cassette (= gene construct, nucleic acid construct) or a vector containing the nucleic acid sequence according to the invention or an organism transformed by the nucleic acid sequences, expression cassette or vector according to the invention all those constructions produced by genetic engineering methods in which either

- a) the nucleic acid sequence depicted in Fig. 1a, 1b or 1c or its derivatives or parts thereof or
- b) a genetic control sequence functionally linked to the nucleic acid sequence described under (a), for example a 3'- and/or 5'- genetic control sequence such as a promoter or terminator, or
- c) (a) and (b)

are not found in their natural, genetic environment or have been modified by genetic engineering methods, wherein the modification may by way of example be a substitution, addition, deletion, inversion or insertion of one or more nucleotide residues. Natural genetic environment means the natural genomic or chromosomal locus in the organism of origin or inside the host organism or presence in a genomic library. In the case of a genomic library the natural genetic environment of the nucleic acid sequence is preferably retained at least in part. The environment borders the nucleic acid sequence at least on one side and has a sequence length of at least 50 bp, preferably at least 500 bp, particularly preferably at least 1,000 bp, most particularly preferably at least 5,000 bp. A naturally occurring expression cassette – for example the naturally occurring combination of the natural promoter of the nucleic acid sequence according to the invention with the corresponding Δ -8-desaturase, Δ -9-elongase and/or Δ -5-desaturase gene – turns into a transgenic expression cassette

when the latter is modified by unnatural, synthetic („artificial“) methods such as by way of example a mutagenation. Appropriate methods are described by way of example in US 5,565,350 or WO 00/15815.

5 0158.0.1 Suitable organisms or host organisms for the nucleic acid, expression cassette or vector according to the invention are advantageously in principle all organisms, which are suitable for the expression of recombinant genes as described above. Further examples which may be mentioned are plants such as Arabidopsis, Asteraceae such as Calendula or crop plants such as soybean, peanut, castor oil plant, sunflower, flax, corn, cotton, flax, oilseed rape, coconut, oil palm, safflower (Carthamus
10 tinctorius) or cocoa bean.

0159.0.1 A further object of the invention relates to the use of a nucleic acid construct, e.g. an expression cassette, containing DNA sequences encoding polypeptides of Fig. 1a, 1b or 1c or DNA sequences hybridizing therewith for the transformation of plant cells, tissues or parts of plants.

15 0160.0.1 In doing so, depending on the choice of promoter, the sequences Fig. 1a, 1b or 1c can be expressed specifically in the leaves, in the seeds, the nodules, in roots, in the stem or other parts of the plant. Those transgenic plants overproducing sequences of Fig. 1a, 1b or 1c, the reproductive material thereof, together with the plant cells, tissues or parts thereof are a further object of the present invention.

20 0161.0.1 The expression cassette or the nucleic acid sequences or construct according to the invention containing sequences of Fig. 1a, 1b or 1c can, moreover, also be employed for the transformation of the organisms identified by way of example above such as bacteria, yeasts, filamentous fungi and plants.

25 0162.0.1 Within the framework of the present invention, altering metabolic activity means, for example, the artificially acquired trait of increased biosynthetic performance due to functional over expression of sequences of Fig. 1a, 1b or 1c in the organisms according to the invention, advantageously in the transgenic plants according to the invention, by comparison with the nongenetically modified initial plants at least for the duration of at least one plant generation.

30 0163.0.1 A constitutive expression of the exogenous sequences of the Fig. 1a, 1b or 1c is, moreover, advantageous. On the other hand, however, an inducible expression may also appear desirable.

35 0164.0.1 The efficiency of the expression of the sequences of the Fig. 1a, 1b or 1c can be determined, for example, in vitro by shoot meristem propagation. In addition, an expression of the sequences of Fig. 1a, 1b or 1c modified in nature and level and its effect on the metabolic pathways performance can be tested on test plants in greenhouse trials.

- 0165.0.1** An additional object of the invention comprises transgenic organisms such as transgenic plants transformed by an expression cassette containing sequences of Fig. 1a, 1b or 1c according to the invention or DNA sequences hybridizing therewith, as well as transgenic cells, tissue, parts and reproduction material of such plants. Particular preference is given in this case to transgenic crop plants such as by way of example barley, wheat, rye, oats, corn, soybean, rice, cotton, sugar beet, oilseed rape and canola, sunflower, flax, hemp, thistle, potatoes, tobacco, tomatoes, tapioca, cassava, arrowroot, alfalfa, lettuce and the various tree, nut and vine species.
- 0166.0.1** For the purposes of the invention plants are mono- and dicotyledonous plants, mosses or algae.
- 0167.0.1** A further refinement according to the invention are transgenic plants as described above which contain a nucleic acid sequence or construct according to the invention or an expression cassette according to the invention.
- 0168.0.1** Furthermore, by derivatives is meant homologues of the sequences of Fig. 1a, 1b or 1c, for example eukaryotic homologues, truncated sequences, single-stranded DNA of the encoding and nonencoding DNA sequence or RNA of the encoding and nonencoding DNA sequence.
- 0169.0.1** In addition, by homologues of the sequences of Fig. 1a, 1b or 1c is meant derivatives such as by way of example promoter variants. These variants may be modified by one or more nucleotide exchanges, by insertion(s) and/or deletion(s) without, however, adversely affecting the functionality or efficiency of the promoters. Furthermore, the promoters can have their efficiency increased by altering their sequence or be completely replaced by more effective promoters even of foreign organisms.
- 0170.0.1** By derivatives is also advantageously meant variants whose nucleotide sequence has been altered in the region from -1 to -2000 ahead of the start codon in such a way that the gene expression and/or the protein expression is modified, preferably increased. Furthermore, by derivatives is also meant variants which have been modified at the 3' end.
- 0171.0.1** Suitable promoters in the expression cassette are in principle all promoters which can control the expression of foreign genes in organisms such as microorganisms like protozoa such as ciliates, algae such as green, brown, red or blue algae such as *Euglenia*, bacteria such as gram-positive or gram-negative bacteria, yeasts such as *Saccharomyces*, *Pichia* or *Schizosaccharomyces* or fungi such as *Mortierella*, *Thraustochytrium* or *Schizochytrium* or plants, advantageously in plants or fungi. Use is preferably made in particular of plant promoters or promoters derived from

a plant virus. Advantageous regulation sequences for the method according to the invention are found for example in promoters such as *cos*, *lac*, *trp*, *tet*, *trp-tet*, *lpp*, *lac*, *lpp-lac*, *lacIq*, T7, T5, T3, *gal*, *trc*, *ara*, SP6, λ -PR or in λ -PL promoters which are employed advantageously in gram-negative bacteria. Other advantageous regulation sequences are found, for example, in the gram-positive promoters *amy* and *SPO2*, in the yeast or fungal promoters *ADC1*, *MF α* , *AC*, *P-60*, *CYC1*, *GAPDH*, *TEF*, *rp28*, *ADH* or in the plant promoters *CaMV/35S* [Franck et al., *Cell* 21(1980) 285-294], *SSU*, *OCS*, *lib4*, *STLS1*, *B33*, *nos* (= Nopaline Synthase Promoter) or in the ubiquitin or phaseolin promoter. The expression cassette may also contain a chemically inducible promoter by means of which the expression of the exogenous sequences of the odd numbers of SEQ. ID No. 1-269 in the organisms can be controlled advantageously in the plants at a particular time. Advantageous plant promoters of this type are by way of example the *PRP1* promoter [Ward et al., *Plant.Mol. Biol.*22(1993), 361-366], a promoter inducible by benzenesulfonamide (EP 388 186), a promoter inducible by tetracycline [Gatz et al., (1992) *Plant J.* 2,397-404], a promoter inducible by salicylic acid (WO 95/19443), a promoter inducible by abscisic acid (EP 335 528) and a promoter inducible by ethanol or cyclohexanone (WO93/21334). Other examples of plant promoters which can advantageously be used are the promoter of cytosolic FBPase from potato, the *ST-LSI* promoter from potato (Stockhaus et al., *EMBO J.* 8 (1989) 2445-245), the promoter of phosphoribosyl pyrophosphate amidotransferase from *Glycine max* (see also gene bank accession number U87999) or a nodiene-specific promoter as described in EP 249 070. Particularly advantageous are those plant promoters which ensure expression in tissue or plant parts/organs in which fatty acid biosynthesis or the precursor stages thereof occurs, as in endosperm or in the developing embryo for example. Particularly noteworthy are advantageous promoters which ensure seed-specific expression such as by way of example the *USP* promoter or derivatives thereof, the *LEB4* promoter, the phaseolin promoter or the napin promoter. The particularly advantageous *USP* promoter cited according to the invention or its derivatives mediate very early gene expression in seed development [Baeumlein et al., *Mol Gen Genet*, 1991, 225 (3): 458-67]. Other advantageous seed-specific promoters which may be used for monocotyledonous or dicotyledonous plants are the promoters suitable for dicotyledons such as napin gene promoters, likewise cited by way of example, from oilseed rape (US 5,608,152), the oleosin promoter from *Arabidopsis* (WO 98/45461), the phaseolin promoter from *Phaseolus vulgaris* (US 5,504,200), the *Bce4* promoter from *Brassica* (WO 91/13980) or the leguminous *B4* promoter (*LeB4*, Baeumlein et al., *Plant J.*, 2, 2, 1992: 233 - 239) or promoters suitable for monocotyledons such as the promoters of the *lpt2* or *lpt1* gene in barley (WO 95/15389

and WO 95/23230) or the promoters of the barley hordein gene, the rice glutelin gene, the rice oryzin gene, the rice prolamin gene, the wheat gliadin gene, the white glutelin gene, the corn zein gene, the oats glutelin gene, the sorghum kasirin gene or the rye socalin gene which are described in WO99/16890.

- 5 **0172.0.1** Furthermore, particularly preferred are those promoters, which ensure the expression in tissues, or plant parts in which, for example, the biosynthesis of fatty acids, oils and lipids or the precursor stages thereof takes place. Particularly noteworthy are promoters, which ensure a seed-specific expression. Noteworthy are the promoter of the napin gene from oilseed rape (US 5,608,152), the USP promoter
10 from *Vicia faba* (USP = unknown seed protein, Bäumlein et al., Mol Gen Genet, 1991, 225 (3): 459-67), the promoter of the oleosin gene from *Arabidopsis* (WO98/45461), the phaseolin promoter (US 5,504,200) or the promoter of the legumin B4 gene (LeB4; Bäumlein et al., 1992, Plant Journal, 2 (2): 233-9). Other promoters to be mentioned are that of the lpt2 or lpt1 gene from barley (WO95/15389 and WO95/23230) which
15 mediate seed-specific expression in monocotyledonous plants. Other advantageous seed specific promoters are promoters such as the promoters from rice, corn or wheat disclosed in WO 99/16890 or Amy32b, Amy6-6 or aleurain (US 5,577,474), Bce4 (rape, US 5,530,149), glycinin (soy bean, EP 571 741), phosphoenol pyruvat carboxylase (soy bean, JP 06/62870), ADR12-2 (soy bean, WO 98/08962), isocitratlyase (rape, US
20 5,669,040) or β -amylase (barley, EP 781 949).

- 0173.0.1** As described above, the expression construct (= gene construct, nucleic acid construct) may contain yet other genes, which are to be introduced into the organisms. These genes can be subject to separate regulation or be subject to the same regulation region as sequences Fig. 1a, 1b or 1c. These genes are by way of
25 example other biosynthesis genes, advantageously for fatty acid biosynthesis, vitamin biosynthesis etc. that allow increased synthesis.

- 0174.0.1** In principle all natural promoters with their regulation sequences can be used like those named above for the expression cassette according to the invention and the method according to the invention. Over and above this, synthetic promoters
30 may also advantageously be used.

- 0175.0.1** In the preparation of an expression cassette various DNA fragments can be manipulated in order to obtain a nucleotide sequence, which usefully reads in the correct direction and is equipped with a correct reading raster. To connect the DNA fragments (= nucleic acids according to the invention) to one another adaptors or
35 linkers may be attached to the fragments.

- 0176.0.1** The promoter and the terminator regions can usefully be provided in the transcription direction with a linker or polylinker containing one or more restriction

points for the insertion of this sequence. Generally, the linker has 1 to 10, mostly 1 to 8, preferably 2 to 6, restriction points. In general the size of the linker inside the regulatory region is less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promoter may be both native or homologous as well as foreign or heterologous to the host organism, for example to the host plant. In the 5'-3' transcription direction the expression cassette contains the promoter, a DNA sequence which encodes of Fig. 1a, 1b or 1c gene and a region for transcription termination. Different termination regions can be exchanged for one another in any desired fashion.

0177.0.1 Furthermore, manipulations which provide suitable restriction interfaces or which remove excess DNA or restriction interfaces can be employed. Where insertions, deletions or substitutions, such as transitions and transversions, come into consideration, in vitro mutagenesis, primer repair, restriction or ligation may be used. In suitable manipulations such as restriction, chewing back or filling of overhangs for blunt ends complementary ends of the fragments can be provided for the ligation.

0178.0.1 For an advantageous high expression the attachment of the specific ER retention signal SEKDEL inter alia can be of importance (Schouten, A. et al., Plant Mol. Biol. 30 (1996), 781-792). In this way the average expression level is tripled or even quadrupled. Other retention signals which occur naturally in plant and animal proteins located in the ER may also be employed for the construction of the cassette. In another preferred embodiment a plastidial targeting sequence is used as described by Napier J.A. [Targeting of foreign proteins to the chloroplast, Methods Mol. Biol., 49, 1995: 369 - 376]. A preferred used vector comprising said plastidial targeting sequence is disclosed by Colin Lazarus [Guerineau F., Woolston S., Brooks L., Mullineaux P. "An expression cassette for targeting foreign proteins into chloroplast; Nucleic. Acids Res., Dec 9, 16 (23), 1988: 11380].

0179.0.1 Preferred polyadenylation signals are plant polyadenylation signals, preferably those which substantially correspond to T-DNA polyadenylation signals from *Agrobacterium tumefaciens*, in particular gene 3 of the T-DNA (octopin synthase) of the Ti plasmid pTiACH5 (Gielen et al., EMBO J.3 (1984), 836 et seq.) or corresponding functional equivalents.

0180.0.1 An expression cassette is produced by fusion of a suitable promoter with suitable sequences of Fig. 1a, 1b or 1c together with a polyadenylation signal by common recombination and cloning techniques as described, for example, in T. Maniatis, E.F. Fritsch and J. Sambrook, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1989) as well as in T.J. Silhavy, M.L. Berman and L.W. Enquist, Experiments with Gene Fusions, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY (1984) and in Ausubel, F.M. et al., Current

Protocols in Molecular Biology, Greene Publishing Assoc. and Wiley-Interscience (1987).

5 **0181.0.1** In the preparation of an expression cassette various DNA fragments can be manipulated to produce a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. Adapters or linkers can be attached to the fragments for joining the DNA fragments.

10 **0182.0.1** The promoter and the terminator regions can usefully be provided in the transcription direction with a linker or polylinker containing one or more restriction points for the insertion of this sequence. Generally, the linker has 1 to 10, mostly 1 to 8, preferably 2 to 6, restriction points. In general the size of the linker inside the regulatory region is less than 100 bp, frequently less than 60 bp, but at least 5 bp. The promoter may be both native or homologous as well as foreign or heterologous to the host organism, for example to the host plant. In the 5'-3' transcription direction the expression cassette contains the promoter, a DNA sequence which either encodes
15 gene of the odd numbers of SEQ. ID No. 1-269 and a region for transcription termination. Different termination regions can be exchanged for one another in any desired fashion.

20 **0183.0.1** In the preparation of an expression cassette various DNA fragments can be manipulated to produce a nucleotide sequence which usefully reads in the correct direction and is equipped with a correct reading raster. Adapters or linkers can be attached to the fragments for joining the DNA fragments.

25 **0184.0.1** The DNA sequences encoding the nucleic acid sequences used in the inventive processes such as the sequences of the Fig. 1a, 1b or 1c contain all the sequence characteristics needed to achieve correct localization of respective biosynthesis. Accordingly, no further targeting sequences are needed per se. However, such a localization may be desirable and advantageous and hence artificially modified or reinforced so that such fusion constructs are also a preferred advantageous embodiment of the invention.

30 **0185.0.1** Particularly preferred are sequences which ensure targeting in plastids. Under certain circumstances targeting into other compartments (reported in: Kermode, Crit. Rev. Plant Sci. 15, 4 (1996), 285-423) may also be desirable, e.g. into vacuoles, the mitochondrion, the endoplasmic reticulum (ER), peroxisomes, lipid structures or due to lack of corresponding operative sequences retention in the compartment of origin, the cytosol.

35 **0186.0.1** As used herein, the term "environmental stress" refers to any sub-optimal growing condition and includes, but is not limited to, sub-optimal conditions associated with salinity, drought, temperature, metal, chemical, pathogenic and

oxidative stresses, or combinations thereof. In preferred embodiments, the environmental stress can be salinity, drought, heat, or low temperature, or combinations thereof, and in particular, can be low water content or low temperature. Wherein drought stress means any environmental stress which leads to a lack of water
5 in plants or reduction of water supply to plants, wherein low temperature stress means freezing of plants below + 4 °C as well as chilling of plants below 15 °C and wherein high temperature stress means for example a temperature above 35 °C. The range of stress and stress response depends on the different plants which are used for the invention, i.e. it differs for example between a plant such as wheat and a plant such as
10 Arabidopsis. A common response of plants to environmental stress is the loss of yield or the loss of quality. It is also to be understood that as used in the specification and in the claims, "a" or "an" can mean one or more, depending upon the context in which it is used. Thus, for example, reference to "a cell" can mean that at least one cell can be utilized.

15 **0187.0.1** As also used herein, the terms "nucleic acid" and "nucleic acid molecule" are intended to include DNA molecules (e.g., cDNA or genomic DNA) and RNA molecules (e.g., mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 1000 nucleotides of
20 sequence upstream from the 5' end of the coding region and at least about 200 nucleotides of sequence downstream from the 3' end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

0188.0.1 An "isolated" nucleic acid molecule is one that is substantially separated
25 from other nucleic acid molecules, which are present in the natural source of the nucleic acid. That means other nucleic acid molecules are present in an amount less than 5% based on weight of the amount of the desired nucleic acid, preferably less than 2% by weight, more preferably less than 1% by weight, most preferably less than 0.5% by weight. Preferably, an "isolated" nucleic acid is free of some of the sequences
30 that naturally flank the nucleic acid (i.e., sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated stress related protein encoding nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid
35 molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be free from some of the other cellular material with which it is naturally associated, or culture medium

when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

0189.0.1 A nucleic acid molecule of the present invention, e.g., a nucleic acid molecule encoding an SRP or a portion thereof which confers tolerance and/or resistance to environmental stress in plants, can be isolated using standard molecular biological techniques and the sequence information provided herein. For example, a *Arabidopsis thaliana* stress related protein encoding cDNA can be isolated from a *A. thaliana* c-DNA library using all or portion of one of the sequences of Fig. 1a, 1b or 1c. Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Fig. 1a, 1b or 1c can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence. For example, mRNA can be isolated from plant cells (e.g., by the guanidinium-thiocyanate extraction procedure of Chirgwin et al., 1979 *Biochemistry* 18:5294-5299) and cDNA can be prepared using reverse transcriptase (e.g., Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Fig. 1a, 1b or 1c. A nucleic acid molecule of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid molecule so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to a SRP encoding nucleotide sequence can be prepared by standard synthetic techniques, e.g., using an automated DNA synthesizer.

0190.0.1 In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in sequences Fig. 1a, 1b or 1c encoding the SRP (i.e., the "coding region"), as well as 5' untranslated sequences and 3' untranslated sequences.

0191.0.1 Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences of the nucleic acid of Fig. 1a, 1b or 1c, for example, a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of a SRP.

0192.0.1 Portions of proteins encoded by the SRP encoding nucleic acid molecules of the invention are preferably biologically active portions described herein. As used herein, the term "biologically active portion of" a SRP is intended to include a portion, e.g., a domain/motif, of stress related protein that participates in a stress tolerance and/or resistance response in a plant. To determine whether a SRP, or a

biologically active portion thereof, results in increased stress tolerance in a plant, a stress analysis of a plant comprising the SRP may be performed. Such analysis methods are well known to those skilled in the art, as detailed in the Examples. More specifically, nucleic acid fragments encoding biologically active portions of a SRP can be prepared by isolating a portion of one of the sequences of the nucleic acid of Fig. 1a, 1b or 1c expressing the encoded portion of the SRP or peptide (e.g., by recombinant expression in vitro) and assessing the activity of the encoded portion of the SRP or peptide.

0193.0.1 Biologically active portions of a SRP are encompassed by the present invention and include peptides comprising amino acid sequences derived from the amino acid sequence of a SRP encoding gene, or the amino acid sequence of a protein homologous to a SRP, which include fewer amino acids than a full length SRP or the full length protein which is homologous to a SRP, and exhibits at least some enzymatic activity of a SRP. Typically, biologically active portions (e.g., peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of a SRP. Moreover, other biologically active portions in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of a SRP include one or more selected domains/motifs or portions thereof having biological activity.

0194.0.1 The term "biological active portion" or "biological activity" means a SRP or a portion of a SRP which still has at least 10 % or 20 %, preferably 20 %, 30 %, 40 % or 50 %, especially preferably 60 %, 70 % or 80 % of the enzymatic activity of the natural or starting enzyme.

0195.0.2 A nucleic acid molecule encompassing a complete sequence of the nucleic acid molecules used in the process, for example the polynucleotide of the invention, or a part thereof may additionally be isolated by polymerase chain reaction, oligonucleotide primers based on this sequence or on parts thereof being used. For example, a nucleic acid molecule comprising the complete sequence or part thereof can be isolated by polymerase chain reaction using oligonucleotide primers which have been generated on the basis of this sequence. For example, mRNA can be isolated from cells (for example by means of the guanidinium thiocyanate extraction method of Chirgwin et al. (1979) Biochemistry 18:5294-5299) and cDNA can be generated by means of reverse transcriptase (for example Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD, or AMV reverse transcriptase, obtainable from Seikagaku America, Inc., St.Petersburg, FL).

0196.0.2 Synthetic oligonucleotide primers for the amplification, e.g. as shown in table 2, by means of polymerase chain reaction can be generated on the basis of a sequence shown herein, for example the sequence shown in Fig. 1a, 1b or 1c or the sequences derived from polypeptides as shown in Fig. 1a, 1b or 1c.

5 **0197.0.2** Moreover, it is possible to identify conserved regions from various organisms by carrying out protein sequence alignments with the polypeptide used in the process of the invention, in particular with sequences of the polypeptide of the invention, from which conserved regions, and in turn, degenerate primers can be derived. Conserved region for the polypeptide of the invention are indicated in the
10 alignment shown in the figure Fig. 1a, 1b or 1c. Conserved regions are those, which show a very little variation in the amino acid in one particular position of several homologs from different origin. The consensus sequences shown in Fig. 2 are derived from said alignments.

0198.0.2 Degenerated primers can then be utilized by PCR for the amplification
15 of fragments of novel proteins having above-mentioned activity, e.g. having an SPR activity or further functional homologs of the polypeptide of the invention from other organisms.

0199.0.2 These fragments can then be utilized as hybridization probe for isolating the complete gene sequence. As an alternative, the missing 5' and 3' sequences can
20 be isolated by means of RACE-PCR (rapid amplification of cDNA ends). A nucleic acid molecule according to the invention can be amplified using cDNA or, as an alternative, genomic DNA as template and suitable oligonucleotide primers, following standard PCR amplification techniques. The nucleic acid molecule amplified thus can be cloned into a suitable vector and characterized by means of DNA sequence analysis.
25 Oligonucleotides, which correspond to one of the nucleic acid molecules used in the process can be generated by standard synthesis methods, for example using an automatic DNA synthesizer.

0200.0.2 Nucleic acid molecules which are advantageously for the process according to the invention can be isolated based on their homology to the nucleic acid
30 molecules disclosed herein using the sequences or part thereof as hybridization probe and following standard hybridization techniques under stringent hybridization conditions. In this context, it is possible to use, for example, isolated nucleic acid molecules of at least 15, 20, 25, 30, 35, 40, 50, 60 or more nucleotides, preferably of at least 15, 20 or 25 nucleotides in length which hybridize under stringent conditions with
35 the above-described nucleic acid molecules, in particular with those which encompass a nucleotide sequence of the nucleic acid molecule used in the process of the invention or encoding a protein used in the invention or of the nucleic acid molecule of the

invention. Nucleic acid molecules with 30, 50, 100, 250 or more nucleotides may also be used.

5 **0201.0.1** In addition to fragments of the SRP described herein, the present invention includes homologs and analogs of naturally occurring SRP and SRP encoding nucleic acids in a plant.

0202.0.1 "Homologs" are defined herein as two nucleic acids or proteins that have similar, or "homologous", nucleotide or amino acid sequences, respectively. Homologs include allelic variants, orthologs, paralogs, agonists and antagonists of SRP as defined hereafter. The term "homolog" further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in sequences with SEQ ID No. **XXX** (and portions thereof) due to degeneracy of the genetic code and thus encode the same SRP as that encoded by the amino acid sequences shown in sequences with SEQ ID No. **XXX**. As used herein a "naturally occurring" SRP refers to a SRP amino acid sequence that occurs in nature.

15 **0203.0.2** The term "homology" means that the respective nucleic acid molecules or encoded proteins are functionally and/or structurally equivalent. The nucleic acid molecules that are homologous to the nucleic acid molecules described above and that are derivatives of said nucleic acid molecules are, for example, variations of said nucleic acid molecules which represent modifications having the same biological function, in particular encoding proteins with the same or substantially the same biological function. They may be naturally occurring variations, such as sequences from other plant varieties or species, or mutations. These mutations may occur naturally or may be obtained by mutagenesis techniques. The allelic variations may be naturally occurring allelic variants as well as synthetically produced or genetically engineered variants. Structurally equivalents can, for example, be identified by testing the binding of said polypeptide to antibodies or computer based predictions. Structurally equivalent have the similar immunological characteristic, e.g. comprise similar epitopes.

0204.0.2 Functional equivalents derived from one of the polypeptides as shown in **SEQ ID NO: YYY** according to the invention by substitution, insertion or deletion have at least 30%, 35%, 40%, 45% or 50%, preferably at least 55%, 60%, 65% or 70% by preference at least 80%, especially preferably at least 85% or 90%, 91%, 92%, 93% or 94%, very especially preferably at least 95%, 97%, 98% or 99% homology with one of the polypeptides as shown in Fig. 1a, 1b or 1c according to the invention and are distinguished by essentially the same properties as the polypeptide as shown in Fig. 1a, 1b or 1c.

0205.0.2 Functional equivalents derived from the nucleic acid sequence as shown in SEQ ID NO: YYY according to the invention by substitution, insertion or deletion have at least 30%, 35%, 40%, 45% or 50%, preferably at least 55%, 60%, 65% or 70% by preference at least 80%, especially preferably at least 85% or 90%, 91%, 92%, 93% or 94%, very especially preferably at least 95%, 97%, 98% or 99% homology with one of the polypeptides as shown in Fig. 1a, 1b or 1c according to the invention and encode polypeptides having essentially the same properties as the polypeptide as shown in Fig. 1a, 1b or 1c.

0206.0.2 "Essentially the same properties" of a functional equivalent is above all understood as meaning that the functional equivalent has above mentioned activity, e.g. conferring an increase in the fine chemical amount while increasing the amount of protein, activity or function of said functional equivalent in an organism, e.g. a microorganism, a plant or plant or animal tissue, plant or animal cells or a part of the same.

0207.0.2 By "hybridizing" it is meant that such nucleic acid molecules hybridize under conventional hybridization conditions, preferably under stringent conditions such as described by, e.g., Sambrook (Molecular Cloning; A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY (1989)) or in Current Protocols in Molecular Biology, John Wiley & Sons, N. Y. (1989), 6.3.1-6.3.6.

0208.0.2 According to the invention, DNA as well as RNA molecules of the nucleic acid of the invention can be used as probes. Further, as template for the identification of functional homologues Northern blot assays as well as Southern blot assays can be performed. The Northern blot assay advantageously provides further informations about the expressed gene product: e.g. expression pattern, occurrence of processing steps, like splicing and capping, etc. The Southern blot assay provides additional information about the chromosomal localization and organization of the gene encoding the nucleic acid molecule of the invention.

0209.0.2 A preferred, nonlimiting example of stringent hybridization conditions are hybridizations in 6 x sodium chloride/sodium citrate (= SSC) at approximately 45°C, followed by one or more wash steps in 0.2 x SSC, 0.1% SDS at 50 to 65°C, for example at 50°C, 55°C or 60°C. The skilled worker knows that these hybridization conditions differ as a function of the type of the nucleic acid and, for example when organic solvents are present, with regard to the temperature and concentration of the buffer. The temperature under "standard hybridization conditions" differs for example as a function of the type of the nucleic acid between 42°C and 58°C, preferably between 45°C and 50°C in an aqueous buffer with a concentration of 0.1 x 0.5 x, 1 x, 2x, 3x, 4x or 5 x SSC (pH 7.2). If organic solvent(s) is/are present in the

abovementioned buffer, for example 50% formamide, the temperature under standard conditions is approximately 40°C, 42°C or 45°C. The hybridization conditions for DNA:DNA hybrids are preferably for example 0.1 x SSC and 20°C, 25°C, 30°C, 35°C, 40°C or 45°C, preferably between 30°C and 45°C. The hybridization conditions for DNA:RNA hybrids are preferably for example 0.1 x SSC and 30°C, 35°C, 40°C, 45°C, 50°C or 55°C, preferably between 45°C and 55°C. The abovementioned hybridization temperatures are determined for example for a nucleic acid approximately 100 bp (= base pairs) in length and a G + C content of 50% in the absence of formamide. The skilled worker knows to determine the hybridization conditions required with the aid of textbooks, for example the ones mentioned above, or from the following textbooks: Sambrook et al., "Molecular Cloning", Cold Spring Harbor Laboratory, 1989; Hames and Higgins (Ed.) 1985, "Nucleic Acids Hybridization: A Practical Approach", IRL Press at Oxford University Press, Oxford; Brown (Ed.) 1991, "Essential Molecular Biology: A Practical Approach", IRL Press at Oxford University Press, Oxford.

0210.0.2 A further example of one such stringent hybridization condition is hybridization at 4XSSC at 65°C, followed by a washing in 0.1XSSC at 65°C for one hour. Alternatively, an exemplary stringent hybridization condition is in 50 % formamide, 4XSSC at 42°C. Further, the conditions during the wash step can be selected from the range of conditions delimited by low-stringency conditions (approximately 2X SSC at 50°C) and high-stringency conditions (approximately 0.2X SSC at 50°C, preferably at 65°C) (20X SSC: 0.3M sodium citrate, 3M NaCl, pH 7.0). In addition, the temperature during the wash step can be raised from low-stringency conditions at room temperature, approximately 22°C, to higher-stringency conditions at approximately 65°C. Both of the parameters salt concentration and temperature can be varied simultaneously, or else one of the two parameters can be kept constant while only the other is varied. Denaturants, for example formamide or SDS, may also be employed during the hybridization. In the presence of 50% formamide, hybridization is preferably effected at 42°C. Relevant factors like i) length of treatment, ii) salt conditions, iii) detergent conditions, iv) competitor DNAs, v) temperature and vi) probe selection can be combined case by case so that not all possibilities can be mentioned herein.

0211.0.2 Thus, in a preferred embodiment, Northern blots are prehybridized with Rothi-Hybri-Quick buffer (Roth, Karlsruhe) at 68°C for 2h. Hybridization with radioactive labelled probe is done overnight at 68°C. Subsequent washing steps are performed at 68°C with 1xSSC.

0212.0.2 For Southern blot assays the membrane is prehybridized with Rothi-Hybri-Quick buffer (Roth, Karlsruhe) at 68°C for 2h. The hybridization with radioactive

labelled probe is conducted over night at 68°C. Subsequently the hybridization buffer is discarded and the filter shortly washed using 2xSSC; 0,1% SDS. After discarding the washing buffer new 2xSSC; 0,1% SDS buffer is added and incubated at 68°C for 15 minutes. This washing step is performed twice followed by an additional washing step using 1xSSC; 0,1% SDS at 68°C for 10 min.

0213.0.2 Some further examples of conditions for DNA hybridization (Southern blot assays) and wash step are shown hereinbelow:

(1) Hybridization conditions can be selected, for example, from the following conditions:

- a) 4X SSC at 65°C,
- b) 6X SSC at 45°C,
- c) 6X SSC, 100 mg/ml denatured fragmented fish sperm DNA at 68°C,
- d) 6X SSC, 0.5% SDS, 100 mg/ml denatured salmon sperm DNA at 68°C,
- e) 6X SSC, 0.5% SDS, 100 mg/ml denatured fragmented salmon sperm DNA, 50% formamide at 42°C,
- f) 50% formamide, 4X SSC at 42°C,
- g) 50% (vol/vol) formamide, 0.1% bovine serum albumin, 0.1% Ficoll, 0.1% polyvinylpyrrolidone, 50 mM sodium phosphate buffer pH 6.5, 750 mM NaCl, 75 mM sodium citrate at 42°C,
- h) 2X or 4X SSC at 50°C (low-stringency condition), or
- i) 30 to 40% formamide, 2X or 4X SSC at 42°C (low-stringency condition).

(2) Wash steps can be selected, for example, from the following conditions:

- a) 0.015 M NaCl/0.0015 M sodium citrate/0.1% SDS at 50°C.
- b) 0.1X SSC at 65°C.
- c) 0.1X SSC, 0.5 % SDS at 68°C.
- d) 0.1X SSC, 0.5% SDS, 50% formamide at 42°C.
- e) 0.2X SSC, 0.1% SDS at 42°C.
- f) 2X SSC at 65°C (low-stringency condition).

0214.0.1 In an other embodiment is meant by standard conditions, for example, depending on the nucleic acid in question temperatures between 42°C and 58°C in an aqueous buffer solution having a concentration of between 0.1 and 5 x SSC (1 X SSC = 0.15 M NaCl, 15 mM sodium citrate, pH 7.2) or additionally in the presence of 50 % formamide, such as by way of example 42°C in 5 x SSC, 50 % formamide. Hybridization conditions for DNA:DNA hybrids are advantageously 0.1 x SSC and temperatures between approximately 20°C and 45°C, preferably between

approximately 30 °C and 45 °C. For DNA:RNA hybrids the hybridization conditions are advantageously 0.1 x SSC and temperatures between approximately 30°C and 55°C, preferably between approximately 45°C and 55°C. These specified temperatures for hybridization are melting temperature values calculated by way of example for a nucleic acid having a length of approximately 100 nucleotides and a G + C content of 50 % in the absence of formamide. The experimental conditions for DNA hybridization are described in relevant genetics textbooks such as by way of example Sambrook et al., „Molecular Cloning“, Cold Spring Harbor Laboratory, 1989, and may be calculated by formulae known to those skilled in the art, for example as a function of the length of the nucleic acids, the nature of the hybrids or the G + C content. Those skilled in the art may draw on the following textbooks for further information on hybridization: Ausubel et al. (eds), 1985, Current Protocols in Molecular Biology, John Wiley & Sons, New York; Hames and Higgins (eds), 1985, Nucleic Acids Hybridization: A Practical Approach, IRL Press at Oxford University Press, Oxford; Brown (ed), 1991, Essential Molecular Biology: A Practical Approach, IRL Press at Oxford University Press, Oxford.

0215.0.2 Polypeptides having above-mentioned activity, i.e. conferring the altered metabolic activity, derived from other organisms, can be encoded by other DNA sequences which hybridize to the sequences shown in Fig. 1a, 1b or 1c under relaxed hybridization conditions and which code on expression for peptides conferring an altered metabolic activity.

0216.0.2 Further, some applications have to be performed at low stringency hybridisation conditions, without any consequences for the specificity of the hybridization. For example, a Southern blot analysis of total DNA could be probed with a nucleic acid molecule of the present invention and washed at low stringency (55°C in 2xSSPE0,1% SDS). The hybridisation analysis could reveal a simple pattern of only genes encoding polypeptides of the present invention or used in the process of the invention, e.g. having herein-mentioned activity of increasing the fine chemical . A further example of such low-stringent hybridization conditions is 4XSSC at 50°C or hybridization with 30 to 40% formamide at 42°C. Such molecules comprise those which are fragments, analogues or derivatives of the polypeptide of the invention or used in the process of the invention and differ, for example, by way of amino acid and/or nucleotide deletion(s), insertion(s), substitution (s), addition(s) and/or recombination (s) or any other modification(s) known in the art either alone or in combination from the above-described amino acid sequences or their underlying nucleotide sequence(s). However, it is preferred to use high stringency hybridisation conditions.

0217.0.2 Hybridization should advantageously be carried out with fragments of at least 5, 10, 15, 20, 25, 30, 35 or 40 bp, advantageously at least 50, 60, 70 or 80 bp,

preferably at least 90, 100 or 110 bp. Most preferably are fragments of at least 15, 20, 25 or 30 bp. Preferably are also hybridizations with at least 100 bp or 200, very especially preferably at least 400 bp in length. In an especially preferred embodiment, the hybridization should be carried out with the entire nucleic acid sequence with conditions described above.

0218.0.2 The terms "fragment", "fragment of a sequence" or "part of a sequence" mean a truncated sequence of the original sequence referred to. The truncated sequence (nucleic acid or protein sequence) can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to or hybridizing with the nucleic acid molecule of the invention or used in the process of the invention under stringent conditions, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence.

0219.0.3 In addition to fragments and fusion polypeptides of the SRPs described herein, the present invention includes homologs and analogs of naturally occurring SRPs and SRP encoding nucleic acids in a plant. "Homologs" are defined herein as two nucleic acids or polypeptides that have similar, or substantially identical, nucleotide or amino acid sequences, respectively. Homologs include allelic variants, orthologs, paralog, agonists and antagonists of SRPs as defined hereafter. The term "homolog" further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Fig. 1a, 1b or 1c (and portions thereof) due to degeneracy of the genetic code and thus encode the same SRP as that encoded by the nucleotide sequences shown in Fig. 1a, 1b or 1c. As used herein a "naturally occurring" SRP refers to a SRP amino acid sequence that occurs in nature. Preferably, a naturally occurring SRP comprises an amino acid sequence selected from the group consisting of polypeptides of Fig. 1a, 1b or 1c.

0220.0.3 An agonist of the SRP can retain substantially the same, or a subset, of the biological activities of the SRP. An antagonist of the SRP can inhibit one or more of the activities of the naturally occurring form of the SRP. For example, the SRP antagonist can competitively bind to a downstream or upstream member of the cell membrane component metabolic cascade that includes the SRP, or bind to a SRP that mediates transport of compounds across such membranes, thereby preventing translocation from taking place.

0221.0.3 Nucleic acid molecules corresponding to natural allelic variants and analogs, orthologs and paralog of a SRP cDNA can be isolated based on their identity

to the *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP nucleic acids described herein using SRP cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. In an alternative embodiment, homologs of the SRP can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of the SRP for SRP agonist or antagonist activity. In one embodiment, a variegated library of SRP variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of SRP variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential SRP sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion polypeptides (e.g., for phage display) containing the set of SRP sequences therein. There are a variety of methods that can be used to produce libraries of potential SRP homologs from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene is then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential SRP sequences. Methods for synthesizing degenerate oligonucleotides are known in the art. See, e.g., Narang, S.A., 1983, *Tetrahedron* 39:3; Itakura et al., 1984, *Annu. Rev. Biochem.* 53:323; Itakura et al., 1984, *Science* 198:1056; Ike et al., 1983, *Nucleic Acid Res.* 11:477.

0222.0.3 In addition, libraries of fragments of the SRP coding regions can be used to generate a variegated population of SRP fragments for screening and subsequent selection of homologs of a SRP. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a SRP coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA, which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal, and internal fragments of various sizes of the SRP.

0223.0.3 Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of SRP homologs. The most widely used techniques, which are amenable to high

through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify SRP homologs (Arkin and Yourvan, 1992, PNAS 89:7811-7815; Delgrave et al., 1993, Polypeptide Engineering 6(3):327-331). In another embodiment, cell based assays can be exploited to analyze a variegated SRP library, using methods well known in the art. The present invention further provides a method of identifying a novel SRP, comprising (a) raising a specific antibody response to a SRP, or a fragment thereof, as described herein; (b) screening putative SRP material with the antibody, wherein specific binding of the antibody to the material indicates the presence of a potentially novel SRP; and (c) analyzing the bound material in comparison to known SRP, to determine its novelty.

0224.0.3 As stated above, the present invention includes SRPs and homologs thereof. To determine the percent sequence identity of two amino acid sequences (e.g., one of the sequences of Fig. 1a, 1b or 1c, and a mutant form thereof), the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one polypeptide for optimal alignment with the other polypeptide or nucleic acid). The amino acid residues at corresponding amino acid positions are then compared. When a position in one sequence (e.g., one of the sequences of Fig. 1a, 1b or 1c) is occupied by the same amino acid residue as the corresponding position in the other sequence (e.g., a mutant form of the sequence selected from the polypeptides of Fig. 1a, 1b or 1c), then the molecules are identical at that position. The same type of comparison can be made between two nucleic acid sequences.

0225.0.3 The percent sequence identity between the two sequences is a function of the number of identical positions shared by the sequences (i.e., percent sequence identity = numbers of identical positions/total numbers of positions x 100). Preferably, the isolated amino acid homologs included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90% or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more identical to an entire amino acid sequence shown in Fig. 1a, 1b or 1c. In yet another embodiment, the isolated amino acid homologs included in the present invention are at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-75%, 75-80%, 80-85%, 85-90% or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more identical to an entire amino

acid sequence encoded by a nucleic acid sequence shown in Fig. 1a, 1b or 1c. In other embodiments, the SRP amino acid homologs have sequence identity over at least 15 contiguous amino acid residues, more preferably at least 25 contiguous amino acid residues, and most preferably at least 35 contiguous amino acid residues of Fig. 1a, 1b or 1c.

0226.0.3 In another preferred embodiment, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which is at least about 50-60%, preferably at least about 60-70%, more preferably at least about 70-75%, 75-80%, 80-85%, 85-90% or 90-95%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical to a nucleotide sequence shown Fig. 1a, 1b or 1c, or to a portion comprising at least 20, 30, 40, 50, 60 consecutive nucleotides thereof. The preferable length of sequence comparison for nucleic acids is at least 75 nucleotides, more preferably at least 100 nucleotides and most preferably the entire length of the coding region.

0227.0.3 It is further preferred that the isolated nucleic acid homolog of the invention encodes a SRP, or portion thereof, that is at least 85% identical to an amino acid sequence of Fig. 1a, 1b or 1c and that functions as a modulator of an environmental stress response in a plant. In a more preferred embodiment, overexpression of the nucleic acid homolog in a plant increases the tolerance of the plant to an environmental stress.

0228.0.3 For the purposes of the invention, the percent sequence identity between two nucleic acid or polypeptide sequences is determined using the Vector NTI 6.0 (PC) software package (Invitrogen, 7600 Wisconsin Ave., Bethesda, MD 20814). A gap opening penalty of 15 and a gap extension penalty of 6.66 are used for determining the percent identity of two nucleic acids. A gap opening penalty of 10 and a gap extension penalty of 0.1 are used for determining the percent identity of two polypeptides. All other parameters are set at the default settings. For purposes of a multiple alignment (Clustal W algorithm), the gap opening penalty is 10, and the gap extension penalty is 0.05 with blosum62 matrix. It is to be understood that for the purposes of determining sequence identity when comparing a DNA sequence to an RNA sequence, a thymidine nucleotide is equivalent to a uracil nucleotide.

0228.1.3 In another aspect, the invention provides an isolated nucleic acid comprising a polynucleotide that hybridizes to the polynucleotide of Fig. 1a, 1b or 1c under stringent conditions. More particularly, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Fig. 1a, 1b or 1c. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in

length. Preferably, an isolated nucleic acid homolog of the invention comprises a nucleotide sequence which hybridizes under highly stringent conditions to the nucleotide sequence shown in Fig. 1a, 1b or 1c, and functions as a modulator of stress tolerance in a plant. In a further preferred embodiment, overexpression of the isolated nucleic acid homolog in a plant increases a plant's tolerance to an environmental stress.

0229.0.3 As used herein with regard to hybridization for DNA to DNA blot, the term "stringent conditions" refers in one embodiment to hybridization overnight at 60°C in 10X Denharts solution, 6X SSC, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA. Blots are washed sequentially at 62°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS and finally 0.1X SSC/0.1% SDS. As also used herein, "highly stringent conditions" refers to hybridization overnight at 65°C in 10X Denharts solution, 6X SSC, 0.5% SDS and 100 µg/ml denatured salmon sperm DNA. Blots are washed sequentially at 65°C for 30 minutes each time in 3X SSC/0.1% SDS, followed by 1X SSC/0.1% SDS and finally 0.1X SSC/0.1% SDS. Methods for nucleic acid hybridizations are described in Meinkoth and Wahl, 1984, Anal. Biochem. 138:267-284; Ausubel et al. eds, 1995, Current Protocols in Molecular Biology, Chapter 2, Greene Publishing and Wiley-Interscience, New York; and Tijssen, 1993, Laboratory Techniques in Biochemistry and Molecular Biology: Hybridisation with Nucleic Acid Probes, Part I, Chapter 2, Elsevier, New York. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent or highly stringent conditions to a sequence of Fig. 1a, 1b or 1c corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural polypeptide). In one embodiment, the nucleic acid encodes a naturally occurring *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP.

0230.0.3 Using the above-described methods, and others known to those of skill in the art, one of ordinary skill in the art can isolate homologs of the SRPs comprising amino acid sequences shown in Fig. 1a, 1b or 1c. One subset of these homologs are allelic variants. As used herein, the term "allelic variant" refers to a nucleotide sequence containing polymorphisms that lead to changes in the amino acid sequences of a SRP and that exist within a natural population (e.g., a plant species or variety). Such natural allelic variations can typically result in 1-5% variance in a SRP nucleic acid. Allelic variants can be identified by sequencing the nucleic acid sequence of interest in a number of different plants, which can be readily carried out by using hybridization probes to identify the same SRP genetic locus in those plants. Any and

all such nucleic acid variations and resulting amino acid polymorphisms or variations in a SRP that are the result of natural allelic variation and that do not alter the functional activity of a SRP, are intended to be within the scope of the invention.

5 **0231.0.3** An isolated nucleic acid molecule encoding a SRP having sequence identity with a polypeptide sequence of Fig. 1a, 1b or 1c can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Fig. 1a, 1b or 1c, respectively, such that one or more amino acid substitutions, additions, or deletions are introduced into the encoded polypeptide. Mutations can be introduced into one of the sequences of Fig. 1a, 1b or 1c by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

15 **0232.0.3** Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a SRP is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a SRP coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for a SRP activity described herein to identify mutants that retain SRP activity. Following mutagenesis of one of the sequences of **SEQ ID NO:XXX**, the encoded polypeptide can be expressed recombinantly and the activity of the polypeptide can be determined by analyzing the stress tolerance of a plant expressing the polypeptide as described herein.

25 **0233.0.3** Additionally, optimized SRP nucleic acids can be created. As used herein, "optimized" refers to a nucleic acid that is genetically engineered to increase its expression in a given plant or animal. To provide plant optimized SRP nucleic acids, the DNA sequence of the gene can be modified to 1) comprise codons preferred by highly expressed plant genes; 2) comprise an A+T content in nucleotide base composition to that substantially found in plants; 3) form a plant initiation sequence; or 35 4) eliminate sequences that cause destabilization, inappropriate polyadenylation, degradation, and termination of RNA, or that form secondary structure hairpins or RNA

splice sites. Increased expression of SRP nucleic acids in plants can be achieved by utilizing the distribution frequency of codon usage in plants in general or a particular plant. Methods for optimizing nucleic acid expression in plants can be found in EPA 0359472; EPA 0385962; PCT Application No. WO 91/16432; U.S. Patent No. 5,380,831; U.S. Patent No. 5,436,391; Perlack et al., 1991, Proc. Natl. Acad. Sci. USA 88:3324-3328; and Murray et al., 1989, Nucleic Acids Res. 17:477-498.

0234.0.3 As used herein, "frequency of preferred codon usage" refers to the preference exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. To determine the frequency of usage of a particular codon in a gene, the number of occurrences of that codon in the gene is divided by the total number of occurrences of all codons specifying the same amino acid in the gene. Similarly, the frequency of preferred codon usage exhibited by a host cell can be calculated by averaging frequency of preferred codon usage in a large number of genes expressed by the host cell. It is preferable that this analysis be limited to genes that are highly expressed by the host cell. The percent deviation of the frequency of preferred codon usage for a synthetic gene from that employed by a host cell is calculated first by determining the percent deviation of the frequency of usage of a single codon from that of the host cell followed by obtaining the average deviation over all codons. As defined herein, this calculation includes unique codons (i.e., ATG and TGG). In general terms, the overall average deviation of the codon usage of an optimized gene from that of a host cell is calculated using the equation $1A = n = 1 \sum X_n - Y_n X_n \text{ times } 100 \sum$ where X_n = frequency of usage for codon n in the host cell; Y_n = frequency of usage for codon n in the synthetic gene; n represents an individual codon that specifies an amino acid; and the total number of codons is Z. The overall deviation of the frequency of codon usage, A, for all amino acids should preferably be less than about 25%, and more preferably less than about 10%.

0235.0.3 Hence, a SRP nucleic acid can be optimized such that its distribution frequency of codon usage deviates, preferably, no more than 25% from that of highly expressed plant genes and, more preferably, no more than about 10%. In addition, consideration is given to the percentage G+C content of the degenerate third base (monocotyledons appear to favor G+C in this position, whereas dicotyledons do not). It is also recognized that the XCG (where X is A, T, C, or G) nucleotide is the least preferred codon in dicots whereas the XTA codon is avoided in both monocots and dicots. Optimized SRP nucleic acids of this invention also preferably have CG and TA doublet avoidance indices closely approximating those of the chosen host plant (i.e., *Brassica napus*, *Glycine max*, or *Oryza sativa*). More preferably these indices deviate from that of the host by no more than about 10-15%.

0236.0.3 In addition to the nucleic acid molecules encoding the SRPs described above, another aspect of the invention pertains to isolated nucleic acid molecules that are antisense thereto. Antisense polynucleotides are thought to inhibit gene expression of a target polynucleotide by specifically binding the target polynucleotide and interfering with transcription, splicing, transport, translation, and/or stability of the target polynucleotide. Methods are described in the prior art for targeting the antisense polynucleotide to the chromosomal DNA, to a primary RNA transcript, or to a processed mRNA. Preferably, the target regions include splice sites, translation initiation codons, translation termination codons, and other sequences within the open reading frame.

0237.0.3 The term "antisense," for the purposes of the invention, refers to a nucleic acid comprising a polynucleotide that is sufficiently complementary to all or a portion of a gene, primary transcript, or processed mRNA, so as to interfere with expression of the endogenous gene. "Complementary" polynucleotides are those that are capable of base pairing according to the standard Watson-Crick complementarity rules. Specifically, purines will base pair with pyrimidines to form a combination of guanine paired with cytosine (G:C) and adenine paired with either thymine (A:T) in the case of DNA, or adenine paired with uracil (A:U) in the case of RNA. It is understood that two polynucleotides may hybridize to each other even if they are not completely complementary to each other, provided that each has at least one region that is substantially complementary to the other. The term "antisense nucleic acid" includes single stranded RNA as well as double-stranded DNA expression cassettes that can be transcribed to produce an antisense RNA. "Active" antisense nucleic acids are antisense RNA molecules that are capable of selectively hybridizing with a primary transcript or mRNA encoding a polypeptide having at least 80% sequence identity with the polypeptide of Fig. 1a, 1b or 1c.

0238.0.3 The antisense nucleic acid can be complementary to an entire SRP coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding a SRP. The term "coding region" refers to the region of the nucleotide sequence comprising codons that are translated into amino acid residues. In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding a SRP. The term "noncoding region" refers to 5' and 3' sequences that flank the coding region that are not translated into amino acids (i.e., also referred to as 5' and 3' untranslated regions). The antisense nucleic acid molecule can be complementary to the entire coding region of SRP mRNA, but more preferably is an oligonucleotide which is antisense to only a

portion of the coding or noncoding region of SRP mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of PKSRP mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. Typically, the antisense molecules of the present invention comprise an RNA having 60-100% sequence identity with at least 14 consecutive nucleotides of one of the nucleic acid of Fig. 1a, 1b or 1c. Preferably, the sequence identity will be at least 70%, more preferably at least 75%, 80%, 85%, 90%, 95%, 98% and most preferably 99%.

0239.0.3 An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylquosine, inosine, N8-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylquosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, quosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

0240.0.3 In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier et al., 1987, Nucleic Acids. Res. 15:6625-6641). The antisense nucleic acid molecule can also comprise a

2'-o-methylribonucleotide (Inoue et al., 1987, Nucleic Acids Res. 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

0241.0.3 The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a SRP to thereby inhibit expression of the polypeptide, e.g., by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic (including plant) promoter are preferred.

0242.0.3 As an alternative to antisense polynucleotides, ribozymes, sense polynucleotides, or double stranded RNA (dsRNA) can be used to reduce expression of a SRP polypeptide. By "ribozyme" is meant a catalytic RNA-based enzyme with ribonuclease activity which is capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which it has a complementary region. Ribozymes (e.g., hammerhead ribozymes described in Haselhoff and Gerlach, 1988, Nature 334:585-591) can be used to catalytically cleave SRP mRNA transcripts to thereby inhibit translation of SRP mRNA. A ribozyme having specificity for a SRP-encoding nucleic acid can be designed based upon the nucleotide sequence of a SRP cDNA, as disclosed herein (i.e., Fig. 1a, 1b or 1c) or on the basis of a heterologous sequence to be isolated according to methods taught in this invention. For example, a derivative of a Tetrahymena I-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a SRP-encoding mRNA. See, e.g., U.S. Patent Nos. 4,987,071 and 5,116,742 to Cech et al. Alternatively, SRP mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W., 1993, Science 261:1411-1418. In preferred embodiments, the ribozyme will contain a portion having at least 7, 8, 9, 10, 12, 14, 16, 18 or 20 nucleotides, and more preferably 7 or 8 nucleotides, that have 100% complementarity to a portion of the target RNA. Methods

for making ribozymes are known to those skilled in the art. See, e.g., U.S. Patent Nos. 6,025,167; 5,773,260; and 5,496,698.

0243.0.3 The term "dsRNA," as used herein, refers to RNA hybrids comprising two strands of RNA. The dsRNAs can be linear or circular in structure. In a preferred embodiment, dsRNA is specific for a polynucleotide encoding either the polypeptide of Fig. 1a, 1b or 1c or a polypeptide having at least 70% sequence identity with a polypeptide of Fig. 1a, 1b or 1c. The hybridizing RNAs may be substantially or completely complementary. By "substantially complementary," is meant that when the two hybridizing RNAs are optimally aligned using the BLAST program as described above, the hybridizing portions are at least 95% complementary. Preferably, the dsRNA will be at least 100 base pairs in length. Typically, the hybridizing RNAs will be of identical length with no over hanging 5' or 3' ends and no gaps. However, dsRNAs having 5' or 3' overhangs of up to 100 nucleotides may be used in the methods of the invention.

0244.0.3 The dsRNA may comprise ribonucleotides or ribonucleotide analogs, such as 2'-O-methyl ribosyl residues, or combinations thereof. See, e.g., U.S. Patent Nos. 4,130,641 and 4,024,222. A dsRNA polyriboninosinic acid:polyribocytidylic acid is described in U.S. patent 4,283,393. Methods for making and using dsRNA are known in the art. One method comprises the simultaneous transcription of two complementary DNA strands, either *in vivo*, or in a single *in vitro* reaction mixture. See, e.g., U.S. Patent No. 5,795,715. In one embodiment, dsRNA can be introduced into a plant or plant cell directly by standard transformation procedures. Alternatively, dsRNA can be expressed in a plant cell by transcribing two complementary RNAs.

0245.0.3 Other methods for the inhibition of endogenous gene expression, such as triple helix formation (Moser et al., 1987, Science 238:645-650 and Cooney et al., 1988, Science 241:456-458) and cosuppression (Napoli et al., 1990, The Plant Cell 2:279-289) are known in the art. Partial and full-length cDNAs have been used for the cosuppression of endogenous plant genes. See, e.g., U.S. Patent Nos. 4,801,340, 5,034,323, 5,231,020, and 5,283,184; Van der Krol et al., 1990, The Plant Cell 2:291-299; Smith et al., 1990, Mol. Gen. Genetics 224:177-181 and Napoli et al., 1990, The Plant Cell 2:279-289.

0246.0.3 For sense suppression, it is believed that introduction of a sense polynucleotide blocks transcription of the corresponding target gene. The sense polynucleotide will have at least 65% sequence identity with the target plant gene or RNA. Preferably, the percent identity is at least 80%, 90%, 95% or more. The introduced sense polynucleotide need not be full length relative to the target gene or transcript. Preferably, the sense polynucleotide will have at least 65% sequence

identity with at least 100 consecutive nucleotides of one of the nucleic acids of Fig. 1a, 1b or 1c. The regions of identity can comprise introns and and/or exons and untranslated regions. The introduced sense polynucleotide may be present in the plant cell transiently, or may be stably integrated into a plant chromosome or extrachromosomal replicon.

0247.0.1 Moreover, nucleic acid molecules encoding SRP from the same or other species such as SRP analogs, orthologs and paralogs, are intended to be within the scope of the present invention. As used herein, the term "analogs" refers to two nucleic acids that have the same or similar function, but that have evolved separately in unrelated organisms. As used herein, the term "orthologs" refers to two nucleic acids from different species that have evolved from a common ancestral gene by speciation. Normally, orthologs encode proteins having the same or similar functions. As also used herein, the term "paralogs" refers to two nucleic acids that are related by duplication within a genome. Paralogs usually have different functions, but these functions may be related (Tatusov, R.L. et al. 1997 Science 278(5338):631-637). Analogs, orthologs and paralogs of a naturally occurring stress related protein can differ from the naturally occurring stress related protein by post-translational modifications, by amino acid sequence differences, or by both. Post-translational modifications include in vivo and in vitro chemical derivatization of polypeptides e.g., acetylation, carboxylation, phosphorylation or glycosylation, and such modifications may occur during polypeptide synthesis or processing or following treatment with isolated modifying enzymes. In particular, orthologs of the invention will generally exhibit at least 80-85%, more preferably 90%, 91%, 92%, 93%, 94%, and most preferably 95%, 96%, 97%, 98% or even 99% identity or homology with all or part of a naturally occurring stress related protein amino acid sequence and will exhibit a function similar to a stress related protein. Orthologs of the present invention are also preferably capable of participating in the stress response in plants.

0248.0.1 In addition to naturally-occurring variants of a stress related protein sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into a nucleotide sequence of the Fig. 1a, 1b or 1c, thereby leading to changes in the amino acid sequence of the encoded stress related protein, without altering the functional ability of the stress related protein or enhancing the functional ability of the stress related protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Fig 1. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of stress related proteins without altering the activity thereof, whereas an "essential" amino acid residue is

required for stress related protein activity. Other amino acid residues, however, (e.g., those that are not conserved or only semi-conserved in the domain having SRP activity) may not be essential for activity and thus are likely to be amenable to alteration without altering SRP activity.

- 5 **0249.0.1** Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding stress related proteins that contain changes in amino acid residues that are not essential for stress related protein activity. Such SRP differ in amino acid sequence from a sequence Fig. 1a, 1b or 1c, yet retain at least one of the stress related protein activities described herein. In one embodiment, the isolated
10 nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Fig. 1a, 1b or 1c. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences of the Fig. 1a, 1b or 1c, more preferably at least about 60 - 70% homologous to one of the
15 sequences of the Fig. 1a, 1b or 1c, even more preferably at least about 70 - 80%, 80 - 90%, more preferably 90%, 91%, 92%, 93%, 94% homologous to one of the sequences of the Fig. 1a, 1b or 1c and most preferably at least about 95%, 97%, 98%, or 99% homologous to one of the sequences of the Fig. 1a, 1b or 1c. The preferred stress related protein homologs of the present invention are preferably capable of
20 participating in the stress tolerance response in a plant. The homology (= identity) was calculated over the entire amino acid range. The program used was PileUp (J. Mol. Evolution., 25 (1987), 351-360, Higgins et al., CABIOS, 5 1989: 151-153).

- 0250.0.1** Homologs of the sequences given in Fig. 1a, 1b or 1c are furthermore to be understood as meaning, for example, homologs, analogs, orthologs and paralogs
25 which have at least 30% homology (= identity) at the derived amino acid level, preferably at least 50 %, 60 %, 70 % or 80 % homology, especially preferably at least 85 % homology, very especially preferably 90 % 91%, 92%, 93%, 94% homology, most preferably 95 %, 96 %, 97 %, 98 % or 99 % homology. The homology (= identity) was calculated over the entire amino acid range. The program used was PileUp (J. Mol.
30 Evolution., 25 (1987), 351 - 360, Higgins et al., CABIOS, 5 1989: 151 - 153) or the program Gap and BestFit [Needleman and Wunsch (J. Mol. Biol. 48; 443 - 453 (1970) and Smith and Waterman respectively (Adv. Appl. Math. 2; 482 - 489 (1981))] which are part of the GCG software package [Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA 53711 (1991)]. The above mentioned percentages of
35 sequence homology are calculated with the program BestFit or Gap, preferably Gap, over the total sequence length with the following parameters used: Gap Weight: 8, Length Weight: 2.

0251.0.1 Variants shall also be encompassed, in particular, functional variants which can be obtained from the sequence shown in the Fig. 1a, 1b or 1c by means of deletion, insertion or substitution of nucleotides, the enzymatic activity of the derived synthetic proteins being retained or enhanced.

5 **0252.0.1** An isolated nucleic acid molecule encoding a stress related protein homologous to a protein sequence of Fig. 1a, 1b or 1c can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Fig. 1a, 1b or 1c such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one
10 of the sequences of Fig. 1a, 1b or 1c by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Another route to the mutagenesis of enzymes, disclosed in the European Publication EP-A-0 909 821, is a method using the specific *Escherichia coli* strain XL1-Red to generate mutants and altered the enzymic activity.

15 **0253.0.1** Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain.

0254.0.1 Families of amino acid residues having similar side chains have been
20 defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g.,
25 threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a stress related protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a stress related protein coding sequence, such as by
30 saturation mutagenesis, and the resultant mutants can be screened for a stress related protein activity as described herein to identify mutants that retain stress related protein activity or show enhanced stress related protein activity. Following mutagenesis of one of the sequences of the nucleic acid of Fig. 1a, 1b or 1c, the encoded protein can be expressed recombinantly and the activity of the protein can be determined by analyzing
35 the stress tolerance of a plant expressing the protein as described in the examples below.

0255.0.1 A useful method to ascertain the level of transcription of the gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel et al., 1988 Current Protocols in Molecular Biology, Wiley: New York). This information at least partially demonstrates the degree of transcription of the gene. Total cellular RNA can be prepared from cells, tissues or organs by several methods, all well-known in the art, such as that described in Bormann, E.R. et al., 1992 Mol. Microbiol. 6:317-326. To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed. These techniques are well known to one of ordinary skill in the art (see, for example, Ausubel et al., 1988 Current Protocols in Molecular Biology, Wiley: New York).

0256.0.1 The present invention also relates to a plant expression cassette comprising a SRP coding nucleic acid selected from the group comprising sequences of SEQ IDs No. XXX and/or homologs or parts thereof operatively linked to regulatory sequences and/or targeting sequences.

0257.0.1 Further, object of the invention is an expression vector comprising a SRP encoding nucleic acid selected from the group comprising sequences of the nucleic acid of Fig. 1a, 1b or 1c and/or homologs or parts thereof or a plant expression cassette as described above, whereby expression of the SRP coding nucleic acid in a host cell results in increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a corresponding non-transformed wild type host cell.

0258.0.1 The invention further provides an isolated recombinant expression vector comprising a stress related protein encoding nucleic acid as described above, wherein expression of the vector or stress related protein encoding nucleic acid, respectively in a host cell results in increased tolerance and/or resistance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to the corresponding non-transformed wild type of the host cell. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Further types of vectors can be linearized nucleic acid sequences, such as transposons, which are pieces of DNA which can copy and insert themselves. There have been 2 types of transposons found: simple transposons, known as Insertion Sequences and composite transposons, which can have several genes as well as the genes that are required for transposition.

0259.0.1 Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

0260.0.1 A plant expression cassette preferably contains regulatory sequences capable of driving gene expression in plant cells and operably linked so that each sequence can fulfill its function, for example, termination of transcription by polyadenylation signals. Preferred polyadenylation signals are those originating from *Agrobacterium tumefaciens* T-DNA such as the gene 3 known as octopine synthase of the Ti-plasmid pTiACH5 (Gielen et al., 1984 EMBO J. 3:835) or functional equivalents thereof but also all other terminators functionally active in plants are suitable.

0261.0.1 As plant gene expression is very often not limited on transcriptional levels, a plant expression cassette preferably contains other operably linked sequences like translational enhancers such as the overdrive-sequence containing the 5'-untranslated leader sequence from tobacco mosaic virus enhancing the protein per RNA ratio (Gallie et al., 1987 Nucl. Acids Research 15:8693-8711).

0262.0.1 Plant gene expression has to be operably linked to an appropriate promoter conferring gene expression in a timely, cell or tissue specific manner. Preferred are promoters driving constitutive expression (Benfey et al., 1989 EMBO J. 8:2195-2202) like those derived from plant viruses like the 35S CaMV (Franck et al., 1980 Cell 21:285-294), the 19S CaMV (see also U.S. Patent No. 5352605 and PCT Application No. WO 8402913) or plant promoters like those from Rubisco small subunit described in U.S. Patent No. 4,962,028.

0263.0.1 Additional advantageous regulatory sequences are, for example, included in the plant promoters such as CaMV/35S [Franck et al., Cell 21 (1980) 285 - 294], PRP1 [Ward et al., Plant Mol. Biol. 22 (1993)], SSU, OCS, lib4, usp, STLS1, B33, LEB4, nos or in the ubiquitin, napin or phaseolin promoter. Also advantageous in this connection are inducible promoters such as the promoters described in EP-A-0

388 186 (benzyl sulfonamide inducible), Plant J. 2, 1992: 397 - 404 (Gatz et al.,
Tetracyclin inducible), EP-A-0 335 528 (abscisic acid inducible) or WO 93/21334
(ethanol or cyclohexanol inducible). Additional useful plant promoters are the cytosolic
FBPase promoter or ST-LSI promoter of the potato (Stockhaus et al., EMBO J. 8,
5 1989, 2445), the phosphorybosyl pyrophosphate amido transferase promoter of
Glycine max (gene bank accession No. U87999) or the noden specific promoter
described in EP-A-0 249 676. Additional particularly advantageous promoters are seed
specific promoters which can be used for monocotyledones or dikotyledones and are
described in US 5,608,152 (napin promoter from rapeseed), WO 98/45461 (phaseolin
10 promoter from Arabidopsis), US 5,504,200 (phaseolin promoter from Phaseolus
vulgaris), WO 91/13980 (Bce4 promoter from Brassica) and Bacumlein et al., Plant J.,
2, 2, 1992: 233-239 (LEB4 promoter from leguminosa). Said promoters are useful in
dikotyledones. The following promoters are useful for example in monocotyledones lpt-
2- or lpt-1- promoter from barley (WO 95/15389 and WO 95/23230) or hordein
15 promoter from barley. Other useful promoters are described in WO 99/16890.

0264.0.1 It is possible in principle to use all natural promoters with their regulatory
sequences like those mentioned above for the novel process. It is also possible and
advantageous in addition to use synthetic promoters.

0265.0.1 The gene construct may also comprise further genes which are to be
20 inserted into the organisms and which are for example involved in stress resistance. It
is possible and advantageous to insert and express in host organisms regulatory genes
such as genes for inducers, repressors or enzymes which intervene by their enzymatic
activity in the regulation, or one or more or all genes of a biosynthetic pathway. These
genes can be heterologous or homologous in origin. The inserted genes may have
25 their own promoter or else be under the control of same promoter as the sequences of
the nucleic acid of Fig. 1a, 1b or 1c or their homologs.

0266.0.1 The gene construct advantageously comprises, for expression of the
other genes present, additionally 3' and/or 5' terminal regulatory sequences to enhance
expression, which are selected for optimal expression depending on the selected host
30 organism and gene or genes.

0267.0.1 These regulatory sequences are intended to make specific expression of
the genes and protein expression possible as mentioned above. This may mean,
depending on the host organism, for example that the gene is expressed or
overexpressed only after induction, or that it is immediately expressed and/or
35 overexpressed.

0268.0.1 The regulatory sequences or factors may moreover preferably have a
beneficial effect on expression of the introduced genes, and thus increase it. It is

possible in this way for the regulatory elements to be enhanced advantageously at the transcription level by using strong transcription signals such as promoters and/or enhancers. However, in addition, it is also possible to enhance translation by, for example, improving the stability of the mRNA.

- 5 **0268.0.1** Other preferred sequences for use in plant gene expression cassettes are targeting-sequences necessary to direct the gene product in its appropriate cell compartment (for review see Kermode, 1996 Crit. Rev. Plant Sci. 15(4):285-423 and references cited therein) such as the vacuole, the nucleus, all types of plastids like amyloplasts, chloroplasts, chromoplasts, the extracellular space, mitochondria, the
10 endoplasmic reticulum, oil bodies, peroxisomes and other compartments of plant cells.

0270.0.1 Plant gene expression can also be facilitated via an inducible promoter (for review see Gatz, 1997 Annu. Rev. Plant Physiol. Plant Mol. Biol. 48:89-108). Chemically inducible promoters are especially suitable if gene expression is wanted to occur in a time specific manner.

- 15 **0271.0.1** Table 1 lists several examples of promoters that may be used to regulate transcription of the stress related protein nucleic acid coding sequences.

0272.0.1 Tab. 1: Examples of Tissue-specific and Stress inducible promoters in plants

Expression	Reference
Cor78- Cold, drought, salt, ABA, wounding-inducible	Ishitani, <i>et al.</i> , Plant Cell 9:1935-1949 (1997). Yamaguchi-Shinozaki and Shinozaki, Plant Cell 8:251-264 (1994).
Rc12A - Cold, dehydration-Inducible	Capel <i>et al.</i> , Plant Physiol 115:568-576 (1997)
Rd22 - Drought, salt	Yamaguchi-Shinozaki and Shinozaki, Mol Gen Genet 238:17-25 (1993).
Cor15A - Cold, dehydration, ABA	Baker <i>et al.</i> , Plant Mol. Biol. 24:701-713 (1994).
GH3- Auxin inducible	Liu <i>et al.</i> , Plant Cell 6:645-657 (1994)
ARSK1-Root, salt inducible	Hwang and Goodman, Plant J 8:37-43 (1995).
PtxA - Root, salt inducible	GenBank accession X67427

SbHRGP3 - Root specific	Ahn <i>et al.</i> , Plant Cell 8:1477-1490 (1998).
KST1 - Guard cell specific	Plesch <i>et al.</i> , Plant Journal. 28(4):455-64, (2001)
KAT1 - Guard cell specific	Plesch <i>et al.</i> , Gene 249:83-89 (2000) Nakamura <i>et al.</i> , Plant Physiol. 109:371-374 (1995)
salicylic acid inducible	PCT Application No. WO 95/19443
tetracycline inducible	Gatz <i>et al.</i> Plant J. 2:397-404 (1992)
Ethanol Inducible	PCT Application No. WO 93/21334
pathogen inducible PRP1	Ward <i>et al.</i> , 1993 Plant. Mol. Biol. 22:361-366
heat inducible hsp80	U.S. Patent No. 5187287
cold inducible alpha-amylase	PCT Application No. WO 95/12814
Wound-inducible pinII	European Patent No. 375091
RD29A - salt-inducible	Yamaguchi-Shinozaki <i>et al.</i> (1993) Mol. Gen. Genet. 238:331-340
plastid-specific viral RNA-polymerase	PCT Application No. WO 95/16783 and. WO 97/06250

0273.0.1 Other promoters, e.g. superpromotor (Ni *et al.*, Plant Journal 7, 1995: 661-676), Ubiquitin promoter (Callis *et al.*, J. Biol. Chem., 1990, 265: 12486-12493; US 5,510,474; US 6,020,190; Kawalleck *et al.*, Plant. Molecular Biology, 1993, 21: 673-684) or 34S promoter (GenBank Accession numbers M59930 and X10673) were similar useful for the present invention and are known to a person skilled in the art.

0274.0.3 Developmental stage-preferred promoters are preferentially expressed at certain stages of development. Tissue and organ preferred promoters include those that are preferentially expressed in certain tissues or organs, such as leaves, roots, seeds, or xylem. Examples of tissue preferred and organ preferred promoters include, but are not limited to fruit-preferred, ovule-preferred, male tissue-preferred, seed-

preferred, integument-preferred, tuber-preferred, stalk-preferred, pericarp-preferred, and leaf-preferred, stigma-preferred, pollen-preferred, anther-preferred, a petal-preferred, sepal-preferred, pedicel-preferred, silique-preferred, stem-preferred, root-preferred promoters, and the like. Seed preferred promoters are preferentially
5 expressed during seed development and/or germination. For example, seed preferred promoters can be embryo-preferred, endosperm preferred, and seed coat-preferred. See Thompson et al., 1989, BioEssays 10:108. Examples of seed preferred promoters include, but are not limited to, cellulose synthase (celA), Cim1, gamma-zein, globulin-1, maize 19 kD zein (cZ19B1), and the like.

10 **0275.0.3** Other promoters useful in the expression cassettes of the invention include, but are not limited to, the major chlorophyll a/b binding protein promoter, histone promoters, the Ap3 promoter, the β -conglycin promoter, the napin promoter, the soybean lectin promoter, the maize 15kD zein promoter, the 22kD zein promoter, the 27kD zein promoter, the g-zein promoter, the waxy, shrunken 1, shrunken 2 and
15 bronze promoters, the Zm13 promoter (U.S. Patent No. 5,086,169), the maize polygalacturonase promoters (PG) (U.S. Patent Nos. 5,412,085 and 5,545,546), and the SGB3 promoter (U.S. Patent No. 5,470,359), as well as synthetic or other natural promoters.

0276.0.3 Additional flexibility in controlling heterologous gene expression in plants
20 may be obtained by using DNA binding domains and response elements from heterologous sources (*i.e.*, DNA binding domains from non-plant sources). An example of such a heterologous DNA binding domain is the LexA DNA binding domain (Brent and Ptashne, 1985, Cell 43:729-736).

0277.0.3 The invention further provides a recombinant expression vector
25 comprising a SRP DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to a SRP mRNA. Regulatory sequences operatively linked to a nucleic acid molecule cloned in the antisense orientation can be
30 chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types. For instance, viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific, or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid, or attenuated virus wherein antisense nucleic acids
35 are produced under the control of a high efficiency regulatory region. The activity of the regulatory region can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense

genes, see Weintraub, H. et al., 1986, Antisense RNA as a molecular tool for genetic analysis, Reviews - Trends in Genetics, Vol. 1(1), and Mol et al., 1990, FEBS Letters 268:427-430.

0279.0.3 Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but they also apply to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein. A host cell can be any prokaryotic or eukaryotic cell. For example, a SRP can be expressed in bacterial cells such as *C. glutamicum*, yeast, *E. coli*, insect cells, fungal cells, or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells), algae, ciliates, plant cells, fungi, or other microorganisms like *C. glutamicum*. Other suitable host cells are known to those skilled in the art.

0280.0.3 A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (i.e., express) a SRP. Accordingly, the invention further provides methods for producing SRPs using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a SRP has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered SRP) in a suitable medium until SRP is produced. In another embodiment, the method further comprises isolating SRPs from the medium or the host cell.

0281.0.3 Another aspect of the invention pertains to isolated SRPs, and biologically active portions thereof. An "isolated" or "purified" polypeptide or biologically active portion thereof is free of some of the cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of SRP in which the polypeptide is separated from some of the cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of a SRP having less than about 30% (by dry weight) of non-SRP material (also referred to herein as a "contaminating polypeptide"), more preferably less than about 20% of non-SRP material, still more preferably less than about 10% of non-SRP material, and most preferably less than about 5% non-PKSRP material.

- 0282.0.3** When the SRP or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of SRP in which the polypeptide is separated from chemical precursors or other chemicals that are involved in the synthesis of the polypeptide. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of a SRP having less than about 30% (by dry weight) of chemical precursors or non-SRP chemicals, more preferably less than about 20% chemical precursors or non-SRP chemicals, still more preferably less than about 10% chemical precursors or non-SRP chemicals, and most preferably less than about 5% chemical precursors or non-SRP chemicals. In preferred embodiments, isolated polypeptides, or biologically active portions thereof, lack contaminating polypeptides from the same organism from which the SRP is derived. Typically, such polypeptides are produced by recombinant expression of, for example, a *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* SRP in plants other than *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*, or microorganisms such as *C. glutamicum*, ciliates, algae or fungi.
- 0283.0.3** The nucleic acid molecules, polypeptides, polypeptide homologs, fusion polypeptides, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* and related organisms; mapping of genomes of organisms related to *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*; identification and localization of *Saccharomyces cerevisiae*, *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa* sequences of interest; evolutionary studies; determination of SRP regions required for function; modulation of a SRP activity; modulation of the metabolism of one or more cell functions; modulation of the transmembrane transport of one or more compounds; modulation of stress resistance; and modulation of expression of SRP nucleic acids.
- 0284.0.3** The SRP nucleic acid molecules of the invention are also useful for evolutionary and polypeptide structural studies. The metabolic and transport processes in which the molecules of the invention participate are utilized by a wide variety of prokaryotic and eukaryotic cells; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are

conserved and which are not, which may aid in determining those regions of the polypeptide that are essential for the functioning of the enzyme. This type of determination is of value for polypeptide engineering studies and may give an indication of what the polypeptide can tolerate in terms of mutagenesis without losing function.

0285.0.3 Manipulation of the SRP nucleic acid molecules of the invention may result in the production of SRPs having functional differences from the wild-type SRPs. These polypeptides may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

0286.0.3 There are a number of mechanisms by which the alteration of a SRP of the invention may directly affect stress response and/or stress tolerance. In the case of plants expressing SRPs, increased transport can lead to improved salt and/or solute partitioning within the plant tissue and organs. By either increasing the number or the activity of transporter molecules which export ionic molecules from the cell, it may be possible to affect the salt tolerance of the cell.

0287.0.3 The effect of the genetic modification in plants, *C. glutamicum*, fungi, algae, or ciliates on stress tolerance can be assessed by growing the modified microorganism or plant under less than suitable conditions and then analyzing the growth characteristics and/or metabolism of the plant. Such analysis techniques are well known to one skilled in the art, and include dry weight, wet weight, polypeptide synthesis, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, etc. (Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al., 1993 Biotechnology, vol. 3, Chapter III: Product recovery and purification, page 469-714, VCH: Weinheim; Belter, P.A. et al., 1988, Bioprocess: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S., 1992, Recovery processes for biological materials, John Wiley and Sons; Shaelwitz, J.A. and Henry, J.D., 1988, Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J., 1989, Separation and purification techniques in biotechnology, Noyes Publications).

0288.0.3 For example, yeast expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into *Saccharomyces cerevisiae* using standard protocols. The resulting transgenic cells can then be assayed for fail or alteration of their tolerance to drought, salt, and temperature stress. Similarly, plant expression vectors comprising the nucleic acids disclosed herein, or fragments thereof, can be constructed and transformed into an appropriate

plant cell such as *Arabidopsis*, soy, rape, maize, wheat, *Medicago truncatula*, etc., using standard protocols. The resulting transgenic cells and/or plants derived therefrom can then be assayed for fail or alteration of their tolerance to drought, salt, temperature stress, and lodging.

- 5 **0289.0.3** The engineering of one or more SRP genes of the invention may also result in SRPs having altered activities which indirectly impact the stress response and/or stress tolerance of algae, plants, ciliates, or fungi, or other microorganisms like *C. glutamicum*. For example, the normal biochemical processes of metabolism result in the production of a variety of products (e.g., hydrogen peroxide and other reactive
10 oxygen species) which may actively interfere with these same metabolic processes. For example, peroxynitrite is known to nitrate tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T., 1999, Curr. Opin. Chem. Biol. 3(2):226-235). While these products are typically excreted, cells can be genetically altered to transport more products than is typical for a wild-type cell. By
15 optimizing the activity of one or more PKSRPs of the invention which are involved in the export of specific molecules, such as salt molecules, it may be possible to improve the stress tolerance of the cell.

- 0290.0.3** Additionally, the sequences disclosed herein, or fragments thereof, can be used to generate knockout mutations in the genomes of various organisms, such as
20 bacteria, mammalian cells, yeast cells, and plant cells (Girke, T., 1998, The Plant Journal 15:39-48). The resultant knockout cells can then be evaluated for their ability or capacity to tolerate various stress conditions, their response to various stress conditions, and the effect on the phenotype and/or genotype of the mutation. For other methods of gene inactivation, see U.S. Patent No. 6,004,804 "Non-Chimeric Mutational Vectors" and Puttaraju et al., 1999, Spliceosome-mediated RNA *trans*-splicing as a tool
25 for gene therapy, Nature Biotechnology 17:246-252.

- 0291.0.3** The aforementioned mutagenesis strategies for SRPs resulting in increased stress resistance are not meant to be limiting; variations on these strategies will be readily apparent to one skilled in the art. Using such strategies, and
30 incorporating the mechanisms disclosed herein, the nucleic acid and polypeptide molecules of the invention may be utilized to generate algae, ciliates, plants, fungi, or other microorganisms like *C. glutamicum* expressing mutated PKSRP nucleic acid and polypeptide molecules such that the stress tolerance is improved.

- 0292.0.3** The present invention also provides antibodies that specifically bind to a
35 SRP, or a portion thereof, as encoded by a nucleic acid described herein. Antibodies can be made by many well-known methods (See, e.g. Harlow and Lane, "Antibodies; A Laboratory Manual," Cold Spring Harbor Laboratory, Cold Spring Harbor, New York,

(1988)). Briefly, purified antigen can be injected into an animal in an amount and in intervals sufficient to elicit an immune response. Antibodies can either be purified directly, or spleen cells can be obtained from the animal. The cells can then fused with an immortal cell line and screened for antibody secretion. The antibodies can be used to screen nucleic acid clone libraries for cells secreting the antigen. Those positive clones can then be sequenced. See, for example, Kelly et al., 1992, *Bio/Technology* 10:163-167; Debbington et al., 1992, *Bio/Technology* 10:168-175.

0283.0.3 The phrases "selectively binds" and "specifically binds" with the polypeptide refer to a binding reaction that is determinative of the presence of the polypeptide in a heterogeneous population of polypeptides and other biologics. Thus, under designated immunoassay conditions, the specified antibodies bound to a particular polypeptide do not bind in a significant amount to other polypeptides present in the sample. Selective binding of an antibody under such conditions may require an antibody that is selected for its specificity for a particular polypeptide. A variety of immunoassay formats may be used to select antibodies that selectively bind with a particular polypeptide. For example, solid-phase ELISA immunoassays are routinely used to select antibodies selectively immunoreactive with a polypeptide. See Harlow and Lane, "Antibodies, A Laboratory Manual," Cold Spring Harbor Publications, New York, (1988), for a description of immunoassay formats and conditions that could be used to determine selective binding.

0294.0.3 In some instances, it is desirable to prepare monoclonal antibodies from various hosts. A description of techniques for preparing such monoclonal antibodies may be found in Stiles et al., eds., "Basic and Clinical Immunology," (Lange Medical Publications, Los Altos, Calif., Fourth Edition) and references cited therein, and in Harlow and Lane, "Antibodies, A Laboratory Manual," Cold Spring Harbor Publications, New York, (1988).

0295.0.1 Gene expression in plants is regulated by the interaction of protein transcription factors with specific nucleotide sequences within the regulatory region of a gene. A common type of transcription factor contains zinc finger (ZF) motifs. Each ZF module is approximately 30 amino acids long folded around a zinc ion. The DNA recognition domain of a ZF protein is a α -helical structure that inserts into the major groove of the DNA double helix. The module contains three amino acids that bind to the DNA with each amino acid contacting a single base pair in the target DNA sequence. ZF motifs are arranged in a modular repeating fashion to form a set of fingers that recognize a contiguous DNA sequence. For example, a three-fingered ZF motif will recognize 9 bp of DNA. Hundreds of proteins have been shown to contain ZF motifs with between 2 and 37 ZF modules in each protein (Isalan M, et al., 1998 *Biochemistry*

37(35):12026-33; Moore M, et al., 2001 Proc. Natl. Acad. Sci. USA 98(4):1432-1436 and 1437-1441; US patents US 6007988 and US 6013453).

5 **0296.0.1** The regulatory region of a plant gene contains many short DNA sequences (cis-acting elements) that serve as recognition domains for transcription factors, including ZF proteins. Similar recognition domains in different genes allow the coordinate expression of several genes encoding enzymes in a metabolic pathway by common transcription factors. Variation in the recognition domains among members of a gene family facilitates differences in gene expression within the same gene family, for example, among tissues and stages of development and in response to environmental conditions.

10 **0297.0.1** Typical ZF proteins contain not only a DNA recognition domain but also a functional domain that enables the ZF protein to activate or repress transcription of a specific gene. Experimentally, an activation domain has been used to activate transcription of the target gene (US patent 5789538 and patent application WO9519431), but it is also possible to link a transcription repressor domain to the ZF and thereby inhibit transcription (patent applications WO00/47754 and WO2001002019). It has been reported that an enzymatic function such as nucleic acid cleavage can be linked to the ZF (patent application WO00/20622).

15 **0298.0.1** The invention provides a method that allows one skilled in the art to isolate the regulatory region of one or more stress related protein encoding genes from the genome of a plant cell and to design zinc finger transcription factors linked to a functional domain that will interact with the regulatory region of the gene. The interaction of the zinc finger protein with the plant gene can be designed in such a manner as to alter expression of the gene and preferably thereby alter metabolic activity to confer increased (or decreased) tolerance of abiotic stress such as drought. The invention provides a method of producing a transgenic plant with a transgene encoding this designed transcription factor, or alternatively a natural transcription factor, that modifies transcription of the Stress-Related Protein, particularly stress related protein gene to provide increased tolerance of environmental stress, which is preferably achieved by altering metabolic activity. Such a regulation of plant genes by artificial polydactyl zinc fingers has been demonstrated by Ordiz et al. (Regulation of transgene Expression in plants with polydactyl zinc finger transcription factors, Ordiz et al., PNAS, 99 (20) 13290-13295, 2002) or Guan et al. (Heritable endogenous gene regulation in plants with designed polydactyl zinc finger transcription factors, PNAS, Vol. 99 (20), 13296-13301 (2002)).

20 **0299.0.1** In particular, the invention provides a method of producing a transgenic plant with a stress related protein coding nucleic acid, wherein expression of the

nucleic acid(s) in the plant results in increased tolerance to environmental stress, which is preferably achieved by altering metabolic activity, as compared to a wild type plant comprising: (a) transforming a plant cell with an expression vector comprising a stress related protein encoding nucleic acid, and (b) generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a wild type plant. For such plant transformation, binary vectors such as pBinAR can be used (Höfigen and Willmitzer, 1990 Plant Science 66:221-230). Moreover suitable binary vectors are for example pBIN19, pBI101, pGPTV or pPZP (Hajdukiewicz, P. et al., 1994, Plant Mol. Biol., 25: 989-994).

0300.0.1 Construction of the binary vectors can be performed by ligation of the cDNA into the T-DNA. 5' to the cDNA a plant promoter activates transcription of the cDNA. A polyadenylation sequence is located 3' to the cDNA. Tissue-specific expression can be achieved by using a tissue specific promoter as listed above. Also, any other promoter element can be used. For constitutive expression within the whole plant, the CaMV 35S promoter can be used. The expressed protein can be targeted to a cellular compartment using a signal peptide, for example for plastids, mitochondria or endoplasmic reticulum (Kermode, 1996 Crit. Rev. Plant Sci. 4(15):285-423). The signal peptide is cloned 5' in frame to the cDNA to achieve subcellular localization of the fusion protein. Additionally, promoters that are responsive to abiotic stresses can be used with, such as the Arabidopsis promoter RD2BA. One skilled in the art will recognize that the promoter used should be operatively linked to the nucleic acid such that the promoter causes transcription of the nucleic acid which results in the synthesis of a mRNA which encodes a polypeptide.

0301.0.1 Alternate methods of transfection include the direct transfer of DNA into developing flowers via electroporation or Agrobacterium mediated gene transfer. Agrobacterium mediated plant transformation can be performed using for example the GV3101(pMP90) (Koncz and Schell, 1986 Mol. Gen. Genet. 204:383-396) or LBA4404 (Ooms et al., Plasmid, 1982, 7: 15-29; Hoekema et al., Nature, 1983, 303: 179-180) Agrobacterium tumefaciens strain. Transformation can be performed by standard transformation and regeneration techniques (Deblaere et al., 1994 Nucl. Acids. Res. 13:4777-4788; Gelvin and Schilperoort, Plant Molecular Biology Manual, 2nd Ed. - Dordrecht : Kluwer Academic Publ., 1995. - in Sect., Ringbuc Zentrale Signatur: BT11-P ISBN 0-7923-2731-4; Glick, B R and Thompson, J E, Methods in Plant Molecular Biology and Biotechnology, Boca Raton : CRC Press, 1993. - 360 S., ISBN 0-8493-5164-2). For example, rapeseed can be transformed via cotyledon or hypocotyl transformation (Moloney et al., 1989 Plant Cell Reports 8:238-242; De Block et al., 1989 Plant Physiol. 91:694-701). Use of antibiotics for Agrobacterium and plant

selection depends on the binary vector and the *Agrobacterium* strain used for transformation. Rapeseed selection is normally performed using kanamycin as selectable plant marker. *Agrobacterium* mediated gene transfer to flax can be performed using, for example, a technique described by Mlynarova et al., 1994 Plant Cell Report 13:282-285. Additionally, transformation of soybean can be performed using for example a technique described in European Patent No. 0424 047, U.S. Patent No. 5,322,783, European Patent No. 0397 687, U.S. Patent No. 5,376,543 or U.S. Patent No. 5,169,770. Transformation of maize can be achieved by particle bombardment, polyethylene glycol mediated DNA uptake or via the silicon carbide fiber technique (see, for example, Freeling and Walbot "The maize handbook" Springer Verlag: New York (1993) ISBN 3-540-97820-7). A specific example of maize transformation is found in U.S. Patent No. 5,990,387 and a specific example of wheat transformation can be found in PCT Application No. WO 93/07256.

0302.0.1 The stress related protein encoding nucleic acid molecules of the invention have a variety of uses. Most importantly, the nucleic acid and amino acid sequences of the present invention can be used to transform plant cells or plants, thereby inducing tolerance to stresses such as drought, high salinity and cold. The present invention therefore provides a transgenic plant transformed by a stress related protein encoding nucleic acid (coding or antisense), wherein expression of the nucleic acid sequence in the plant results in increased tolerance to environmental stress as compared to a wild type plant. The increased stress tolerance is apparent as an increase in the yield or quality of the plant. The transgenic plant can be a monocot or a dicot or a gymnosperm plant. The invention further provides that the transgenic plant can be selected from maize, wheat, rye, oat, laticals, rice, barley, soybean, peanut, cotton, borago, sunflower, linseed, primrose, rapeseed, canola and turnip rape, manihot, pepper, sunflower, tagetes, solanaceous plant such as potato, tobacco, eggplant and tomato, *Vicia* species, pea, alfalfa, bushy plants such as coffee, cacao, tea, *Salix* species, trees such as oil palm, coconut, perennial grass, such as ryegrass and fescue, and forage crops, such as alfalfa and clover and *Arabidopsis thaliana*. Further the transgenic plant can be selected from spruce, pine or fir for example.

0303.0.1 In particular, the present invention describes using the expression of stress related proteins to engineer drought-tolerant, salt-tolerant and/or cold-tolerant plants. This strategy has herein been demonstrated for *Arabidopsis thaliana*, Ryegrass, Alfalfa, Rapeseed/Canola, Soybean, Corn and Wheat but its application is not restricted to these plants. Accordingly, the invention provides a transgenic plant containing a stress related protein encoding gene selected from the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences, wherein the

environmental stress is drought, increased salt or decreased or increased temperature but its application is not restricted to these adverse environments. Protection against other adverse conditions such as heat, air pollution, heavy metals and chemical toxicants, for example, may be obtained. In preferred embodiments, the environmental stress is drought.

0304.0.1 The present invention also provides methods of modifying stress tolerance of a plant comprising, modifying the expression of a stress related protein encoding gene in the plant. The invention provides that this method can be performed such that the stress tolerance is increased. This can for example be done by the use of transcription factors. In particular, the present invention provides methods of producing a transgenic plant having an increased tolerance to environmental stress as compared to a wild type plant due to increased expression of a stress related protein in the plant.

0306.0.1 Growing the modified plants under stress conditions and then screening and analyzing the growth characteristics and/or metabolic activity assess the effect of the genetic modification in plants on stress tolerance and/or resistance. Such analysis techniques are well known to one skilled in the art. They include next to screening (Römpf Lexikon Biotechnologie, Stuttgart/New York: Georg Thieme Verlag 1992, "screening" p. 701) dry weight, wet weight, protein syntheses, carbohydrate synthesis, lipid synthesis, evapotranspiration rates, general plant and/or crop yield, flowering, reproduction, seed setting, root growth, respiration rates, photosynthesis rates, etc. (Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm et al., 1993 Biotechnology, vol. 3, Chapter III: Product recovery and purification, page 489-714, VCH: Weinheim; Belter, F.A. et al., 1988 Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S., 1992 Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D., 1988 Biochemical separations, In: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications).

0306.0.1 The engineering of one or more stress related protein encoding genes of the invention may also result in stress related proteins having altered activities which indirectly impact the stress response and/or stress tolerance of plants. For example, the normal biochemical processes of metabolism result in the production of a variety of products (e.g., hydrogen peroxide and other reactive oxygen species) which may actively interfere with these same metabolic processes (for example, peroxynitrite is known to react with tyrosine side chains, thereby inactivating some enzymes having tyrosine in the active site (Groves, J.T., 1999 Curr. Opin. Chem. Biol. 3(2):226-235). By

optimizing the activity of one or more stress related proteins (enzymes) of the invention, it may be possible to improve the stress tolerance of the cell.

0307.0.1 Throughout this application, various publications are referenced. The disclosures of all of these publications and those references cited within those publications in their entireties are hereby incorporated by reference into this application in order to more fully describe the state of the art to which this invention pertains.

0308.0.1 It should also be understood that the foregoing relates to preferred embodiments of the present invention and that numerous changes and variations may be made therein without departing from the scope of the invention. The invention is further illustrated by the following examples, which are not to be construed in any way as limiting. On the contrary, it is to be clearly understood that various other embodiments, modifications and equivalents thereof, which, after reading the description herein, may suggest themselves to those skilled in the art without departing from the spirit of the present invention and/or the scope of the claims.

0309.0.1 The invention also pertains to the use of SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences for preparing a plant cell with increased environmental stress tolerance, which is preferably achieved by altering metabolic activity. The said sequences can also be used for preparing a plant with increased environmental stress tolerance.

0310.0.1 Object of the invention is further the use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group of sequences of the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for selection of plants with increased tolerance to environmental stress or as markers for detection of stress in plants or plant cells.

0311.0.1 Example 1

0312.0.1 Engineering stress-tolerant Arabidopsis plants by over-expressing stress related protein genes.

0313.0.1 Gene cloning and transformation of Arabidopsis thaliana

0314.0.1 Amplification

0315.0.1 The standard protocol of Pfu DNA polymerase or a Pfu/Taq DNA polymerase mix (Herculase) was used for the amplification procedure. Amplified ORF fragments were analysed by gel electrophoresis. Each primer consists of a universal 5' end and ORF specific 3' end whereby the universal sequences differ for the forward and reverse primers (forward primer sequence contains an EcoRI for yeast or SmaI for E.coli and the reverse primer sequence a SmaI for yeast or SacI for E.coli restriction site) allowing generally a unidirectional cloning success.

- 0316.0.1** Amplification using the protocol of Pfu or Herculanse DNA polymerase (Stratagene). Conditions: 1x PCR buffer, 0.2 mM dNTP, 100 ng genomic DNA *Saccharomyces cerevisiae* (S288C) or 80 ng genomic DNA *Escherichia coli* K-12 (MG1655), 25 pmol forward primer, 25 pmol reverse primer, 2.5 u Pfu or Herculanse DNA polymerase. 1st cycle for 3' for yeast or 2' for E.coli at 94 °C, followed by 25 cycles for 30'' at 94 °C, 30'' 55°C for yeast or 60°C for E.coli and 5-6' 72 °C, followed by 1 cycle for 610' at 72 °C, final for 4 °C at ∞.
- 5

0317.0.1 Table 2: Forward and reverse primer sequences used for ORF amplification

Gene	Forward Seq
YGL283W	GGAATTCAGCTGACCACCATGGATGGAGCCAAATTTGAAAATAC
YGH004W	GGAATTCAGCTGACCACCATGAGCGAAATAAATAATGAAAATCTAG
YGH014W	GGAATTCAGCTGACCACCATGCAGTTTCCATTGCTTGTCTC
YGL239C	GGAATTCACCTGACCACCATGAAATTTTTCAAGAACAAGCACC
YBL060W	GGAATTCAGCTGACCACCATGTGCGCCAGTTTAAACGAGGTA
YGL186W	GGAATTCAGCTGACCACCATGGTCGTAATTAACGGGGTCAAAAT
YDL202W	GGAATTCAGCTGACCACCATGTTGCAGCTAAGGTTTATGCGT
YAL040C	GGAATTCAGCTGACCACCATGAAGCTCCACAGACCATGCT
YDR101C	GGAATTCAGCTGACCACCATGGCTCTAGCTATCTCCACGA
YDR108W	GGAATTCAGCTGACCACCATGTTTTTTCTTATGAGCACTATATG
YAL064W	GGAATTCAGCTGACCACCATGCGATATACTGCAACTTTTCGG
YDR134C	GGAATTCAGCTGACCACCATGCAATTCTCTACCGTCGCTTCT
YFL031W	GGAATTCAGCTGACCACCATGAATACCGAGTACGATTACCTGT
YFL052W	GGAATTCAGCTGACCACCATGCCCCGCAATAGACAAGCGT
YFL042C	GGAATTCAGCTGACCACCATGTCCGATGTAGATAACTGGGAA
YBR025C	GGAATTCAGCTGACCACCATGCCTCCAAAGAAGCAAGTCGAA
YER174C	GGAATTCAGCTGACCACCATGACTGTGGTTGAAATAAAAAGCC
YBR051W	GGAATTCAGCTGACCACCATGCACATCTTTTCTTGTATTATTTTC
YER175C	GGAATTCAGCTGACCACCATGTCTACCTTTTCTGCTTCTGATT
YDR521W	GGAATTCAGCTGACCACCATGAAAGGTTCAAAATCGCACCTTG
YER167W	GGAATTCAGCTGACCACCATGCCGAAGAATAGTCACCACCAT
YER123W	GGAATTCAGCTGACCACCATGTCCCAACGATCTTCACAACAC
YDR115C	GGAATTCAGCTGACCACCATGGCCGATGAGGAACGTTTAAAG
YEL052W	GGAATTCAGCTGACCACCATGATCCCTTTGAAGCCCAATGCT
YDH536W	GGAATTCAGCTGACCACCATGAAGGATTTAAATTATCGAATTTCA
YDR513W	GGAATTCAGCTGACCACCATGCAGACCAATTTTTCCTTCGACT
YEL045C	GGAATTCAGCTGACCACCATGAAATGTCACGCGAAACGGAC
YEL041W	GGAATTCAGCTGACCACCATGAAAATGATAGATTACTGATTAAC
YDL238C	GGAATTCAGCTGACCACCATGACAAAAGTGATTTATTATTGATAA
YBR282W	GGAATTCAGCTGACCACCATGAAAGGCTCACCCATTTCTCAAT
YBR258C	GGAATTCAGCTGACCACCATGGCGTATAATCAAGAAGATAGTAA
YCL001W-A	GGAATTCAGCTGACCACCATGACCTTTTACAATTTATCAATAATAATA

YBR274W	GGAATTCAGCTGACCACCATGAGTCTCTCGCAGGTGTCAC
YHR090C	GGAATTCAGCTGACCACCATGGATCCAAGTTTAGTTTTAGAGC
YGR121C	GGAATTCAGCTGACCACCATGGAGAGTCGAACTACAGGGC
YGR127W	GGAATTCAGCTGACCACCATGTGCATTTTAATGGCCACAAGG
YGR150C	GGAATTCAGCTGACCACCATGTACATGGCCAGATGTGGCC
YKL037W	GGAATTCAGCTGACCACCATGCAGACAATGGCGGGGAG
YKL051W	GGAATTCAGCTGACCACCATGATTCAATTTAAAAGTCAGGTAAC
YKL120W	GGAATTCAGCTGACCACCATGTCATCTGACAACTCTAAACAAG
YKL011C	GGAATTCAGCTGACCACCATGTGACAGCACAGAAAGCTAAG
YKL017C	GGAATTCAGCTGACCACCATGAACAAAGAATTGGCTTCTAAGTT
YKL049C	GGAATTCAGCTGACCACCATGGAAACTGAAGTACCTGCACCA
YKL132C	GGAATTCAGCTGACCACCATGGATGATATAAGCGGAAGGCAAA
YGR126W	GGAATTCAGCTGACCACCATGCGTGTCCCATCTGTAGTGT
YKL070W	GGAATTCAGCTGACCACCATGTACATTCTAAACATTTTGAGTC
YKL058W	GGAATTCAGCTGACCACCATGGCAGTACCCGGGTATTACGA
YHR130C	GGAATTCAGCTGACCACCATGACTAAAAGTATATATATTATCATCG
YIL070C	GGAATTCAGCTGACCACCATGTTCTTAAGAAGCGTTAACCGTG
YHR195W	GGAATTCAGCTGACCACCATGACTCGTCCCCCATTTGGTTC
YIR022W	GGAATTCAGCTGACCACCATGAATCTAAGATTTGAATTGCAGAAA
YJL089W	GGAATTCAGCTGACCACCATGGCCAAGAGGAAATATGGCAG
YJL172W	GGAATTCAGCTGACCACCATGATGCGCTTACCAGTAGAGAAG
YHR118W	GGAATTCAGCTGACCACCATGTTCCAGGATACAACCTGAGAACTA
YHR175W	GGAATTCAGCTGACCACCATGGATGATAAGAAAACATGGAGTAC
YGR212W	GGAATTCAGCTGACCACCATGAATCTTAAACTTTCTGCTATTGAA
YJL024C	GGAATTCAGCTGACCACCATGATTCATCCAGTTCTAATATGTATG
YGR180C	GGAATTCAGCTGACCACCATGGAAAGCACATAACCAATTTTGAA
YJL178W	GGAATTCAGCTGACCACCATGTCCACAGATGCCACAAGAAATGA
YJL001W	GGAATTCAGCTGACCACCATGAATGGAAATCAAGTGGACATCA
YJL208C	GGAATTCAGCTGACCACCATGTGCAGTAGGATACTCTTGTCG
YJL152W	GGAATTCAGCTGACCACCATGCCGCAATTTAGCCGCCGAAG
YJL131C	GGAATTCAGCTGACCACCATGTTAAAAGTTCTTTGAGTGATGT
YJL151C	GGAATTCAGCTGACCACCATGGACAGAGACCATATTAAAGACC
YLR441C	GGAATTCAGCTGACCACCATGGCTGTCCGAAAGAAATAGAGA
YLR415C	GGAATTCAGCTGACCACCATGTATCTCAGTCCCAGCTTATG
YLR212C	GGAATTCAGCTGACCACCATGGGTGGAGAAATTATTACTTTGC
YLR029C	GGAATTCAGCTGACCACCATGGGTGCGTACAAATATTTGGAAG
YLL041C	GGAATTCAGCTGACCACCATGTGAACTGTCTATTGAGAAGGA
YLR105C	GGAATTCAGCTGACCACCATGTCTAAAGGGAGGGTCAATCAG
YIL136W	GGAATTCAGCTGACCACCATGTCTCAAGAATAATTGTCCGGA
YLR215C	GGAATTCAGCTGACCACCATGTCTCACAAGAATATACAACCTTT
YLR321C	GGAATTCAGCTGACCACCATGTGCGACCAAAACAGCTTATT
YMR260C	GGAATTCAGCTGACCACCATGGGTAAAGAAAAACACTAAGGTG
YML120C	GGAATTCAGCTGACCACCATGATAAAGTCGATACTTCCGATG
YLR407W	GGAATTCAGCTGACCACCATGACTGTTTCTACTTCCAAGACC
YMR197C	GGAATTCAGCTGACCACCATGAGTTCCCTATTAAATATCATACGA
YMR100W	GGAATTCAGCTGACCACCATGAGAGACTCTAATCATCGATCAT

YMR210W	GGAATTCCAGCTGACCACCATGCGTCTAAAAGAATTGTTACCTAA
YMR318C	GGAATTCCAGCTGACCACCATGTCTTATCCTGAGAAATTTGAAGG
YMR069W	GGAATTCCAGCTGACCACCATGCGTCTTCGGTATATAGTGAGA
YNL076W	GGAATTCCAGCTGACCACCATGTGCGGGAGGCCAIIIGATGI
YNL024C	GGAATTCCAGCTGACCACCATGGAGAGTATATTTGGTGGGTTTG
YNL125C	GGAATTCCAGCTGACCACCATGTCAACGCACTCAAACGACTAC
YNL020C	GGAATTCCAGCTGACCACCATGTTGCTAATAAGAAGGACGATAAA
YMR115W	GGAATTCCAGCTGACCACCATGCTTTTACAAGGAATCCGTTTATC
YNL244C	GGAATTCCAGCTGACCACCATGTCCATTGAGAATCTGAAATCATT
YNL334C	GGAATTCCAGCTGACCACCATGACCGTCGTTATCCAGTCTT
YNR018W	GGAATTCCAGCTGACCACCATGAAGATTTTAACCCAAGACGAAAT
YNL277W	GGAATTCCAGCTGACCACCATGTCCCATACTTTAAATCGAAAAC
YOL118C	GGAATTCCAGCTGACCACCATGTCTTTTAGAAAGAAAAAACTCAAAC
YOL123W	GGAATTCCAGCTGACCACCATGAGCTCTGACGAAGAAGATTTCA
YOR020C	GGAATTCCAGCTGACCACCATGTCCACCTTTTGAAGTCTGCT
YOL116W	GGAATTCCAGCTGACCACCATGGCAAGTAACCAGCACATAGGA
YOR305W	GGAATTCCAGCTGACCACCATGATAAAAACTATTTGGGACGAAG
YPL267W	GGAATTCCAGCTGACCACCATGATATCACCACAAAAAAGAGAAC
YPL229W	GGAATTCCAGCTGACCACCATGATGCCCTACAACACCCCTC
YPL038W	GGAATTCCAGCTGACCACCATGAAACTGGCCCAAGACATGAAT
YPR047W	GGAATTCCAGCTGACCACCATGGAGGTAACCTTCATGTTTCTCA
YPL011C	GGAATTCCAGCTGACCACCATGACTACAATAATGACTTCTATTTTG
YPR143C	GGAATTCCAGCTGACCACCATGTCTGGTTATTTTTTCAGGGTTTTTC
YOL103W	GGAATTCCAGCTGACCACCATGGCTGAATGAAGAATTCGACAG
YOR016C	GGAATTCCAGCTGACCACCATCCCGCTTTTACTTTGATTGCGA
YPL079W	GGAATTCCAGCTGACCACCATGGGTAAATCGTATGTCCATATAAC
YOR280W	GGAATTCCAGCTGACCACCATGTCAAIICAGGCTTTGTCTTTTG
YOH350C	GGAATTCCAGCTGACCACCATGTCCACCTTTTCTGATTGGAA
YDL060W	GGAATTCCAGCTGACCACCATGGCAGGTCATTTCACACAGGTC
YDL05C	GGAATTCCAGCTGACCACCATGGTAGTACAAAATAGCCCAGTTT
YPL210C	GGAATTCCAGCTGACCACCATGAAAGAAAAGCAAAAAAATGGCTAAA
YMR118C	GGAATTCCAGCTGACCACCATGAAAGCAACCATTCAAAGAGTAAC
YPR052C	GGAATTCCAGCTGACCACCATGGTCACCCCAAGAGAACCTAA
YLR224W	GGAATTCCAGCTGACCACCATGAATCAGAGCGATAGCAGCTTG
YLR275W	GGAATTCCAGCTGACCACCATGTCTGTATGTTTGATCTTAACCAAT
YMR154C	GGAATTCCAGCTGACCACCATGAATGATTGGCATGATTCATG
YDR205W	GGAATTCCAGCTGACCACCATGGATAGAGGCAGCTGCTGTTT
YPR037C	GGAATTCCAGCTGACCACCATGAAACAGATAGTCAAAAGAAGCC
YNR008W	GGAATTCCAGCTGACCACCATGGGCACACTGTTTCGAAGAAAT
YOR084W	GGAATTCCAGCTGACCACCATGGAACAGAACAGGTTCAAGAAAG
YGR054W	GGAATTCCAGCTGACCACCATGTCATCTCAGTTTTTCTGAAAAC
YGL106W	GGAATTCCAGCTGACCACCATGTCAGCCACCAGAGCCAATAAA
YAL067C	GGAATTCCAGCTGACCACCATGTATTCAATTGTTAAAGAGATTATTG
YIL023C	GGAATTCCAGCTGACCACCATGAAGGCGTCGCACATTTGCTC
YBR064W	GGAATTCCAGCTGACCACCATGGATATGGTATCACCAGTCTTGA
b0019	TTGCTCTTCCATGAACATCTGCATCGATTCTTTAG

b2148	TTGCTCTTCCATGAGTGCGTTAAATAAGAAAAG
b2795	TTGCTCTTCCATGGAAACGACTCAAACGAGCAC
b2082	TTGCTCTTCCATGTTTCATTGTCCCTTATGCCAGC
b5124	TTGCTCTTCCATGGCAATTAACAATACAGGCTCG
b3116	TTGCTCTTCCATGAGTACTTCAGATAGCATTGTATC
b1830	TTGCTCTTCCATGAACATGTTTTTTAGGCTTACC
b1453	TTGCTCTTCCATGTTTCATGGCAACTTATATGACTTTT
b2864	TTGCTCTTCCATGATCAGGAGTCACACCATGA
b2799	TTGCTCTTCCATGATGGCTAACAGAATGATTCTGA
b3327	TTGCTCTTCCATGAATTATCGCTATCGCGCCA
b0970	TTGCTCTTCCATCCATCGTATTGTTACTTCTTCAC
YER003C	GGAATTCAGCTGACCACCATGTCCAACAAGCTGTTCCAGGTTA
YCL027W	GGAATTCAGCTGACCACCATGGTAGCAACAATAATGCAGACGA
YBR112C	GGAATTCAGCTGACCACCATGAATCCGGGCGGTGAACAAAC
YNL079C	GGAATTCAGCTGACCACCATCCACAAAATCAGACAAAAGCTAAG
YFR042W	GGAATTCAGCTGACCACCATGGCAGGTATCAAGTTGACGCAT
YER137C	GGAATTCAGCTGACCACCATGTGTGAATCATCAAATAAGACTGA
YKL103C	GGAATTCAGCTGACCACCATGGAGGAACAACGTGAAATACTG
YNL080W	GGAATTCAGCTGACCACCATGTCTGAAAAGGCCGTTAGAAGG
YGR161C	GGAATTCAGCTGACCACCATGATCGCTACCTCCAGAGCCG
YDH071C	GGAATTCAGCTGACCACCATGGCCTCCTCAAGTAGCACGC

Gene	Reverse Seq
YGL283W	GATCCCCGGGAATTGCCATGTTACACATGATTGCAAGCTGATTGT
YGR004W	GATCCCCGGGAATTGCCATGTTATAGAGAAGGAGACATTGAAACAT
YGR014W	GATCCCCGGGAATTGCCATGTCAAACCTTCGTTCCAACCCAGGG
YGL289C	GATCCCCGGGAATTGCCATGTCAATTGCAGGGATTATGGAATAAAA
YBL080W	GATCCCCGGGAATTGCCATGTTAGAACTGAACAGAACCCATGGC
YGL166W	GATCCCCGGGAATTGCCATGTTATTGTGAATGTGAGTTATGCGAAG
YDL202W	GATCCCCGGGAATTGCCATGTTACTTTGATCCCTTCCATTCTGCA
YAL046C	GATCCDCGGGAATTGCCATGTTCATGATGATGCCGGACCCCTTC
YDR101C	GATCCCCGGGAATTGCCATGCTACATTTTCATGGTTTCTTCAACTG
YDH108W	GATCCCCGGGAATTGCCATGTCAATCCAATAAAGCTAACACTTGTTC
YAL064W	GATCCCCGGGAATTGCCATGCTATGGTTGCTATTCAATATTAGAA
YDR134C	GATCCCCGGGAATTGCCATGTTACAAATAAAGCGGCAGCACCC
YFL031W	GATCCCCGGGAATTGCCATGTCAACAGCAGCCCCCACCGBT
YFL052W	GATCCCCGGGAATTGCCATGTTAAGGAAGCGCATCTACATCTTCT
YFL042C	GATCCCCGGGAATTGCCATGTCAACCATACCTTTGATCCAACCTG
YBR025C	GATCCCCGGGAATTGCCATGTCAATTGTTACCAGCACCAAGCTCT
YER174C	GATCCCCGGGAATTGCCATGTTACTGTAGAGCATGTTGGAAATATT
YBR051W	GATCCCCGGGAATTGCCATGTTATATATGGCATGTCTTCGCATGT
YER175C	GATCCCCGGGAATTGCCATGTCAAGACCCCTTTGCCAAGTTGTAA

YDR521W	GATCCCCGGGAATTGCCATGTTACTCACCATTAAAACATCTTTCCG
YER167W	GATCCCCGGGAATTGCCATGTTAGTTGCTATTATCAAAATAAAAGAGAC
YER123W	GATCCCCGGGAATTGCCATGTCAAAAAAAAAAAGGAAAAAGAGAAAAAG
YDR415C	GATCCCCGGGAATTGCCATGTCAACATTTTTTCIAAATTCACTTAGGAC
YEL052W	GATCCCCGGGAATTGCCATGTTAGTATGTAGGCTTAGTACCCAA
YDR536W	GATCCCCGGGAATTGCCATGTCAAAGCTCAAAATTGCTTTATCG
YDR513W	GATCCCCGGGAATTGCCATGCTATTCAAATACCGGCTTCAATATTT
YEL045C	GATCCCCGGGAATTGCCATGCTAGGAAAGGAGGTGGTACGAA
YEL041W	GATCCCCGGGAATTGCCATGTTAGATIGCAAAATGAGCCTGACGA
YDL238C	GATCCCCGGGAATTGCCATGCTAAATCTGGTAGACTTGCTGGC
YBR282W	GATCCCCGGGAATTGCCATGTTATCCAGCTCCTTATAACATGAA
YBR258C	GATCCCCGGGAATTGCCATGTTACGTACTTCCATTTGCTTCCCTGT
YCL001W-A	GATCCCCGGGAATTGCCATGTCAAGTTCATCAAAATTGAAATTTCTAACCA
YBR274W	GATCCCCGGGAATTGCCATGTCAAGTTCGGAATTAGGATAATATCC
YHR090C	GATCCCCGGGAATTGCCATGTCAAGTTAGGTTTTCTTTCAAGTTGT
YGR121C	GATCCCCGGGAATTGCCATGTTACCTATTGGCAGGATCTTCTTGA
YGR127W	GATCCCCGGGAATTGCCATGTTACAATTTGAATTTAAACCTTTTTC
YGR150C	GATCCCCGGGAATTGCCATGCTACATGTTAABTTCTTGTTCTCTCC
YKL037W	GATCCCCGGGAATTGCCATGTTATATACTCAATCCAAAACAGGGAA
YKL051W	GATCCCCGGGAATTGCCATGTCAACGACTACTTGAATAGATTGG
YKL120W	GATCCCCGGGAATTGCCATGTTAATTATGGCCTAAAACCTCTCGAC
YKL011C	GATCCCCGGGAATTGCCATGTTAGTCAATTGTTGTAAGTGTCTCGC
YKL017C	GATCCCCGGGAATTGCCATGTTACAAATAATCGTCAATGTTGGGG
YKL049C	GATCCCCGGGAATTGCCATGCTAAATAAACTGTCCCTGATTCTT
YKL132C	GATCCCCGGGAATTGCCATGCTATACTGGCAAGTGACAGTTGTG
YGR126W	GATCCCCGGGAATTGCCATGTTAATCGAAAATTCTATGAAAAAACCC
YKL070W	GATCCCCGGGAATTGCCATGTCAAGAAAGCTCCACTTTAGTTGG
YKL058W	GATCCCCGGGAATTGCCATGTTACTCGCTCTTTTGGAGTTACATG
YHR130C	GATCCCCGGGAATTGCCATGCTAATTCCTGATGCCAAGTAACGA
YIL070C	GATCCCCGGGAATTGCCATGTTAGTGGAAAACTTCTTCATCTTTTC
YHR195W	GATCCCCGGGAATTGCCATGTTAGTATCTAAATGGTTGAGAGTATG
YIR022W	GATCCCCGGGAATTGCCATGCTACTCGCCGCCAGCAGAG
YJL089W	GATCCCCGGGAATTGCCATGTTAGAAGGTGGAGTTCAAAATATTCT
YJL172W	GATCCCCGGGAATTGCCATGTTAAGCGTATTCTTTAACATTAAACGA
YHR113W	GATCCCCGGGAATTGCCATGTTAGACAACAATTTACATTCTATGG
YHR175W	GATCCCCGGGAATTGCCATGTTAATGGCAGGCGAAGGAGCTG
YDR212W	GATCCCCGGGAATTGCCATGCTAGTATAAATTTAAGTAATCTTTCATAT
YJL024C	GATCCCCGGGAATTGCCATGTTATTGCCCGTTGCCCATTTGTG
YGR180C	GATCCCCGGGAATTGCCATGTTAGAAGTCATCATCAAGTTAATTTTC
YJL179W	GATCCCCGGGAATTGCCATGTTAATTCCTTCATCAATGCCCTTAGATT
YJL061W	GATCCCCGGGAATTGCCATGTTATAGTTGTTCAATTTCATCAGGGT
YJL208C	GATCCCCGGGAATTGCCATGCTCAATTCCTTTTGTGGAGGAGGT
YJL152W	GATCCCCGGGAATTGCCATGTCAAGCAGACATGCCAGTGGG
YJL131C	GATCCCCGGGAATTGCCATGTTACATTTCAITTCATTTTTTCTCTGA
YJL151C	GATCCCCGGGAATTGCCATGCTAAGTACGGCCGGAAGAGAGC
YLR441C	GATCCCCGGGAATTGCCATGTTACACAGTTTCCAAGACTTCGTG

YLR415C	GATCCCCGGGAATTGCCATGCTACTTCCAAACAAGTGGTCCAGA
YLR212C	GATCCCCGGGAATTGCCATGTTATACTAATTTATGATCACCGTCGG
YLR029C	GATCCCCGGGAATTGCCATGTTATTTTCTGTATCTCCACAAGGAC
YLL041C	GATCCCCGGGAATTGCCATGCTAGGCAAAATGCCAAAGATTTCTTA
YLR105C	GATCCCCGGGAATTGCCATGCTAGTCTCTATTTCTTCCGGGAAC
YIL136W	GATCCCCGGGAATTGCCATGCTAGTCCTTTTTCGAGCTCCAQAA
YLR215C	GATCCCCGGGAATTGCCATGCTAAGTTTCATTCTCACTATCACTG
YLR321C	GATCCCCGGGAATTGCCATGCTACATTCTCATTGTGGTTTCTAAG
YMR260C	GATCCCCGGGAATTGCCATGTTAATCATAAATAGTTTCATAAGTGTGT
YNL120C	GATCCCCGGGAATTGCCATGTCAGTTCCCTATGCAAAATGCTTAATA
YLR407W	GATCCCCGGGAATTGCCATGTCAGTCATGGCATGCCCTTGGCA
YMR197C	GATCCCCGGGAATTGCCATGCTAAAATGAAGACAGCCACAATCTG
YMR100W	GATCCCCGGGAATTGCCATGCTATTGATTGTTTGTTCACGGGACT
YMR210W	GATCCCCGGGAATTGCCATGTTATGAAGTCCATGGTAAATTCGTG
YMR318C	GATCCCCGGGAATTGCCATGTTACATGAGGTTTCATGTTTCATGTTAG
YMR069W	GATCCCCGGGAATTGCCATGTTATTTTACTTAATTTTCATCCATTTAG
YNL076W	GATCCCCGGGAATTGCCATGTTATGTATCACAAGTATTAAATTCAGTT
YNL024C	GATCCCCGGGAATTGCCATGTTAATCTCTTTCAAAACAGACAGCAA
YNL125C	GATCCCCGGGAATTGCCATGCTATTTTTCAGTTTGGGTGTTGCC
YNL028C	GATCCCCGGGAATTGCCATGTTAACTCTCTTGTCCCAATTTCTC
YMR115W	GATCCCCGGGAATTGCCATGTTAGTTTCTCAAGTGACTATTGTGA
YNL244C	GATCCCCGGGAATTGCCATGTTACGAATCAGTCCBATTGGACTT
YNL334C	GATCCCCGGGAATTGCCATGTTAAGCTGGAAGAGGCCAATCTCTT
YMR018W	GATCCCCGGGAATTGCCATGTTATTTCAAAGTCTTCAAACAATTTTCT
YNL277W	GATCCCCGGGAATTGCCATGTTAGTCTTCATGCTTATCAGAGAAC
YOL118C	GATCCCCGGGAATTGCCATGTCAGTTCAAAGTCTCTGGAATATGA
YOL123W	GATCCCCGGGAATTGCCATGTTATTCGTCTTCTTCCAAAGTTTGAG
YOR020C	GATCCCCGGGAATTGCCATGCTATGAGGATCCCGTTTTGTGA
YOL116W	GATCCCCGGGAATTGCCATGTTAATAATTGAATTTAATTTTACTTCTGTT
YOR305W	GATCCCCGGGAATTGCCATGTCACCGACTCATTTTGTTAAGCTTG
YPL287W	GATCCCCGGGAATTGCCATGTTACTCATCTTCATAACGCTGGGAAG
YPL229W	GATCCCCGGGAATTGCCATGCTAACATTTCTTATTATCTCTATATATC
YPL038W	GATCCCCGGGAATTGCCATGCTAACTGCTTTTTTCTGTGTTGAGTA
YPR047W	GATCCCCGGGAATTGCCATGTCATTTTGTCCCTTTATATCAATTTTT
YPL011C	GATCCCCGGGAATTGCCATGTTAGCGTTTTTTTTTGCCCTTCTTC
YPR148C	GATCCCCGGGAATTGCCATGCTAAATTTCCAAACCATTTAGAAGTTT
YOL103W	GATCCCCGGGAATTGCCATGCTAAGACTTGAAATTAATTAATTCGGG
YOR016C	GATCCCCGGGAATTGCCATGTCAGTGTATCTCGCTGTCAACAATC
YPL079W	GATCCCCGGGAATTGCCATGCTATTGTAATTCCTTATAGTGTTCAT
YOR260W	GATCCCCGGGAATTGCCATGTTATTTAAGCTCGAAATGGCTATTGA
YOR360C	GATCCCCGGGAATTGCCATGTCATTGTGGAAGAGGTCTTCTAGG
YDL060W	GATCCCCGGGAATTGCCATGTTACATACCATTCCAAGGTAACGAA
YDL005C	GATCCCCGGGAATTGCCATGCTATATATTGAAGCCGCTGAGGTC
YPL210C	GATCCCCGGGAATTGCCATGCTACTTACGTACTAAAATAGTCTCTT
YMR118C	GATCCCCGGGAATTGCCATGTTACTGAGCCAGTAAATACGTTCCCT
YPR052C	GATCCCCGGGAATTGCCATGCTAAGCCAAAGTGGCGTTATATAAC

YLR224W	GATCCCCGGGAATTGCCATGTCATCTTCGAAGATAAGGGGTATTG
YLR275W	GATCCCCGGGAATTGCCATGTTACTCAACAGGGGTTTTTAACACA
YMR154C	GATCCCCGGGAATTGCCATGTTATTTTGGTATCACATCATCGGAG
YDH205w	GATCCCCGGGAATTGCCATGTCGAATTTGCTATAGGCTGTAGCGG
YPR037C	GATCCCCGGGAATTGCCATGTTAGAACTGAATTATTTACATTGTCT
YNR008W	GATCCCCGGGAATTGCCATGTTACATTGGGAAGCCCATCTGAGA
YOR084W	GATCCCCGGGAATTGCCATGTTACAGTTTTTGTTTAGTCGTTTTAAC
YGR054W	GATCCCCGGGAATTGCCATGTTATTCATCCTTCCAACCCAACITTT
YGL108W	GATCCCCGGGAATTGCCATGTCATTGTCTCAAAACATCTTCGATG
YAL067C	GATCCCCGGGAATTGCCATGTTATTTTTTCATCAGATACTGATAAGGT
YIL023c	GATCCCCGGGAATTGCCATGTCGAATCCTCATCCATCAGCGCCA
YBR061W	GATCCCCGGGAATTGCCATGCTAAAATATGGAGGAAGTAGGTTTAA
b0019	TTGCTCTTCGTTAAACTGATGGACGCAAAAGGAACG
b2148	TTGCTCTTCGTTATTTCTTACGCGCGTATTTCAAGTG
b2796	TTGCTCTTCGTTAGCTGAACAGAGAGTAGAAGATT
l2082	TTGCTCTTCGTTACATCCACATAATTTGCTGCCC
b0124	TTGCTCTTCGTTACTTCACATCATCGGCGAGCG
b3118	TTGCTCTTCGTTAAACAGTTTGTATACCATGTTTAC
b1830	TTGCTCTTCGTTACTTGACGGGAGCGGGTTGT
b1453	TTGCTCTTCGTTAACTCGCCGTTTCAGGCTTAAA
b2564	TTGCTCTTCGTTAATTGCCAGCCATCGGCTG
b2792	TTGCTCTTCGTTACCAGGCGGTATGCTAAAGCT
b3327	TTGCTCTTCGTTAATTAAATCATTGAGTTAAGTTGAAGA
b0970	TTGCTCTTCGTTAATCGGCGGTAGCGAAGCCC
YER003C	GATCCCCGGGAATTGCCATGCTGAATTTGGTTCCACAAAGGCTCTA
YGL027W	GATCCCCGGGAATTGCCATGTCAGTCGTATTCTTGGAGACAGTC
YER112C	GATCCCCGGGAATTGCCATGTTAGTCGTCTAGTTTTTCATCTTCT
YNL079C	GATCCCCGGGAATTGCCATGTCACAAAGTTTTCCAGAGATGCAGC
YFR042W	GATCCCCGGGAATTGCCATGTCATTTTGTAAAGTTTTTTGTATGCT
YER137C	GATCCCCGGGAATTGCCATGTTATTTCTTGGGTATAAGTGTACATC
YKL103C	GATCCCCGGGAATTGCCATGTCAGAACTCGCCGAATTCATCGTA
YNL090W	GATCCCCGGGAATTGCCATGTTATAAAATTATGCAACAGTTAGCCC
YGR161C	GATCCCCGGGAATTGCCATGCTATTTCAATGAACAGTTTGAATTC
YDR071C	GATCCCCGGGAATTGCCATGCTAGTTGTCTGTTCTTCTTAATTA

0318.0.1 Vector preparation

- 0319.0.1 The preferred binary vector 1bxbigResgen for yeast and 1bSuperColiC for E.coli, which is based on the modified pPZP binary vector backbone (comprising the kanamycin-gene for bacterial selection; Hajukiewicz, P. et al., 1994, Plant Mol. Biol., 25: 989-994) carried the selection marker bar-gene (De Block et al., 1987, EMBO J. 6, 2513-2518) driven by the mas1 promoter (Velten et al., 1984, EMBO J. 3, 2723-2730; Mengiste, Amedeo and Paszkowski, 1997, Plant J., 12, 945-948) on its T-DNA. In addition the T-DNA contained the strong double 35S(Kay et al., 1987, Science 236,

1299-1302) for yeast or Super promotor (Ni et al., 1995, Plant Journal 7, 861-876) for E.coli in front of a cloning cassette followed by the nos-terminator (Depicker A. Stachel S. Dhaese P. Zambryski P. Goodman HM. Nopaline synthase: transcript mapping and DNA sequence. Journal of Molecular & Applied Genetics. 1(6):561-73, 1982.). The

5 cloning cassette consists of the following sequence:

0320.0.1 Yeast: 5'-GGAATTCGAGCTGACCACCATGGCAATTCCTCGGGGATC-3 or

0321.0.1 E.coli: 5'-TTG CTC TTC CAT GGC AAT GAT TAA TTA ACG AAG AGC AA-3', respectively.

10 **0322.0.1** Other selection marker systems, like the AHAS marker or other promoters, e.g. superpromotor (see above), 35S promotor (see above), Ubiquitin promotor (Callis et al., J. Biol. Chem., 1990, 265: 12488-12493; US 5,510,474; US 6,020,190; Kawalleck et al., Plant. Molecular Biology, 1993, 21: 673-684) or 34S promotor (GenBank Accession numbers M59930 and X16673) were similar useful for
15 the instant invention and are known to a person skilled in the art. The vector was linearised with EcoR and SmaI for yeast or SmaI and SacI for E.coli using the standard protocol provided by the supplier (MBI Fermentas, Germany) and purified using Qiagen columns (Qiagen, Hilden, Germany).

0323.0.1 Ligation and transformation

20 **0324.0.1** Present ORF fragments (~ 100 ng) were digested by EcoRI and SmaI for yeast and SmaI and SacI for E.coli using the standard protocol provided by the supplier (MBI Fermentas, Germany), purified using Qiagen columns (Qiagen, Hilden, Germany) and were ligated into the cloning cassette of the binary vector systems (~ 30 ng) using standard procedures (Maniatis et al.).

25 **0325.0.1** In the case of internal EcoRI, SmaI and SacI restriction sites a blunt end cloning procedure was applied. The undigested ORF fragments were directly purified and ligated into the cloning cassette of the binary vector. In this case the EcoRI site was refilled by Klenow reaction and the SacI site blunted Pfu DNA polymerase.

0326.0.1 Ligation products were transformed into E.coli (DH5alpha) using a
30 standard heat shock protocol (Maniatis et al.). Transformed colonies were grown on LB media and selected by respective antibiotics (Km) for 16h at 37 °C. Positive clones were identified by control PCR reactions using a combination of a vector specific and the respective ORF specific primers.

0327.0.1 Plasmid preparation

35 **0328.0.1** Plasmid DNA was prepared from positive clones using standard protocols (Qiagen Hilden, Germany).

0329.0.1 Transformation of *Agrobacteria*

0330.0.1 Plasmids were transformed into *Agrobacterium tumefaciens* (GV3101pMP90; Koncz and Schell, 1986, Mol. Gen. Genet. 204: 383-396) using heat shock or electroporation protocols. Transformed colonies were grown on YEP media and selected by respective antibiotics (Rif/Gent/Km) for 2d at 28 °C. These *Agrobacterium* cultures were used for the plant transformation.

0331.0.1 *Arabidopsis thaliana* was grown and transformed according to standard conditions Bechtold 1993 (Bechtold, N., Ellis, J., Pelletier, G. 1993. In planta *Agrobacterium* mediated gene transfer by infiltration of *Arabidopsis thaliana* plants C.R. Acad.Sci.Paris. 316:1194-1199); Bent et al. 1994 (Bent, A., Kunkel, B.N., Dahlbeck, D., Brown, K.L., Schmidt, R., Giraudat, J., Leung, J., and Staskawicz, B.J. 1994; PPCS2 of *Arabidopsis thaliana*: A leucine-rich repeat class of plant disease resistant genes; Science 265: 1856-1860).

0332.0.1 Transgenic *A. thaliana* plants were grown individually in pots containing a 4:1 (v/v) mixture of soil and quartz sand in a York growth chamber. Standard growth conditions were: photoperiod of 16 h light and 8 h dark, 20 °C, 60% relative humidity, and a photon flux density of 150 µE. To induce germination, sown seeds were kept at 4 °C, in the dark, for 3 days. Plants were watered daily until they were approximately 3 weeks old at which time drought was imposed by withholding water. Parallely, the relative humidity was reduced in 10% increments every second day to 20%. After approximately 12 days of withholding water, most plants showed visual symptoms of injury, such as wilting and leaf browning, whereas tolerant plants were identified as being visually turgid and healthy green in color. Plants were scored for symptoms of drought injury in comparison to neighbouring plants for 3 days in succession.

0333.0.1 Three successive experiments were conducted. In the first experiment, 10 independent T2 lines were sown for each gene being tested. The percentage of plants not showing visual symptoms of injury was determined. In the second experiment, the lines that had been scored as tolerant in the first experiment were put through a confirmation screen according to the same experimental procedures. In this experiment, plants of each tolerant line were grown and treated as before. In the third experiment, at least 7 replicates of the most tolerant line were grown and treated as before. The average and maximum number of days of drought survival after wild-type control had visually died were determined. Additionally measurements of chlorophyll fluorescence were made in stressed and non-stressed plants using a Mini-PAM (Heinz Walz GmbH, Effeltrich, Germany).

0334.0.1 In the first experiment, after 12 days of drought, the control, non-transgenic *Arabidopsis thaliana* and most transgenic lines expressing other transgenes

in the test showed extreme visual symptoms of stress including necrosis and cell death. Several plants expressing the genes retained viability as shown by their turgid appearance and maintenance of green color.

0335.0.1 The second experiment compared a smaller number of independent transgenic lines for each gene but a greater number of progeny within each independent transformation event. This experiment confirmed the previous results. Those lines containing the specific SRP encoding yeast genes survived longer than the controls. In some cases the transgenic line survived more than 3 days after the controls had died.

0336.0.1 According to the results of the first and second experiments some major lines containing the specific SRP encoding yeast genes were identified, which showed the best results with regard to the average days of survival after wild type and/or the hit percentage.

0337.0.1 In a third experiment these major lines were tested with multiple replicates (4-80 plants per line). The average number of days the plants of the major line survived longer than wild-type was measured. I.e., the number '1' means that, on average, the plants overexpressing this ORF, on averaged survived 1 day longer than wild-type. The value for WT in this column is '0'. The results are summarised in table 3.

0338.0.1 Table 3: Drought tolerance of transgenic *Arabidopsis thaliana* expressing the various SRP encoding genes from *Saccharomyces cerevisiae* or *E. coli* after imposition of drought stress on 3 week old plants in a third experiment using several plants from one transgenic line (experiment 3). Drought tolerance is measured for the indicated number of transgenic plants (Plants tested) as the average number of days (Average days of survival after WT) that the transgenic plants survived after the control (untransformed wild type). The hit percentage indicates the fraction of the tested plants of the major line that was actually resistant, i.e. the number '50' indicates that half of the tested plants were resistant (survived longer than WT). For WT, this column has the value '0'.

Sequ. ID No.	Gene	Plants tested	Average days of survival after WT
1	YGL263W	12	1,17
3	YGR004W	11	1,36
5	YGR014W	11	0,82
7	YGL238C	13	2,4
9	YBL060W	14	1,6
11	YGL166W	14	1,07
13	YDL202W	15	0,47

15	YAL046C	14	1,9
17	YDR101C	14	3,57
19	YDR108W	14	0,5
21	YAL064W	33	2,29
23	YDR134C	13	0,8
25	YFL031W	13	1,3
27	YFL052W	14	1,1
29	YFL042C	11	1,3
31	YBR025C	11	1,4
33	YER174C	22	1,05
35	YBR051W	10	1,2
37	YER175C	11	1,7
39	YDR521W	14	0,5
41	YER167W	35	0,66
43	YER123W	11	2,2
45	YDR415C	7	2,71
47	YEL052W	4	1,5
49	YDR536W	14	1,5
51	YDR513W	7	3,14
53	YEL045C	14	1,64
55	YEL041W	13	1,77
57	YDL238C	35	1,2
59	YBR282W	14	1,79
61	YBR258C	9	3,4
63	YCL001W-A	36	1,78
65	YBR274W	14	2
67	YHR090C	8	4,5
69	YGR121C	40	1,6
71	YGR127W	8	1,4
73	YGR150C	12	2,6
75	YKL037W	14	0,79
77	YKL051W	16	2,4
79	YKL120W	14	0,64
81	YKL011C	12	1,9
83	YKL017C	10	1,8
85	YKL049C	80	1,92
87	YKL132C	33	1,82
89	YGR126W	8	2,3
91	YKL070W	14	2,1
93	YKL058W	9	1,14
95	YHR130C	9	1,8
97	YIL070C	13	0,69

99	YHR195W	14	1,9
101	YIR022W	14	1,07
103	YJL089W	14	0,86
105	YJL172W	11	0,82
107	YHR119W	15	2
109	YHR175W	9	0,78
111	YGR212W	13	1,48
113	YJL024C	13	0,69
115	YGR180c	14	2,9
117	YJL179W	18	1,3
119	YJL001W	14	1,6
121	YJL208C	12	1,4
123	YJL152W	13	1,3
125	YJL131C	14	0,6
127	YJL151C	14	1,9
129	YLR441C	10	2
131	YLR415C	14	1,6
133	YLR212C	13	0,64
135	YLR029C	14	1,56
137	YLL041C	13	0,92
139	YLR105C	14	0,86
141	YIL136W	8	2,25
143	YLR215C	13	1,77
145	YLR321C	14	1,29
147	YMR260C	11	2,08
149	YNL120C	7	2
151	YLR407W	12	1,17
153	YMR197C	14	0,57
155	YMR100W	12	1,25
157	YMR210W	10	1,1
159	YMR318C	13	0,85
161	YMR069W	8	1,25
163	YNL076W	13	1,31
165	YNL024C	13	1,08
167	YNL125C	4	1,75
169	YNL029C	13	1,92
171	YMR115W	12	0,75
173	YNL244C	11	1,55
175	YNL334C	14	1,5
177	YNR018W	14	1,29
179	YNL277W	14	1,14
181	YOL118C	14	1,71

183	YOL123W	14	0,71
185	YOR020C	12	1,83
187	YOL116W	13	1,08
189	YOR305w	15	1,2
191	YPL267W	6	2,5
193	YPL229w	5	2
195	YPL038W	10	1,3
197	YPR047W	11	1
199	YPL011C	12	0,75
201	YPR148C	10	1,1
203	YOL103W	12	0,75
205	YOR016C	14	0,79
207	YPL079W	15	1,33
209	YOR260W	7	1,29
211	YOR360C	15	1,53
213	YDL060W	15	0,67
215	YDL005C	15	1
217	YPL210C	15	1,13
219	YMR118C	14	1,14
221	YPR052C	14	1,07
223	YLR224W	10	2,1
225	YLR275W	9	2,44
227	YMR154C	15	1,27
229	YDR205w	12	1,08
231	YPR067C	12	2,17
233	YNR006W	14	2,29
235	YOR084W	10	2,2
237	YGR054W	14	1,5
239	YGL106W	13	3,46
241	YAL067C	13	1,62
243	YIL023c	15	1,73
245	YBR064W	15	1,13
247	b0020	13	0,78
249	b2143	15	3,13
251	b2796	15	2,33
253	b2082	14	2,43
255	b0124	15	2,87
257	b3118	15	1,07
259	b1830	15	2,07
261	b1453	14	2,29
263	b2664	13	1,85
265	b2799	15	1,87

267	b3327	15	1,47
269	b0970	15	1,33
271	YER003C	5	1
273	YGL027W	9	0,56
275	YBR112C	10	0,5
277	YNL079C	9	0,67
279	YFR042W	9	0,78
281	YER137C	3	0
283	YKL103C	9	1
285	YNL090W	6	0,83
287	YGR161C	7	0,86
289	YDR071C	9	0,78

0339.0.1 In a further experiment, for individual major lines, other lines containing the same gene construct, but resulting from a different transformation event were tested. In these lines, the specific SRP encoding yeast genes is incorporated at a different site in the plant genom. The results are summarised in table 4 in accordance to table 3. The results demonstrate the dependence of the stress tolerance and/or resistance in plants on the expression of the SRP, rather than the insertion event.

0340.0.1 Table 4: Drought tolerance of transgenic *Arabidopsis thaliana* expressing selected SRP encoding genes from *Saccharomyces cerevisiae* or *E. coli* after imposition of drought stress on 3 week old plants in a third experiment using one plant from several independent transgenic lines each (experiment 3). Drought tolerance is measured for the indicated number of transgenic plants (Plants tested) as the average number of days (Average days of survival after WT) that the transgenic plants survived after the control (untransformed wild type). The hit percentage indicates the fraction of the tested plants of the major line that was actually resistant, i.e. the number '50' indicates that half of the tested plants were resistant (survived longer than WT). For WT, this column has the value '0'.

Sequ. ID No.	Gene	Number other lines tested	Average days of survival after WT
1	YGL263W	7	1,43
3	YGR004W	8	1
5	YGI1014W	9	0,75
7	YGL239C	5	1
9	YBL060W	8	2
11	YGL166W	8	0,63
13	YDL202W	8	0,25

15	YAL046C	7	1,3
17	YDR101C	9	1,1
19	YDR108W	9	0,22
21	YAL084W	8	3
23	YDR134C	6	2,2
25	YFL031W	9	2,3
27	YFL052W	5	1,4
31	YBR025C	5	1,2
33	YER174C	9	0,5
35	YBR051W	6	1,3
37	YER175C	4	1,4
39	YDR521W	3	0,7
43	YER123W	6	0,3
45	YDR415C	7	1,4
47	YEL052W	3	1,33
49	YDR536W	8	1,25
51	YDR513W	4	1,5
53	YEL045C	5	1,2
55	YEL041W	8	0,88
57	YDL238C	8	0,17
59	YDR282W	2	2,2
61	YBR258C	7	1,7
63	YCL001W-A	7	0,57
65	YBR274W	9	0,78
67	YHR090C	6	2,7
69	YGR121C	9	0,8
71	YGR127W	6	2,5
73	YGR130C	5	3
75	YKL037W	9	0,78
77	YKL051W	5	1,8
79	YKL120W	8	0,63
81	YKL011C	5	1,4
83	YKL017C	5	0,6
85	YKL049C	9	1,4
87	YKL132C	7	0,7
89	YGR126W	6	1,3
91	YKL070W	6	2
93	YKL058W	8	0,88
95	YHR130C	9	2,1
97	YIL070C	7	0,71
99	YHR1195W	9	2,1
101	YIR022W	9	1,22
103	YJL089W	7	0,8
105	YJL172W	4	1
107	YHR113W	7	1,6
109	YHR175W	3	1

111	YGR212W	8	0,88
113	YJL024C	6	1,33
115	YGR180C	8	2,7
117	YJL179W	8	1,8
119	YJL001W	9	0,7
121	YJL208C	6	1,7
123	YJL152W	8	0,3
125	YJL131C	6	1
127	YJL151C	8	1,6
129	YLR441C	7	2,6
131	YLR415C	9	0,3
133	YLR212C	7	2,14
135	YLR029C	8	0,25
137	YLL041C	7	0,86
139	YLR105C	7	0,29
141	YIL136W	9	1,75
143	YLR215C	8	1,25
145	YLR321C	7	0,86
147	YMR260C	8	0,60
149	YNL120C	9	1,56
151	YLR407W	5	0,4
153	YMR197C	9	1,22
155	YMR100W	8	0,88
157	YMR210W	6	0,88
159	YMR318C	8	0,63
161	YMR069W	9	0,44
163	YNL076W	4	1,75
165	YNL024C	9	1,70
167	YNL125C	7	2,14
169	YNL029C	9	1,80
171	YMR115W	9	1,44
173	YNL244C	8	0,25
175	YNL331C	8	1,33
177	YNR018W	9	1,22
179	YNL277W	8	1
181	YOL118C	9	0,89
183	YOL128W	8	0,88
185	YOR020C	9	0,44
187	YOL116W	9	1,67
189	YOR305W	7	0,28
191	YPL267W	4	0,75
193	YPL229W	5	1,6
195	YPL038W	5	0,4
197	YPR047W	2	1
199	YPL011C	6	0,5
201	YPR148C	9	0,33

203	YOL103W	9	0,33
205	YOR016C	9	0,56
211	YOR360C	8	0,38
213	YDL060W	8	0,5
215	YDL005C	9	0,44
217	YPL210C	8	1,5
219	YMR110C	10	1,1
221	YPR052C	7	0,86
223	YLR224W	9	1,22
225	YLR275W	8	1,75
227	YMR151C	9	1,11
229	YDR205w	4	1
231	YPR037C	5	3,4
233	YNR008W	8	0,75
235	YOR084W	6	0,5
239	YGL103W	7	2,14
241	YAL067C	6	1,83
243	YIL023c	1	3
245	YBR064W	7	0,71
247	b0020	4	1,5
249	b2146	10	0,1
251	b2786	11	0,72
253	b2082	9	1,22
255	b0124	9	3,3
257	b3116	8	1
259	b1830	7	1,71
261	b1453	8	1,13
263	b2664	9	1
267	b3327	10	0,8
269	b0970	8	1,5
271	YER003C	12	2,08
273	YOL027W	14	2,14
275	YBH112C	11	3,3
277	YNL079C	13	2,69
279	YFR042W	7	2,3
281	YER137C	13	2,2
283	YKL103C	10	2,8
285	YNL090W	12	4,33
287	YGR161C	12	2,7
289	YDR071C	11	3

0341.0.1 Chlorophyll fluorescence measurements of photosynthetic yield confirmed that severe drought stress completely inhibited photosynthesis in the control

plants, but the transgenic major lines maintained photosynthetic function longer (Table 5).

- 0342.0.1 Table 5: Drought tolerance of transgenic *Arabidopsis thaliana* expressing the various SRP encoding genes from *Saccharomyces cerevisiae* or *E. coli* after imposition of drought stress on 3 week old plants in a third experiment using several plants from one transgenic line (experiment 3). Drought tolerance is reported as photosynthetic yield measured by chlorophyll fluorescence measured at three different time point during the drought stress experiment, and compared to the untransformed wild type control. For each transgenic line, the average of 5 replicate plants is indicated, the wild type value is the average of 20-25 plants measured in the same experiment.

Sequ. ID No.	Gene	Photosynthetic yield 6 days after final watering	wild type	Photosynthetic yield 10 days after final watering	wild type	Photosynthetic yield 14 days after final watering	wild type
1	YGL283W	751	766	765	654	254	106
3	YGR004W	759	766	755	654	216	106
5	YGR014W	759	766	752	654		
7	YGL239C	782	757	786	610		
9	YBL080W	743	757	782	610	108	16
11	YGL166W	752	736	747	709		
13	YDL202W	780	766	508	548		
15	YAL046C	788	730	758	518	216	20
19	YDR108W	756	736	739	709	0	20
23	YDR134C	757	730	765	549	273	20
25	YFL031w	763	760	766	549	784	20
27	YFL062W	757	757	753	610		
29	YFL042C	743	757	780	610		
31	YBR025C	763	760	762	549	831	20
35	YBR051W	741	760	696	549	456	20
37	YER175C	749	757	627	610	140	16
43	YER123W	767	757	780	610	147	16
47	YEL052W	750	736	773	710	177	20
49	YDR536W	753	736	772	709	293	20
51	YDR513W	782	794	660	413	411	54
53	YEL045C	755	736	553	709	147	20
55	YELD41W	758	736	769	709	129	20

59	YBR282W	758	760	724	549	221	20
61	YBR258C	759	757	772	610	144	16
65	YBR274W	749	736	769	709	148	20
67	YHR090C	749	760	765	549	620	20
71	YGR127W	740	549	576	20		
73	YGR150C	771	760	742	549	618	20
75	YKL037W	761	736	760	709	134	20
77	YKL051W	733	760	740	549	153	20
79	YKL120W	759	736	518	709		
81	YKL011C	750	760	694	549	434	20
83	YKL017C	744	549	734	549	754	20
89	YGR128W	784	760	750	549	159	20
91	YKL070W	774	760	734	549	244	20
93	YKL058W	752	766	765	654	495	20
95	YHR190C	772	760	756	549	147	20
97	YIL070C	768	766	755	654		
99	YHR195W	753	757	693	610	141	16
101	YIR022W	761	736	771	709		
105	YJL172W	756	766	758	654	298	20
107	YHR113W	749	760	754	549	142	20
109	YHR175W	768	766	758	654	485	106
111	YGR212W	777	766	748	654		
113	YJL024C	762	766	758	654	736	106
115	YGR180C	763	757	779	610		
117	YJL179W	744	760	706	549	310	20
119	YJL001W	748	757	519	610	135	16
121	YJL208C	685	549	49	20		
123	YJL152W	754	757	723	610		
125	YJL131C	750	757	758	610		
127	YJL151C	755	760	764	549	152	20
129	YLR441C	745	760	762	549	277	20
131	YLR415C	739	757	503	610	144	16
133	YLR212C	740	736	759	709	103	20
135	YLR029C	746	736	790	700	292	20
139	YLR105C	751	736	784	709		
141	YIL138W	749	736	779	710	422	20
143	YLR215C	752	736	774	709	151	20
145	YLR321C	749	736	767	709	145	20
147	YMR260C	774	766	763	654	691	106
149	YNL120C	764	766	740	654	298	20
151	YLR407W	774	766	640	654	138	106
153	YMR197C	751	736	723	709	63	20
155	YMR100W	770	766	596	654	171	20
157	YMD210W	753	766	755	654	733	20
159	YMR318C	761	736	780	709	135	20
161	YMR069W	756	766	750	654	519	20

163	YNL076W	765	766	757	654	244	20
165	YNL024C	767	766	761	654	273	20
167	YNL125C	761	766	750	654	263	20
169	YNL029C	764	766	758	654		
171	YMR115W	755	736	739	709		
173	YNL244C	774	766	686	654	94	20
175	YNL334C	761	736	756	709		
177	YNR018W	756	736	749	709		
181	YOL118C	727	736	756	709	280	20
183	YOL123W	747	736			140	20
185	YOR020C	764	766	748	654	207	20
187	YOL116W	774	766	735	654	135	20
189	YOR305w	773	769	585	245		
191	YPL267W	757	767	756	548		
193	YPL229w	781	769	752	245		
197	YPR047W	761	769	597	245		
199	YPL011C	766	769	582	245		
201	YPR148C	771	769	401	245		
203	YOL103W	769	769	237	245		
205	YOR016C	770	769	523	245		
211	YOR360C	771	769	651	245		
215	YDL005C	782	769	702	245		
217	YPL210C	794	769	735	245		
219	YMR119C	777	766	499	272		
221	YPR052C	772	766	293	272		
223	YLR224W	767	765	434	272		
225	YLR275W	741	766	760	272		
227	YMR154C	750	766	734	272		
229	YDR205w	767	766	241	272		
231	YPR037C	759	766	740	272		
233	YNR008W	746	766	782	272		
235	YOR064W	758	766	765	272		
237	YOR054W	766	766	140	272		
239	YGL106W	760	766	477	272		
241	YAL037C	759	766	681	272		
243	YIL023c	769		814			
245	YBR064W	745	750	770	576	117	31
249	b2148	736	766	740	272		
251	b2796	761	766	319	272		
253	b2082	756	766	706	272		
255	b0124	756	766	571	272		
257	b3116	765	766	600	272		
259	b1830	757	766	772	272		
261	b1458	750	766	648	272		
263	b2604	764	766	521	272		
265	b2799	768	766	615	272		

267	b8327	766	768	799	272		
269	b0070	764	768	560	272		
271	YER003C	758	760	769	549	729	20
273	YCL027W	749	760	770	549	145	20
275	YBR112C	760	760	760	549	731	20
277	YNL078C	763	766	762	654	216	20
279	YFR042W	789	760	739	549	232	20
281	YER137C	760	760	728	549	468	20
283	YKL103C	747	760	763	549	791	20
285	YNL090W	757	760	783	549	403	20
287	YGR161C	742	760	753	549	225	20
289	YDR071C	737	757	793	610	707	10

0343.0.4 Metabolic analysis of transgenic plants

The described metabolic changes in transgenic plants were identified using the following experimental procedure:

5 0344.0.4 a) Growth and treatment of plants

0345.0.4 Plants were grown in climate chambers under standard conditions on pot soil for three weeks (see above). Eight days prior to harvest, water was withheld for part of the plants (8-day treatment). Four days prior to harvest, water was withheld for another group of plants (4-day treatment). The plants of "control treatment" were normally watered throughout the growth period. Plants due to be analysed in the same analytical sequence were grown side-by-side to avoid environmental influences.

10 0346.0.4 b) Sampling and storage of samples

0347.0.4 Sampling took place in the climate chamber. Green parts were cut with a pair of scissors, quickly weighed, and immediately put into a liquid nitrogen pre-cooled extraction thimble. Racks with extraction thimbles were stored at -80°C until extraction.

15 0348.0.4 c) Freeze-drying

Plants were not allowed to thaw or reach temperatures > -40°C until either the first contact with solvents or the removal of water by freeze-drying.

0349.0.4 The sample rack with extraction thimbles was put into the pre-cooled (-40°C) freeze-dryer. The starting temperature for the main drying phase was -35°C, pressure was 0.120 mbar. For the drying process, parameters were changed according to a pressure and temperature program. The final temperature (after 12 hours) was +30°C, pressure was 0.001 - 0.004 mbar. After shutting down the vacuum pump and cooling machine, the system was aired with dried air or Argon.

25 0350.0.4 d) Extraction

0351.0.4 Extraction thimbles with plant material were transferred to 5 mL extraction cells on the ASE (Accelerated Solvent Extractor ASE 200 with Solvent Controller and AutoASE-Software (DIONEX)) immediately after freeze-drying.

0352.0.4 Polar substances were extracted with approximately 10 mL
5 **Methanol/Water (80/20, v/v)** at $T = 70\text{ }^{\circ}\text{C}$ und $p = 140\text{ bar}$, 5 min heating phase, 1 min static Extraction. Lipid substances were extracted with approximately 10 mL **Methanol/Dichlormethan (40/60, v/v)** at $T = 70\text{ }^{\circ}\text{C}$ und $p = 140\text{ bar}$, 5 min heating phase, 1 min static Extraction. Both extracts were collected in one extraction vial (Centrifuge tubes, 50 mL with screw-on lid and Septum for ASE (DIONEX)).

10 **0353.0.4** The following internal standards were added to the extracts: LC-Standards L-Methionine-d3, Boc-Ala-Gly-Gly-Gly-OH, L-Tryptophan-d5, Arginine- $^{18}\text{C}_6$ - $^{15}\text{N}_3$, CoEnzyme Q1,2,4 and ribitol, L-glycine-2,2-d2, L-alanine-2,3,3,3-d4, alpha-methyl-glucopyranoside, nonadecanoic acid methyl ester, undecanoic acid methyl ester, tridecanoic acid, pentadecanoic acid, nonacosanoic acid. To the resulting
15 mixture, 8 mL water were added. The solid residues of plant and extraction thimble were discarded.

0354.0.4 The extract was centrifuged at 1400 g for 5-10 minutes to speed-up phase-separation. For GC and LC analysis, 1 mL each was taken from the colourless methanol/water upper (polar) phase. The remaining upper phase was discarded. Of the
20 dark-green, organic bottom phase 0.5 mL was taken for GC and LC analysis, respectively. All sample aliquots were evaporated using a IR-Dancer Infrared vacuum evaporator (Hettich), using a temperature maximum of 40°C and a maximum pressure of 10 mbar.

0355.0.4 e) LC/MS- and LC/MSMS-Analysis
25 HPLC mobile phase was added to the lipid and polar residues, respectively (volume adjusted to the weighted sample) and an HPLC analysis using gradient elution was performed.

0356.0.4 f) Derivatisation of the lipid phase for GC/MS-Analysis

0357.0.4 For transesterification, a mixture of 140 μL chloroform, 38 μL HCl (37%
30 HCl in water), 320 μL methanol and 20 μL toluol was added to the residue. The sample container was carefully closed and reaction was carried out at 100°C for 2 hours. Subsequently, the solution was evaporated and the pellet was dried completely.

0358.0.4 The methoxylation of carbonyl groups was achieved by a reaction with 100 μL methoxyamine-hydrochloride (5 mg/mL in Pyridine) for 1.5 hours at 60°C, in a
35 closed vial. 20 μL of a mixture of linear, odd-numbered fatty acids was added to provide a time standard. Finally, derivatisation with 100 μL N-Methyl-N-(trimethylsilyl)-

2,2,2-trifluoroacetamide (MSTFA) took place in a closed vial for 30 minutes at 60°C. The final volume for GC Injection was 220 µL.

0359.0.4 g) Derivatisation of the polar phase for GC/MS-Analysis

0360.0.4 The methoximation of carbonyl groups was achieved by a reaction with 50 µL methoxyamine-hydrochloride (5 mg/mL in Pyridine) for 1.5 hours at 60°C, in a closed vial. 10 µL of a mixture of linear, odd-numbered fatty acids was added to provide a time standard. Finally, derivatisation with 50 µL N-methyl-N-(trimethylsilyl)-2,2,2-trifluoroacetamide (MSTFA) took place in a closed vial for 30 minutes at 60°C. The final volume for GC injection was 110 µL.

0361.0.4 h) Analysis of different plant samples

0362.0.4 Samples were measured in sequences of 20. Each sequence contained 5 wild type and 5 transgenic plants grown under control conditions, as well as 5 wild type and 5 transgenic plants from either the 4 day or 8 day drought treatment.

0363.0.4 The peak height or peak area of each analyte (metabolite) was divided through the peak area of the respective internal standards. Data was normalised using the individual sample fresh weight. The resulting values were divided by the mean values found for wild type plants grown under control conditions and analysed in the same sequence, resulting in the so-called X-folds or ratios (see table 7 - 14), which represent values independent of the analytical sequence. These ratios indicate the behavior of the metabolite concentration of the target plants in comparison to the concentration in the wild type control plants.

0364.0.4 In table 6 the results of the metabolite screening for the plants transformed in genes YOL027W, YBR112C, YNL079C, YER137C, YNL103C, YNL090W, YGR161C, YDR071C are shown.

0365.0.4 Tables 6: Details on screening of metabolic activity.

metabolite	wild type			YDR071C		
	control	4 days	8 days	control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54			
2-hydroxy-palmitic acid	1,00	1,11	1,26	1,18		
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,96			

beta-apo-8' carotenal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26			
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienoic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienoic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 mc)	1,00	1,19	1,28			
delta-15-cis-tetracosenoic acid (c24:1 mc)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
cerotic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthin	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42	0,98		
gamma-linolenic acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,21	3,08			
glucose	1,00	14,27	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,69			
glycerate	1,00	1,87	2,04			
glycinaldehyde	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,20	1,66			
iso-maltose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,80	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38			
luteine	1,00	1,26	1,33			
malate	1,00	2,91	3,46			
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			

methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,16	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
stapline acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,98	3,48			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,09			
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,86	1,18			
zearcanthine	1,00	1,27	1,34			

	wild type			YER137C		
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,50	2,15		5,67
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,66	1,81	1,55		1,73
alanine	1,00	0,64	0,64	1,32		0,94
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16		1,26	0,63
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,96			
beta-apo-8' carotenal	1,00	1,21	1,22			
beta-carotene	1,00	1,26	1,26			
beta-sitosterol	1,00	1,39	1,51	0,88	1,17	1,35
beta-tocopherol	1,00	0,54	0,60	2,70		5,03
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid	1,00	1,01	1,04			

(c16:2 me)						
hexadecatrienoic acid (c16:3 mc)	1,00	1,19	1,29			
myristic acid (c14:0 mc)	1,00	1,19	1,28			
delta-15-cis-tetradecenoic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,66		1,10	1,29
cerotic acid (c26:0)	1,00	0,74	1,00	3,24	1,78	
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32	4,44		10,51
gamma-tocopherol	1,00	0,54	0,60	2,78		5,83
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,89			
glycerate	1,00	1,87	2,04	1,17	2,32	
glyceraldehyde	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41	1,12	1,57	2,06
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,60			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,26	1,66			
iso-maltose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,80	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02	2,01	1,74	2,03
linoleic acid (c18:2 (c0, c12))	1,00	1,19	1,38			
lutidine	1,00	1,28	1,33			
malate	1,00	2,91	3,46	1,67	5,70	8,01
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			

putrescine	1,00		0,89			
pyruvate	1,00	1,80	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	8,48			
serine	1,00	0,88	1,18			
shikimate	1,00	1,11	1,07		1,40	1,50
sinapine acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,95			
succinate	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,58	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,58	1,94			
valine	1,00	0,98	1,18			
zeaxanthine	1,00	1,27	1,34			

metabolite	wild type			YBR112C		
	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54	0,63		
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydro- γ -phenylalanine (=dopa)	1,00	1,89	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,58	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40	1,12		1,42
alpha-tocopherol	1,00	1,05	1,14			
aminocaproic acid	1,00	1,73	1,65	3,90	12,95	
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,98			
beta-apo-8' carotenol	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,28	1,35		
beta-sitosterol	1,00	1,38	1,51	1,19		
beta-tocopherol	1,00	0,54	0,60	0,70		
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienoic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28			
delta-15-cis-tetradecenoic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65	1,42		
cerotic acid (c28:0)	1,00	0,74	1,00			

citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferric acid	1,00	1,37	1,47	1,20		
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42			
γ -aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60	0,70		
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,69			
glycerate	1,00	1,87	2,04			
glyceraldehyde	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,88	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,80	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38			
lutine	1,00	1,28	1,33	1,17		
malate	1,00	2,91	3,46			
mannose	1,00	16,10	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38	1,11		
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,70			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			

sinapine acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,99	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,58	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,98	1,18			
zeaxanthine	1,00	1,27	1,34			

	wild type			YGR161C		
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54			
2-hydroxy-palmitic acid	1,00	1,11	1,28			
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,88	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,78	1,68			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,29	0,33			
aspartic acid	1,00	2,72	2,86			
beta-eps-8' carotinal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26			
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid (c16:2 me)	1,00	1,01	1,04	1,14		
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28	1,22		
delta-15-cis-tetraacsenic acid (c24:1 me)	1,00	1,16	1,31			
campesterol	1,00	1,32	1,65			
carotic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosanoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			

fructose	1,00	14,10	19,79			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42	1,15		
γ -aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,69			
glycerate	1,00	1,87	2,04			
glyceralinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,28	1,66			
iso-mallose	1,00	2,63	3,02			
isopentenyl pyrophosphate	1,00	1,60	2,62			
leucine	1,00	1,34	1,71			
lignoceric acid (c24:0)	1,00	0,91	1,09			
linoleic acid (c18:2 (c9, c12))	1,00	1,10	1,38			
lutetins	1,00	1,28	1,33			
malate	1,00	2,91	3,46			
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,21	1,49			
methylgalactopyranoside	1,00	1,25	1,36	1,18		
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,78			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
stearic acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			

threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,56	2,01			
ubiquinolone	1,00	1,02	1,20			
udp-glucose	1,00	1,58	1,94			
valine	1,00	0,98	1,18			
zeaxanthine	1,00	1,27	1,34			

YKL103C						
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54			
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminosadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,96			
beta-apo-8' carotenol	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26			
beta-cholesterol	1,00	1,30	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid (c16:2 me)	1,00	1,01	1,04	1,18	1,16	1,30
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28			
delta-15-cis-tetradecenoic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
corolic acid (c26:0)	1,00	0,74	1,00			
citrutline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	11,10	19,70			
fumarate	1,00	5,19	9,33			
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
glucuronic acid	1,00	2,24	3,08			

glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,69			
glycerate	1,00	1,87	2,04			
glycerinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,26	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,83	3,02			
isopentenyl pyrophosphate	1,00	1,50	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38			
lutein	1,00	1,26	1,33			
malate	1,00	2,91	3,46			
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine					1,70	1,52
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylethamine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	1,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
sinapine acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,28	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,98	1,18			

zeaxanthine	1,00	1,27	1,34			
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YCL027W						
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54			
2-hydroxy-palmitic acid	1,00	1,11	1,25			
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00					
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,61	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			
alpha-tocopherol	1,00	1,05	1,14			
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,98			
beta-apo-8' carotenal	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,28			
beta-sitosterol	1,00	1,38	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid (c18:2 me)	1,00	1,01	1,04			
hexadecadienic acid (c16:3 me)	1,00	1,19	1,28			
margaric acid (c17:0 me)	1,00	1,19	1,28			
delta-15-cis-tetacosenic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
cerotic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosanoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47	0,79	0,74	0,80
fructose	1,00	14,10	19,78			
lumarate	1,00	5,18	9,33			
galactose	1,00	1,29	1,42			
g-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,87	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,69			
glycerate	1,00	1,87	2,04			
glyceraldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			

glycerol-3-phosphate	1,00	1,88	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	6,32			
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,89	3,02			
isopentenyl pyrophosphate	1,00	1,80	2,62			
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38			
luteine	1,00	1,28	1,33			
malate	1,00	2,91	3,48			
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,76			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
sinapic acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,98	3,19			
sulfate	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophan	1,00	1,13	1,89			
tyrosine	1,00	1,58	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,94			
valine	1,00	0,98	1,19			
zeaxanthine	1,00	1,27	1,34			

YNL079C						
metabolite	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,54	0,59		
2-hydroxy-palmitic acid	1,00	1,11	1,25			

3,4-dihydroxyphenylalanine (=dopa)	1,00	1,83	3,37			
3-hydroxy-palmitic acid	1,00		1			
5-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c0, c12, c15))	1,00	1,24	1,40		1,53	1,56
alpha-tocopherol	1,00	1,05	1,14		2,64	3,68
aminoadipic acid	1,00	1,73	1,65			
anhydroglucose	1,00	1,02	1,16			
arginine	1,00	0,39	0,33			
aspartic acid	1,00	2,72	2,96			
beta-apo-8' carotenol	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,26		1,26	1,20
beta-sitosterol	1,00	1,38	1,51			
beta-tocopherol	1,00	0,54	0,60	0,73		0,56
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10 cis-hexadecadienic acid (c18:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28	1,22	1,53	1,36
delta-15-cis-tetracosenic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65		1,79	1,62
cerotic acid (c26:0)	1,00	0,74	1,00			
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,81			
ferulic acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumaric	1,00	5,12	9,33			
galactose	1,00	1,28	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			
gluconic acid	1,00	2,24	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,60			
glycerate	1,00	1,87	2,04			
glycerinaldehyd	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,11			
glycine	1,00	0,26	0,26			
homocysteine	1,00	3,61	0,69			
inositol	1,00	4,19	6,32		4,73	6,12
isoleucine	1,00	1,28	1,66			
iso-maltose	1,00	2,63	3,02		4,42	4,93

isopentenyl pyrophosphate	1,00	1,80	2,82			
leucine	1,00	1,34	1,74		1,51	2,19
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,10	1,38			
lutine	1,00	1,26	1,33			
malate	1,00	2,81	3,46	1,49		5,72
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,18	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
ribonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
sinapic acid	1,00	2,74	3,11		3,89	2,79
stearic acid (c18:0)	1,00	1,18	1,35			
succinate	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,28	1,38			
tryptophane	1,00	1,15	1,89		2,68	2,98
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20		0,88	1,02
udp-glucose	1,00	1,53	1,84			
valine	1,00	0,93	1,18			
zeaxanthine	1,00	1,27	1,34			

metabolite	wild type			YNL090W		
	Control	4 days	8 days	Control	4 days	8 days
2,3-dimethyl-5-phytylquinol	1,00	0,50	0,64			
2-hydroxy-palmitic acid	1,00	1,11	1,25	1,15	1,25	
3,4-dihydroxyphenylalanine (=dopa)	1,00	1,88	3,37			
3-hydroxy-palmitic acid	1,00					
6-oxoproline	1,00	1,56	1,81			
alanine	1,00	0,64	0,64			
alpha linolenic acid (c18:3 (c9, c12, c15))	1,00	1,24	1,40			

alpha-tocopherol	1,00	1,05	1,14	1,30		5,28
aminoadipic acid	1,00	1,73	1,85			
anhydroglucose	1,00	1,02	1,18			
arginine	1,00	0,39	0,33		0,85	
aspartic acid	1,00	2,77	2,98			
beta-apo-8' carotene	1,00	1,21	1,22			
beta-carotene	1,00	1,25	1,28	1,15		1,31
beta-sitosterol	1,00	1,39	1,51			
beta-tocopherol	1,00	0,54	0,60			
palmitic acid	1,00	1,07	1,25			
delta-7-cis,10-cis-hexadecadienic acid (c16:2 me)	1,00	1,01	1,04			
hexadecatrienic acid (c16:3 me)	1,00	1,19	1,29			
margaric acid (c17:0 me)	1,00	1,19	1,28			
delta-15-cis-tetraacosenic acid (c24:1 me)	1,00	1,16	1,34			
campesterol	1,00	1,32	1,65			
cerotic acid (c26:0)	1,00	0,74	1,00	2,98	3,93	
citrulline	1,00	0,51	0,33			
cryptoxanthine	1,00	1,00	0,90			
eicosenoic acid (20:1)	1,00	0,81	0,61			
isuric acid	1,00	1,37	1,47			
fructose	1,00	14,10	19,78			
fumarate	1,00	5,19	8,33	0,78		
galactose	1,00	1,29	1,42			
gamma-aminobutyric acid	1,00	1,16	1,32			
gamma-tocopherol	1,00	0,54	0,60			1,69
gluconic acid	1,00	2,21	3,08			
glucose	1,00	14,97	20,73			
glutamine	1,00	0,98	1,17			
glutamic acid	1,00	2,01	2,39			
glycerate	1,00	1,87	2,04			
glycerinaldehyde	1,00	1,11	1,12			
glycerol	1,00	1,22	1,29			
glycerol-3-phosphate	1,00	1,86	2,41			
glycine	1,00	0,25	0,26			
homoserine	1,00	0,61	0,69			
inositol	1,00	4,19	8,32	1,46		9,70
isoleucine	1,00	1,28	1,68		3,54	4,86
iso-maltose	1,00	2,63	3,02	3,59	20,72	14,65
isupentenyl pyrophosphate	1,00	1,80	2,62	1,79		
leucine	1,00	1,34	1,74			
lignoceric acid (c24:0)	1,00	0,91	1,02			
linoleic acid (c18:2 (c9, c12))	1,00	1,19	1,38			

luteine	1,00	1,26	1,33			
malate	1,00	2,91	3,46	2,12		14,49
mannose	1,00	16,40	17,80			
triacontanoic acid	1,00	1,26	1,23			
methionine	1,00	1,13	1,12			
methylgalactofuranoside	1,00	1,24	1,49			
methylgalactopyranoside	1,00	1,25	1,36			
ornithine						
palmitic acid (c16:0)	1,00	1,16	1,38			
phenylalanine	1,00	0,92	1,10			
phosphate	1,00	2,15	2,73			
proline	1,00	1,23	4,77			
putrescine	1,00		0,39			
pyruvate	1,00	1,30	1,21			
raffinose	1,00	17,04	74,78			
r-bonic acid	1,00	2,32	3,43			
serine	1,00	0,98	1,13			
shikimate	1,00	1,11	1,07			
sinapine acid	1,00	2,74	3,44			
stearic acid (c18:0)	1,00	1,18	1,35			
succinic	1,00	2,98	3,49			
sucrose	1,00	1,42	1,70			
threonine	1,00	1,26	1,68			
tryptophane	1,00	1,13	1,89			
tyrosine	1,00	1,56	2,01			
ubichinone	1,00	1,02	1,20			
udp-glucose	1,00	1,53	1,91			
valine	1,00	0,98	1,18	1,13	1,53	1,80
zeaxanthine	1,00	1,27	1,34			

0366.0.1 Example 2

0367.0.1 Engineering stress-tolerant *Arabidopsis* plants by over-expressing stress related protein encoding genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa* using stress-inducible and tissue-specific promoters.

0368.0.1 Transgenic *Arabidopsis* plants were created as in example 1 to express the stress related protein encoding transgenes under the control of either a tissue-specific or stress-inducible promoter. Constitutive expression of a transgene may cause deleterious side effects. Stress inducible expression was achieved using promoters selected from those listed above in Table 1.

0369.0.1 T2 generation plants were produced and treated with drought stress in two experiments. For the first drought experiment, the plants were deprived of water until the plant and soil were desiccated. At various times after withholding water, a normal watering schedule was resumed and the plants were grown to maturity. Seed yield was determined as seeds per plant. At an equivalent degree of drought stress, tolerant plants were able to resume normal growth and produced more seeds than non-transgenic control plants. Proline content of the leaves and stomatal aperture were also measured at various times during the drought stress. Tolerant plants maintained a lower proline content and a greater stomatal aperture than the non-transgenic control plants.

0370.0.1 An alternative method to impose water stress on the transgenic plants was by treatment with water containing an osmolyte such as polyethylene glycol (PEG) at specific water potential. Since PEG may be toxic, the plants were given only a short term exposure and then normal watering was resumed. As above, seed yields were measured from the mature plants. The response was measured during the stress period by physical measurements, such as stomatal aperture or osmotic potential, or biochemical measurements, such as accumulation of proline. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels.

0371.0.1 The transgenic plants with a constitutive promoter controlling transcription of the transgene were compared to those plants with a drought-inducible promoter in the absence of stress. The results indicated that the metabolite and gene expression changes did not occur when plants with the stress-inducible promoter were grown in the absence of stress. These plants also had higher seed yields than those with the constitutive promoter.

0372.0.1 Example 3

0373.0.1 Over-expression of stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa* provides tolerance of multiple abiotic stresses.

0374.0.1 Plants that exhibit tolerance of one abiotic stress often exhibit tolerance of another environmental stress or an oxygen free radical generating herbicide. This phenomenon of cross-tolerance is not understood at a mechanistic level (McKersie and Leshem, 1994). Nonetheless, it is reasonable to expect that plants exhibiting enhanced drought tolerance due to the expression of a transgene might also exhibit tolerance of low temperatures, freezing, salt, air pollutants such as ozone, and other abiotic

stresses. In support of this hypothesis, the expression of several genes are up or down-regulated by multiple abiotic stress factors including cold, salt, osmoticum, ABA, etc (e.g. Hong et al. (1992) Developmental and organ-specific expression of an ABA- and stress-induced protein in barley. *Plant Mol Biol* 18: 663-674; Jagendorf and Takabe (2001) Inducers of glycinebetaine synthesis in barley. *Plant Physiol* 127: 1827-1835); Mizoguchi et al. (1996) A gene encoding a mitogen-activated protein kinase is induced simultaneously with genes for a mitogen-activated protein kinase and an S6 ribosomal protein kinase by touch, cold, and water stress in *Arabidopsis thaliana*. *Proc Natl Acad Sci U S A* 93: 765-769; Zhu (2001) Cell signaling under salt, water and cold stresses. *Curr Opin Plant Biol* 4: 401-406).

0375.0.1 To determine salt tolerance, seeds of *Arabidopsis thaliana* were sterilized (100% bleach, 0.1% TritonX for five minutes two times and rinsed five times with ddH₂O). Seeds were plated on non-selection media (1/2 MS, 0.6% phytagar, 0.5g/L MES, 1% sucrose, 2 µg/ml benamyl). Seeds are allowed to germinate for approximately ten days. At the 4-5 leaf stage, transgenic plants were potted into 5.5cm diameter pots and allowed to grow (22 °C, continuous light) for approximately seven days, watering as needed. To begin the assay, two liters of 100 mM NaCl and 1/8 MS was added to the tray under the pots. To the tray containing the control plants, three liters of 1/8 MS was added. The concentrations of NaCl supplementation were increased stepwise by 50 mM every 4 days up to 200 mM. After the salt treatment with 200 mM, fresh and dry weights of the plants as well as seed yields were determined.

0376.0.1 To determine cold tolerance, seeds of the transgenic and cold lines were germinated and grown for approximately 10 days to the 4-5 leaf stage as above. The plants were then transferred to cold temperatures (5 °C) and grown through the flowering and seed set stages of development. Photosynthesis was measured using chlorophyll fluorescence as an indicator of photosynthetic fitness and integrity of the photosystems. Seed yield and plant dry weight were measured as an indicator of plant biomass production.

0377.0.1 Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0378.0.1 Example 4

0379.0.1 Engineering stress-tolerant alfalfa plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

0380.0.1 A regenerating clone of alfalfa (*Medicago sativa*) was transformed using the method of (McKersie et al., 1998 *Plant Physiol* 119: 839-847). Regeneration and transformation of alfalfa is genotype dependent and therefore a regenerating plant is

required. Methods to obtain regenerating plants have been described. For example, these can be selected from the cultivar Rangelander (Agriculture Canada) or any other commercial alfalfa variety as described by Brown DCW and A Atanassov (1985. Plant Cell Tissue Organ Culture 4: 111-112). Alternatively, the RA3 variety (University of Wisconsin) has been selected for use in tissue culture (Walker et al., 1978 Am J Bot 65:654-659).

0381.0.1 Petiole explants were cocultivated with an overnight culture of *Agrobacterium tumefaciens* C58C1 pMP90 (McKersie et al., 1999 Plant Physiol 119: 839-847) or LBA4404 containing a binary vector. Many different binary vector systems have been described for plant transformation (e.g. Art, G. in *Agrobacterium Protocols*, Methods in Molecular Biology vol 44, pp 47-62, Garland KMA and MR Davey eds. Humana Press, Totowa, New Jersey). Many are based on the vector pBIN19 described by Bevan (Nucleic Acid Research, 1984, 12:8711-8721) that includes a plant gene expression cassette flanked by the left and right border sequences from the Ti plasmid of *Agrobacterium tumefaciens*. A plant gene expression cassette consists of at least two genes – a selection marker gene and a plant promoter regulating the transcription of the cDNA or genomic DNA of the trait gene. Various selection marker genes can be used including the *Arabidopsis* gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patents 57673666 and 6225105). Similarly, various promoters can be used to regulate the trait gene that provides constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M59930 and X16673) was used to provide constitutive expression of the trait gene.

0382.0.1 The explants were cocultivated for 3 d in the dark on SH Induction medium containing 288 mg/ L Pro, 53 mg/ L thioproline, 4.35 g/ L K₂SO₄, and 100 µm acetosyringone. The explants were washed in half-strength Murashige-Skoog medium (Murashige and Skoog, 1962) and plated on the same SH induction medium without acetosyringone but with a suitable selection agent and suitable antibiotic to inhibit *Agrobacterium* growth. After several weeks, somatic embryos were transferred to B0i2Y development medium containing no growth regulators, no antibiotics, and 50 g/ L sucrose. Somatic embryos were subsequently germinated on half-strength Murashige-Skoog medium. Rooted seedlings were transplanted into pots and grown in a greenhouse.

0383.0.1 The T0 transgenic plants were propagated by node cuttings and rooted in Turface growth medium. The plants were defoliated and grown to a height of about 10 cm (approximately 2 weeks after defoliation). The plants were then subjected to drought stress in two experiments.

- 0384.0.1** For the first drought experiment, the seedlings received no water for a period up to 3 weeks at which time the plant and soil were desiccated. At various times after withholding water, a normal watering schedule was resumed. At one week after resuming watering, the fresh and dry weights of the shoots was determined. At an equivalent degree of drought stress, tolerant plants were able to resume normal growth whereas susceptible plants had died or suffered significant injury resulting in less dry matter. Proline content of the leaves and stomatal aperture were also measured at various times during the drought stress. Tolerant plants maintained a lower proline content and a greater stomatal aperture than the non-transgenic control plants.
- 0385.0.1** An alternative method to impose water stress on the transgenic plants was by treatment with a solution at specific water potential, containing an osmolyte such as polyethylene glycol (PEG). The PEG treatment was given to either detached leaves (e.g. Djilianov et al., 1997 Plant Science 129: 147-158) or to the roots (Wakabayashi et al., 1997 Plant Physiol 113: 967-973). Since PEG may be toxic, the plants were given only a short term exposure. The response was measured as physical measurements such as stomatal aperture or osmotic potential, or biochemical measurements such as accumulation of proline. Tolerant plants maintained their stomatal aperture and showed only slight changes in osmotic potential, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential. In addition the changes in proline and other metabolites were less in the tolerant transgenic plants than in the non-transgenic control plants.
- 0386.0.1** Tolerance of salinity and cold were measured using methods as described in example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.
- 0387.0.1 Example 5**
- 0388.0.1 Engineering stress-tolerant ryegrass plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa***
- 0389.0.1** Seeds of several different ryegrass varieties may be used as explant sources for transformation, including the commercial variety Gunne available from Svalof Weibull seed company or the variety Affinity. Seeds were surface-sterilized sequentially with 1% Tween-20 for 1 minute, 100 % bleach for 60 minutes, 3 rinses with 5 minutes each with de-ionized and distilled H₂O, and then germinated for 3-4 days on moist, sterile filter paper in the dark. Seedlings were further sterilized for 1 minute with 1% Tween-20, 5 minutes with 75% bleach, and rinsed 3 times with ddH₂O, 5 min each.

0390.0.1 Surface-sterilized seeds were placed on the callus induction medium containing Murashige and Skong basal salts and vitamins, 20 g/l sucrose, 150 mg/l asparagine, 500 mg/l casein hydrolysate, 3 g/l Phytigel, 10 mg/l BAP, and 5 mg/l dicamba. Plates were incubated in the dark at 25C for 4 weeks for seed germination and embryogenic callus induction.

0391.0.1 After 4 weeks on the callus induction medium, the shoots and roots of the seedlings were trimmed away, the callus was transferred to fresh media, maintained in culture for another 4 weeks, and then transferred to MSO medium in light for 2 weeks. Several pieces of callus (11-17 weeks old) were either strained through a 10 mesh sieve and put onto callus induction medium, or cultured in 100 ml of liquid ryegrass callus induction media (same medium as for callus induction with agar) in a 250 ml flask. The flask was wrapped in foil and shaken at 175 rpm in the dark at 23 C for 1 week. Sieving the liquid culture with a 40-mesh sieve collected the cells. The fraction collected on the sieve was plated and cultured on solid ryegrass callus induction medium for 1 week in the dark at 25C. The callus was then transferred to and cultured on MS medium containing 1% sucrose for 2 weeks.

0392.0.1 Transformation can be accomplished with either Agrobacterium or with particle bombardment methods. An expression vector is created containing a constitutive plant promoter and the cDNA of the gene in a pUC vector. The plasmid DNA was prepared from E. coli cells using Qiagen kit according to manufacturer's instruction. Approximately 2 g of embryogenic callus was spread in the center of a sterile filter paper in a Petri dish. An aliquot of liquid MSO with 10 g/l sucrose was added to the filter paper. Gold particles (1.0 µm in size) were coated with plasmid DNA according to method of Sanford et al., 1993 and delivered to the embryogenic callus with the following parameters: 500 µg particles and 2 µg DNA per shot, 1300 psi and a target distance of 8.5 cm from stopping plate to plate of callus and 1 shot per plate of callus.

0393.0.1 After the bombardment, calli were transferred back to the fresh callus development medium and maintained in the dark at room temperature for a 1-week period. The callus was then transferred to growth conditions in the light at 25 °C to initiate embryo differentiation with the appropriate selection agent, e.g. 250 nM Arsenal, 5 mg/l PPT or 50 mg/L kanamycin. Shoots resistant to the selection agent appeared and once rooted were transferred to soil.

0394.0.1 Samples of the primary transgenic plants (T0) are analyzed by PCR to confirm the presence of T-DNA. These results are confirmed by Southern hybridization in which DNA is electrophoresed on a 1% agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit

(Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.

0395.0.1 Transgenic T0 ryegrass plants were propagated vegetatively by excising tillers. The transplanted tillers were maintained in the greenhouse for 2 months until well established. The shoots were defoliated and allowed to grow for 2 weeks.

0396.0.1 The first drought experiment was conducted in a manner similar to that described in example 3. The seedlings received no water for a period up to 3 weeks at which time the plant and soil were desiccated. At various times after withholding water, a normal watering schedule was resumed. At one week after resuming watering, the lengths of leaf blades, and the fresh and dry weights of the shoots was determined. At an equivalent degree of drought stress, tolerant plants were able to resume normal growth whereas susceptible plants had died or suffered significant injury resulting in shorter leaves and less dry matter. Proline content of the leaves and stomatal aperture were also measured at various times during the drought stress. Tolerant plants maintained a lower proline content and a greater stomatal aperture than the non-transgenic control plants.

0397.0.1 A second experiment imposing drought stress on the transgenic plants was by treatment with a solution of PEG as described in the previous examples. Tolerance of salinity and cold were measured using methods as described in example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0398.0.1 Example 6

0399.0.1 Engineering stress-tolerant soybean plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

0400.0.1 Soybean was transformed according to the following modification of the method described in the Texas A&M patent US 5,164,310. Several commercial soybean varieties are amenable to transformation by this method. The cultivar Jack (available from the Illinois Seed Foundation) is a commonly used for transformation. Seeds were sterilized by immersion in 70% (v/v) ethanol for 8 min and in 25 % commercial bleach (NaOCl) supplemented with 0.1% (v/v) Tween for 20 min, followed by rinsing 4 times with sterile double distilled water. Seven-day seedlings were propagated by removing the radicle, hypocotyl and one cotyledon from each seedling. Then, the epicotyl with one cotyledon was transferred to fresh germination media in petri dishes and incubated at 25 °C under a 16-hr photoperiod (approx. 100 $\mu\text{E}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) for three weeks. Axillary nodes (approx. 4 mm in length) were cut from 3 – 4 week-old plants. Axillary nodes were excised and incubated in *Agrobacterium* LBA4404 culture.

0401.0.1 Many different binary vector systems have been described for plant transformation (e.g. An, G. In *Agrobacterium Protocols. Methods in Molecular Biology* vol 44, pp 17-82, Gartland KMA and MR Davey eds. Humana Press, Totowa, New Jersey). Many are based on the vector pBIN19 described by Bevan (*Nucleic Acid Research*, 1984, 12:8711-8721) that includes a plant gene expression cassette flanked by the left and right border sequences from the T1 plasmid of *Agrobacterium tumefaciens*. A plant gene expression cassette consists of at least two genes – a selection marker gene and a plant promoter regulating the transcription of the cDNA or genomic DNA of the trait gene. Various selection marker genes can be used including the *Arabidopsis* gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patents 57673666 and 6225105). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M59930 and X16673) was used to provide constitutive expression of the trait gene.

0402.0.1 After the co-cultivation treatment, the explants were washed and transferred to selection media supplemented with 500 mg/L timentin. Shoots were excised and placed on a shoot elongation medium. Shoots longer than 1 cm were placed on rooting medium for two to four weeks prior to transplanting to soil.

0403.0.1 The primary transgenic plants (T0) were analyzed by PCR to confirm the presence of T-DNA. These results were confirmed by Southern hybridization in which DNA is electrophoresed on a 1 % agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR DIG Probe Synthesis Kit (Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.

0404.0.1 Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels.

0405.0.1 Tolerance of drought, salinity and cold were measured using methods as described in example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0406.0.1 Example 7

0407.0.1 Engineering stress-tolerant Rapeseed/Canola plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

0408.0.1 Cotyledonary petioles and hypocotyls of 5-6 day-old young seedlings were used as explants for tissue culture and transformed according to Babic et al.(1998, Plant Cell Rep 17: 183-186). The commercial cultivar Westar (Agriculture Canada) is the standard variety used for transformation, but other varieties can be used.

0409.0.1 *Agrobacterium tumefaciens* LBA4404 containing a binary vector was used for canola transformation. Many different binary vector systems have been described for plant transformation (e.g. An, G. in *Agrobacterium Protocols, Methods in Molecular Biology* vol 44, pp 47-62, Gartland KMA and MR Davey eds. Humana Press, Totowa, New Jersey). Many are based on the vector pBIN19 described by Bevan (Nucleic Acid Research, 1984, 12:8711-8721) that includes a plant gene expression cassette flanked by the left and right border sequences from the Ti plasmid of *Agrobacterium tumefaciens*. A plant gene expression cassette consists of at least two genes – a selection marker gene and a plant promoter regulating the transcription of the cDNA or genomic DNA of the trait gene. Various selection marker genes can be used including the *Arabidopsis* gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patents 5787366 and 6225105). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M58930 and X16673) was used to provide constitutive expression of the trait gene.

0410.0.1 Canola seeds were surface-sterilized in 70% ethanol for 2 min., and then in 30% Clorox with a drop of Tween-20 for 10 min, followed by three rinses with sterilized distilled water. Seeds were then germinated in vitro 5 days on half strength MS medium without hormones, 1% sucrose, 0.7% Phytagar at 23°C, 16 hr. light. The cotyledon petiole explants with the cotyledon attached were excised from the in vitro seedlings, and inoculated with *Agrobacterium* by dipping the cut end of the petiole explant into the bacterial suspension. The explants were then cultured for 2 days on MSBAP-3 medium containing 3 mg/l BAP, 3 % sucrose, 0.7 % Phytagar at 23 °C, 16 hr light. After two days of co-cultivation with *Agrobacterium*, the petiole explants were transferred to MSBAP-3 medium containing 3 mg/l BAP, cefotaxime, carbenicillin, or timentin (300 mg/l) for 7 days, and then cultured on MSBAP-3 medium with cefotaxime, carbenicillin, or timentin and selection agent until shoot regeneration. When the shoots were 5 – 10 mm in length, they were cut and transferred to shoot elongation medium (MSBAP-0.5, containing 0.5 mg/l BAP). Shoots of about 2 cm in length were transferred to the rooting medium (MS0) for root induction.

0411.0.1 Samples of the primary transgenic plants (T0) were analyzed by PCR to confirm the presence of T-DNA. These results were confirmed by Southern hybridization in which DNA is electrophoresed on a 1 % agarose gel and transferred to a positively charged nylon membrane (Roche Diagnostics). The PCR Dig Probe Synthesis Kit (Roche Diagnostics) is used to prepare a digoxigenin-labelled probe by PCR, and used as recommended by the manufacturer.

0412.0.1 The transgenic plants were then evaluated for their improved stress tolerance according to the method described in Example 3. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels.

0413.0.1 Tolerance of drought, salinity and cold were measured using methods as described in the previous example 3. Plants that had tolerance to salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0414.0.1 Example 8

0415.0.1 Engineering stress-tolerant corn plants by over-expressing stress-related genes from *Saccharomyces cerevisiae* or *E. coli* or *Brassica napus*, *Glycine max*, and *Oryza sativa*

0416.0.1 Transformation of maize (*Zea Mays* L.) is performed with a modification of the method described by Ishida et al. (1996, *Nature Biotech* 14:745-50). Transformation is genotype-dependent in corn and only specific genotypes are amenable to transformation and regeneration. The inbred line A188 (University of Minnesota) or hybrids with A188 as a parent are good sources of donor material for transformation (Fromm et al. 1990 *Biotech* 8:833-839), but other genotypes can be used successfully as well. Ears are harvested from corn plants at approximately 11 days after pollination (DAP) when the length of immature embryos is about 1 to 1.2 mm. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors and transgenic plants are recovered through organogenesis. The super binary vector system of Japan Tobacco is described in WO patents WO94/00977 and WO95/06722. Vectors were constructed as described. Various selection marker genes can be used including the maize gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patent 6025541). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of gene transcription. In this example, the 34S promoter (GenBank Accession numbers M58930 and X16673) was used to provide constitutive expression of the trait gene.

0417.0.1 Excised embryos are grown on callus induction medium, then maize regeneration medium, containing imidazolinone as a selection agent. The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to maize rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the imidazolinone herbicides and which are PCR positive for the transgenes.

0418.0.1 The T1 transgenic plants were then evaluated for their improved stress tolerance according to the method described in Example 3. The T1 generation of single locus insertions of the T-DNA will segregate for the transgene in a 3:1 ratio. Those progeny containing one or two copies of the transgene are tolerant of the imidazolinone herbicide, and exhibit greater tolerance of drought stress than those progeny lacking the transgenes. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels. Homozygous T2 plants exhibited similar phenotypes. Hybrid plants (F1 progeny) of homozygous transgenic plants and non-transgenic plants also exhibited increased environmental stress tolerance.

0419.0.1 Tolerance of salinity and cold were measured using methods as described in the previous example 3. Plants that had tolerance to drought, salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0420.0.1 **Example 9**

0421.0.1 **Engineering stress-tolerant wheat plants by over-expressing stress related genes from *Saccharomyces cerevisiae* or *E. coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa***

0422.0.1 Transformation of wheat is performed with the method described by Ishida et al. (1998 Nature Biotech. 14745-50). The cultivar Bobwhite (available from CYMMIT, Mexico) is commonly used in transformation. Immature embryos are co-cultivated with *Agrobacterium tumefaciens* that carry "super binary" vectors, and transgenic plants are recovered through organogenesis. The super binary vector system of Japan Tobacco is described in WO patents WO94/00977 and WO95/06722. Vectors were constructed as described. Various selection marker genes can be used including the maize gene encoding a mutated acetohydroxy acid synthase (AHAS) enzyme (US patent 6025541). Similarly, various promoters can be used to regulate the trait gene to provide constitutive, developmental, tissue or environmental regulation of

gene transcription. In this example, the 34S promoter (GenBank Accession numbers M59930 and X16673) was used to provide constitutive expression of the trait gene.

0423.0.1 After incubation with *Agrobacterium*, the embryos are grown on callus induction medium, then regeneration medium, containing imidazolinone as a selection agent. The Petri plates are incubated in the light at 25 °C for 2-3 weeks, or until shoots develop. The green shoots are transferred from each embryo to rooting medium and incubated at 25 °C for 2-3 weeks, until roots develop. The rooted shoots are transplanted to soil in the greenhouse. T1 seeds are produced from plants that exhibit tolerance to the imidazolinone herbicides and which are PCR positive for the transgenes.

0424.0.1 The T1 transgenic plants were then evaluated for their improved stress tolerance according to the method described in the previous example 3. The T1 generation of single locus insertions of the T-DNA will segregate for the transgene in a 3:1 ratio. Those progeny containing one or two copies of the transgene are tolerant of the imidazolinone herbicide, and exhibit greater tolerance of drought stress than those progeny lacking the transgenes. Tolerant plants had higher seed yields, maintained their stomatal aperture and showed only slight changes in osmotic potential and proline levels, whereas the susceptible non-transgenic control plants closed their stomata and exhibited increased osmotic potential and proline levels. Homozygous T2 plants exhibited similar phenotypes. Tolerance of salinity and cold were measured using methods as described in the previous examples. Plants that had tolerance to drought, salinity or cold had higher seed yields, photosynthesis and dry matter production than susceptible plants.

0425.0.3 Example 14

0426.0.3 Identification of Identical and Heterologous Genes

0427.0.3 Gene sequences can be used to identify identical or heterologous genes from cDNA or genomic libraries. Identical genes (e. g. full-length cDNA clones) can be isolated via nucleic acid hybridization using for example cDNA libraries. Depending on the abundance of the gene of interest, 100,000 up to 1,000,000 recombinant bacteriophages are plated and transferred to nylon membranes. After denaturation with alkali, DNA is immobilized on the membrane by e. g. UV cross linking. Hybridization is carried out at high stringency conditions. In aqueous solution, hybridization and washing is performed at an ionic strength of 1 M NaCl and a temperature of 68°C. Hybridization probes are generated by e.g. radioactive (³²P) nick transcription labeling (High Prime, Roche, Mannheim, Germany). Signals are detected by autoradiography.

0428.0.3 Partially identical or heterologous genes that are related but not identical can be identified in a manner analogous to the above-described procedure using low

stringency hybridization and washing conditions. For aqueous hybridization, the ionic strength is normally kept at 1 M NaCl while the temperature is progressively lowered from 68 to 42°C.

- 5 **0429.0.3** Isolation of gene sequences with homology (or sequence identity/similarity) only in a distinct domain of (for example 10-20 amino acids) can be carried out by using synthetic radio labeled oligonucleotide probes. Radiolabeled oligonucleotides are prepared by phosphorylation of the 5-prime end of two complementary oligonucleotides with T4 polynucleotide kinase. The complementary oligonucleotides are annealed and ligated to form concatemers. The double stranded
- 10 concatemers are then radiolabeled by, for example, nick translation. Hybridization is normally performed at low stringency conditions using high oligonucleotide concentrations.

Oligonucleotide hybridization solution:

- 6 x SSC
- 15 0.01 M sodium phosphate
1 mM EDTA (pH 8)
0.5 % SDS
100 µg/ml denatured salmon sperm DNA
0.1 % nonfat dried milk
- 20

- 0430.0.3** During hybridization, temperature is lowered stepwise to 5-10°C below the estimated oligonucleotide T_m or down to room temperature followed by washing steps and autoradiography. Washing is performed with low stringency such as 3 washing steps using 4 x SSC. Further details are described by Sambrook, J. et al.,
- 25 1989, "Molecular Cloning: A Laboratory Manual," Cold Spring Harbor Laboratory Press or Ausubal, F.M. et al., 1994, "Current Protocols in Molecular Biology," John Wiley & Sons.

0431.0.3 Example 15

- 0432.0.3 Identification of Identical Genes by Screening Expression Libraries**
- 30 **with Antibodies**

- 0433.0.3** c-DNA clones can be used to produce recombinant polypeptide for example in *E. coli* (e.g. Qiagen QIAexpress pQE system). Recombinant polypeptides are then normally affinity purified via Ni-NTA affinity chromatography (Qiagen). Recombinant polypeptides are then used to produce specific antibodies for example by
- 35 using standard techniques for rabbit immunization. Antibodies are affinity purified using a Ni-NTA column saturated with the recombinant antigen as described by Gu et al., 1994, BioTechniques 17:257-262. The antibody can then be used to screen expression cDNA libraries to identify identical or heterologous genes via an immunological screening (Sambrook, J. et al., 1989, "Molecular Cloning: A Laboratory

Manual," Cold Spring Harbor Laboratory Press or Ausubel, F.M. et al., 1994, "Current Protocols in Molecular Biology", John Wiley & Sons).

0434.0.3 Example 16

0435.0.3 In vivo Mutagenesis

- 5 **0436.0.3** *In vivo* mutagenesis of microorganisms can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (e.g. *Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (e.g., mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D., 1996, DNA repair mechanisms, in: *Escherichia coli* and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those skilled in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M., 1994, Strategies 7: 32-34. Transfer of mutated DNA molecules into plants is preferably done after selection and testing in microorganisms. Transgenic plants are generated according to various examples within the exemplification of this document.

0437.0.3 Example 17

0438.0.3 Identification and Analysis of YNL090W Homologs

- 15 **0439.0.3** Transgenic Arabidopsis plants overexpressing YNL 090W (ORF 3165) lived 4.33 days longer than the wild type control under drought conditions. The protein sequence of YNL090W was used to identify related gene sequences of expressed sequence tags (ESTs) proprietary libraries constructed from *Oryza sativa* cv. Noppon-Brarre (a japonica rice), *Brassica napus* cv. "AG Excel" "Quantum" and "Cresor" (canola), and *Glycine max* cv. Resuick (soybean) by Blast analysis (Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ. 1990 J Mol Biol 21593:403-10).

- 20 **0440.0.3** The plant cDNA sequences were translated into a predicated amino acid sequences, and relationship among the amino acids sequences was determined by sequence alignment using the clustal W algorithm in Vector NTI Version 7 (Figure 2). They have 75% similarity overall. In general, proteins having conserved domains referred to as I (GXXXGKT), II (DXXG), III (VGTK), IV (EXSS), and E (FXXXYXX), are classified as small GTPases. All five domains in the proteins in Figure 1 are more conserved than in other known small GTPases, particularly Domain I (KXVXXGDXXXGKT), Domain E (FXXXYXXTV), Domain II (WDTAGQE) and Domain III (VGTKXDL). In addition, polybasic amino acids in C terminus are shown in the Figure 2, as well as a C-terminal CAAL domain (wherein A is an aliphatic amino acid), which is the signature sequence for post translational modification by the enzyme geranylgeranyltransferase I. Another important Ptho-specific feature was shown in

most proteins in Figure 1 is the highly conserved amino acids between Domain II and Domain III.

CLAIMS

1. A transformed plant cell with altered metabolic activity compared to a corresponding non transformed wild type plant cell, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell.
2. The transformed plant cell of claim 1, wherein metabolic activity is altered concerning one or more metabolites selected from the group consisting of 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4-dihydroxyphenyl-alanine (= dopa), 3-hydroxy-palmitic acid, 5-oxoproline, alanine, alpha linolenic acid (c18:3 (c9, c12, c15)), alpha-tocopherol, aminoadipic acid, anhydroglucose, arginine, aspartic acid, beta-apo-8' carotenal, beta-carotene, beta-sitosterol, beta-tocopherol, (delta-7-cis,10-cis)-hexadecadienic acid, hexadecatrienic acid, margaric acid, delta-15-cis-tetracosenic acid, ferulic acid, campesterol, cerotic acid (c26:0), citrullino, cryptoxanthine, eicosenoic acid (20:1), fructose, fumarate, galactose, gamma-aminobutyric acid, gamma-tocopherol, gluconic acid, glucose, glutamic acid, glutamine, glycerate, glyceraldehyde, glycerol, glycerol-3-phosphate, glycine, homoserine, inositol, isoleucine, iso-maltose, isopentenyl pyrophosphate, leucine, lignocoric acid (c24:0), linoleic acid (c18:2 (c8, c12)), luteine, lycopene, malate, mannose, methionine, methylgalactofuranoside, methylgalactopyranoside, methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate, proline, putrescine, pyruvat, raffinose, ribonic acid, serine, shikimate, sinapine acid, stearic acid (c18:0), succinate, sucrose, threonine, triacontanoic acid, tryptophane, tyrosine, ubiquinone, udp-glucose, valine, zeaxanthine.
3. The transgenic plant cell of claim 1 or 2, wherein the metabolic activity is altered by transformation with a Stress-Related Protein (SRP) coding nucleic acid selected from the group consisting of:
 - a) nucleic acid molecule encoding one of the polypeptides shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;
 - b) nucleic acid molecule comprising one of the nucleic acid molecules shown in Fig. 1a, 1b or 1c;
 - c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;

- d) nucleic acid molecule which encodes a polypeptide which has at least 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;
- 5 c) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- 10 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- 15 h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring an altered metabolic activity in an organism or a part thereof.
- 20 or comprising a sequence which is complementary thereto.
4. The transgenic plant cell of claim 3, wherein the environmental stress is selected from the group consisting of salinity, drought, temperature, metal, chemical, pathogenic and oxidative stresses, or combinations thereof.
5. The transgenic plant cell of any of claims 1 – 4 derived from a monocotyledonous plant.
- 30 6. The transgenic plant cell of any of claims 1 – 5 derived from a dicotyledonous plant.
7. The transgenic plant cell of any of claims 1 – 6, wherein the plant is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, pepper, sunflower, flax, borage, safflower, linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco,
- 35

eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass, forage crops and *Arabidopsis thaliana*.

8. The transgenic plant cell of any of claims 1 – 4, derived from a gymnosperm plant.

5 9. The transgenic plant cell of any of claims 1 – 4 or 6, wherein the plant is selected from the group of spruce, pine and fir.

10. A transgenic plant generated from a plant cell according to any of claims 1 – 7 and which is a monocot or dicot plant.

10 11. A transgenic plant of claim 10, which is selected from the group consisting of maize, wheat, rye, oat, triticale, rice, barley, soybean, peanut, cotton, rapeseed, canola, manihot, popper, sunflower, flax, borage, safflower, linseed, primrose, rapeseed, turnip rape, tagetes, solanaceous plants, potato, tobacco, eggplant, tomato, *Vicia* species, pea, alfalfa, coffee, cacao, tea, *Salix* species, oil palm, coconut, perennial grass, forage crops and *Arabidopsis thaliana*.

15 12. A transgenic plant generated from a plant cell according to any of claims 1 – 4, 8 or 9 and which is a gymnosperm plant.

13. A transgenic plant of claim 12, which is selected from the group consisting of spruce, pine and fir.

20 14. A seed produced by a transgenic plant of any of claims 10 - 13, wherein the seed is genetically homozygous for a transgene conferring altered metabolic activity resulting in an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant.

15. An isolated nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:

25 a) nucleic acid molecule encoding of the polypeptide shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;

b) nucleic acid molecule comprising of the nucleic acid molecule shown in Fig. 1a, 1b or 1c;

30 c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;

35 d) nucleic acid molecule which encodes a polypeptide which has at least 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;

- e) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- 5 f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- 10 g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig. 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- 15 i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring altered
- 20 metabolic activity in an organism or a part thereof;

whereby the nucleic acid molecule distinguishes over the sequence as shown in Fig. 1a, 1b or 1c by one or more nucleotides.

16. An isolated nucleic acid molecule comprising a nucleic acid molecule selected from the group consisting of:
- 25 a) nucleic acid molecule encoding of the polypeptide shown in Fig. 1a, 1b or 1c or a fragment thereof, which confers an altered metabolic activity in an organism or a part thereof;
- b) nucleic acid molecule comprising of the nucleic acid molecule shown in Fig. 1a, 1b or 1c;
- 30 c) nucleic acid molecule whose sequence can be deduced from a polypeptide sequence encoded by a nucleic acid molecule of (a) or (b) as a result of the degeneracy of the genetic code and conferring an altered metabolic activity in an organism or a part thereof;
- d) nucleic acid molecule which encodes a polypeptide which has at least
- 35 50% identity with the amino acid sequence of the polypeptide encoded by the nucleic acid molecule of (a) to (c) and conferring an altered metabolic activity in an organism or a part thereof;

- e) nucleic acid molecule which hybridizes with a nucleic acid molecule of (a) to (c) under stringent hybridisation conditions and conferring an altered metabolic activity in an organism or a part thereof;
- f) nucleic acid molecule which encompasses a nucleic acid molecule which is obtained by amplifying nucleic acid molecules from a cDNA library or a genomic library using the primers in table 2 and conferring an altered metabolic activity in an organism or a part thereof;
- g) nucleic acid molecule encoding a polypeptide which is isolated with the aid of monoclonal antibodies against a polypeptide encoded by one of the nucleic acid molecules of (a) to (f) and conferring an altered metabolic activity in an organism or a part thereof;
- h) nucleic acid molecule encoding a polypeptide comprising the consensus sequence shown in Fig. 2 and conferring an altered metabolic activity in an organism or a part thereof; and
- i) nucleic acid molecule which is obtainable by screening a suitable nucleic acid library under stringent hybridization conditions with a probe comprising one of the sequences of the nucleic acid molecule of (a) to (k) or with a fragment thereof having at least 15 nt, preferably 20 nt, 30 nt, 50 nt, 100 nt, 200 nt or 500 nt of the nucleic acid molecule characterized in (a) to (k) and conferring altered metabolic activity in an organism or a part thereof.
17. A nucleic acid construct which confers the expression of the nucleic acid molecule of claim 15 or 16, comprising one or more regulatory elements, whereby expression of the SRP coding nucleic acid in a host cell results altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell.
18. A vector comprising the nucleic acid molecule as claimed in claim 15 or 16 or the nucleic acid construct of claim 17, whereby expression of the SRP coding nucleic acid in a host cell results altered metabolic activity resulting in increased tolerance to environmental stress as compared to a corresponding non-transformed wild type host cell.
19. A host cell, which has been transformed stably or transiently with the vector as claimed in claim 18 or the nucleic acid molecule as claimed in claim 15 or 16 or the nucleic acid construct of claim 17.
20. An isolated Stress Related Protein (SRP) which is selected from the group comprising Fig. 1a, 1b or 1c and/or homologs thereof.

21. An isolated Stress Related Protein (SRP) of claim 20 which is selected from yeast, preferably *Saccharomyces cerevisiae*, or *E.coli*, *Brassica napus*, *Glycine max*, or *Oryza sativa*.
22. A method of producing a transgenic plant with altered metabolic activity
5 compared to a corresponding non transformed wild type plant cell, wherein the metabolic activity is altered by expression of a Stress-Related Protein (SRP) coding nucleic acid and results in increased tolerance and/or resistance to an environmental stress as compared to a corresponding non-transformed wild type plant cell, comprising
- 10 a. transforming a plant cell with an expression vector according to claim 18 and
b. generating from the plant cell a transgenic plant with an increased tolerance to environmental stress as compared to a corresponding non-transformed wild type plant.
- 15 23. The method of claim 22, wherein the SRP coding nucleic acid is selected from the group comprising the nucleic acids of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences.
24. The method of any of claims 22 or 23, wherein the SRP coding nucleic acid is at least about 50% homologous to one of the nucleic acids of Fig. 1a, 1b or 1c.
- 20 25. A method of modifying stress tolerance of a plant comprising, modifying the level of expression of an SRP in the plant.
26. The method of claim 25, wherein the SRP encoding nucleic acid is selected from the group comprising the nucleic acids of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences.
- 25 27. The method of any of claims 25 or 26, wherein the SRP coding nucleic acid is at least about 50% homologous to one of the nucleic acid of Fig. 1a, 1b or 1c.
28. The method of any of claims 25 - 27, wherein an expression vector is used according to any of claims 17 or 18.
29. The method of any of claims 25 - 28, wherein the stress tolerance is decreased.
- 30 30. The method of any of claims 25 - 29, wherein the plant is transgenic.
31. The method of any of claims 25 - 30, wherein the plant is transformed with an inducible promoter that directs expression of the SRP.
32. The method of any of claims 25 - 31, wherein the promoter is tissue specific.
33. The method of any of claims 25 - 32, wherein the promoter is developmentally
35 regulated.
34. The method of any of claims 25 - 33, wherein SRP expression is modified by administration of an targeting nucleic sequence complementary to the regulatory region

of the SRP encoding nucleic acid and/or by a transcription factor and/or by a zinc finger protein.

35. A method of detecting environmental stress in plant cells or plants comprising screening the plant cells for altered metabolic activity as compared to non-stress conditions.

36. A method of screening plant cells or plants for increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions.

37. A method of breeding plant cells or plants towards increased tolerance and/or resistance to environmental stress comprising screening the plant cells under stress conditions for altered metabolic activity as compared to non-stress conditions and selecting those with increased tolerance and/or resistance to environmental stress.

38. The method of one of claims 35 - 37, wherein metabolite activity is altered concerning one or more metabolites selected from the group consisting of 2,3-dimethyl-5-phytylquinol, 2-hydroxy-palmitic acid, 3,4-dihydroxyphenylalanine (= dopa), 3-hydroxy-palmitic acid, 5-oxoprolino, alanine, alpha linolenic acid (c18:3 (c9, c12, c15)), alpha-tocopherol, amino adipic acid, anhydroglucose, arginine, aspartic acid, beta-apo-8' carotenal, beta-carotene, beta-sitosterol, beta-tocopherol, (delta-7-cis,10-cis)-hexadecadienic acid, hexadecatrienic acid, margaric acid, delta-15-cis-tetracosenic acid, nerolic acid, campesterol, cerotic acid (c26:0), citrulline, cryptoxanthine, eicosenoic acid (20:1), fructose, fumarates, galactose, gamma-aminobutyric acid, gamma-tocopherol, gluconic acid, glucose, glutamic acid, glutamine, glycerate, glycerinaldehyd, glycerol, glycerol-3-phosphate, glycine, homoserine, inositol, isoleucine, iso-maltose, isopentenyl pyrophosphate, leucine, lignoceric acid (c24:0), linoleic acid (c18:2 (c9, c12)), luteine, lycopene, malates, mannose, methionine, methylgalactofuranoside, methylgalactopyranoside, methylgalactopyranoside, palmitic acid (c16:0), phenylalanine, phosphate, proline, putrescine, pyruvat, raffinose, ribonic acid, serine, shikimate, sinapine acid, stearic acid (c18:0), succinates, sucrose, threonine, triacontenoic acid, tryptophane, tyrosine, ubiquinone, udp-glucose, valine, zeaxanthine.

39. The method of one of the claims 35 - 38, wherein the altered metabolic activity is by transformation with a Stress-Related Protein (SRP) coding nucleic acid.

40. The method of one of the claims 35 - 39, wherein metabolic activity is altered by transformation with one or more Stress-Related Protein (SRP) coding nucleic acids selected from the group comprising at least one of the nucleic acids of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences.

41. Use of a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences for preparing a plant cell with increased environmental stress tolerance.
42. Use of altered metabolic activity and/or a SRP encoding nucleic acid selected
5 from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the afore mentioned sequences or parts thereof as markers for selection of plants or plant cells with increased tolerance to environmental stress.
43. Use of altered metabolic activity and/or a SRP encoding nucleic acid selected from the group comprising the nucleic acid of Fig. 1a, 1b or 1c and/or homologs of the
10 afore mentioned sequences or parts thereof as markers for detection of stress in plants or plant cells.
44. A nucleic acid construct which confers the expression of the nucleic acid molecule of claim 15 or 16, comprising one or more regulatory elements, whereby expression of the SRP coding nucleic acid in a host cell results in increased tolerance
15 to environmental stress as compared to a corresponding non-transformed wild type host cell.
45. A vector comprising the nucleic acid molecule as claimed in claim 15 or 16 or the nucleic acid construct of claim 44, whereby expression of the SRP coding nucleic acid in a host cell results in increased tolerance to environmental stress as compared
20 to a corresponding non-transformed wild type host cell.
46. A plant cell comprising a nucleic acid construct of claim 44 or a vector of claim 45.
47. A plant comprising a cell of claim 46.
48. An isolated nucleic acid, comprising a polynucleotide selected from the group
25 consisting of:
- a. a nucleic acid sequence of Fig. 1c;
 - b. a polynucleotide encoding a polypeptide of Fig. 1c;
 - c. a polynucleotide having at least 70% sequence identity with a nucleic acid sequence of Fig. 1c, wherein expression of said polynucleotide confers
30 increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant; and
 - d. a polynucleotide hybridizing under stringent conditions to a nucleic acid sequence of Fig. 1c, wherein expression of said polynucleotide confers
35 increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant.
49. A vector comprising the isolated nucleic acid of claim 48.

50. A plant stably transformed with the isolated nucleic acid of claim 48.
51. A plant stably transformed with the vector of claim 49.
52. A seed of the plant of claim 50, wherein said seed comprises the isolated nucleic acid of claim 48.
- 5 53. A seed of the plant of claim 50, wherein said seed comprises the vector of claim 49.
54. A method of increasing tolerance of a plant to at least one abiotic stress, comprising: transforming a plant with an isolated nucleic acid of claim 48.
55. A method of increasing tolerance of a plant to at least one abiotic stress, comprising: transforming a plant with a vector of claim 49.
- 10 56. A plant transformed with a nucleic acid selected from the group consisting of:
- a. a nucleic acid sequence of Fig. 1a or Fig. 1b;
 - b. a polynucleotide encoding a polypeptide of Fig. 1a or Fig. 1b;
 - c. a polynucleotide having at least 70% sequence identity with a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant; and
 - d. a polynucleotide hybridizing under stringent conditions to a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant.
- 15 57. A seed of the plant of claim 56.
- 20 58. A method of increasing tolerance of a plant to at least one abiotic stress, comprising: transforming a plant with a nucleic acid selected from the group consisting of:
- a. a nucleic acid sequence of Fig. 1a or Fig. 1b;
 - b. a polynucleotide encoding a polypeptide of Fig. 1a or Fig. 1b;
 - c. a polynucleotide having at least 70% sequence identity with a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic stress in a plant as compared to a corresponding non-transformed plant; and
 - d. a polynucleotide hybridizing under stringent conditions to a nucleic acid sequence of Fig. 1a or Fig. 1b, wherein expression of said polynucleotide confers increased tolerance to one or more abiotic in a plant as compared to a corresponding non-transformed plant.
- 25 30 35

SEQUENCES

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 435 440 445

aaa tta ata caa ata tct gat gtc tca atg tct cct tct cta taa 1388
 Lys Leu Ile Gln Ile Ser Asp Val Ser Met Ser Pro Ser Leu
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<211> 462

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 4

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Lys Arg Arg Gly Lys Leu Ser Ala Gln Thr Tyr Glu Glu Asp Gln Glu			
35	40	45	
Ala Ile Leu Ser Ser Pro Leu Leu Thr Ser Thr Pro Lys Thr Val Ser			
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Arg Ser Leu Val Arg Leu Tyr Pro Tyr Leu Ile Val Val Asp Asn Phe			
65	70	75	80
Leu Ser Ile Ile Thr Trp Ser Asn Asp Asn Val Ser Ala Asn Leu Leu			
85	90	95	
Gly Ile Phe Leu Phe Thr Val Cys Val Leu Tyr Phe Gly Phe Ile Thr			
100	105	110	
Arg Tyr Phe Gly His Leu Met Ile Val Gly Ile Ile Trp Val Tyr Leu			
115	120	125	
Leu Ile Asp Lys His Val Gln Glu Thr Met Ala Ser Cys Pro Ser Leu			
130	135	140	
Asp Asp Ile Ile His Val Met Asp Arg Val Ser Met Lys Ser Ser Ala			
145	150	155	160
Val Leu Ser Pro Ile Thr Ile Leu Ser Ala Gln Asp Val Arg Arg Leu			
165	170	175	
Leu Phe Thr Ile Ala Phe Leu Ser Pro Val Tyr Ile Phe Leu Thr Val			
180	185	190	
Phe Val Leu Ser Pro Asn Tyr Leu Met Leu Ile Gly Gly Leu Tyr Val			
195	200	205	
Leu Thr Tyr His Ser Lys Leu Ile Arg Arg Met Arg Arg Tyr Leu Trp			
210	215	220	
Lys Phe Arg Val Val Arg Leu Leu Val Phe Phe Ile Thr Gly Leu Asp			

225	230	235	240
Leu Gly Gly Pro Asp Asn Asn Arg Arg Leu Phe Ala Ser Val Asn Lys			
245	250	255	
Lys Ile Arg Ser Phe Val Trp Asn Glu Val Gly Asn Thr Ser Asn Thr			
260	265	270	
Lys Lys Thr Val Leu Phe Lys Val Ala Leu Phe Glu Asn Glu Arg Arg			
275	280	285	
Trp Leu Gly Ile Gly Trp Thr Ser Thr Met Leu Ser Tyr Glu Arg Ala			
290	295	300	
Ser Trp Thr Asp Glu Phe Leu Asn Thr Ser Pro Ser Pro Glu Val Phe			
305	310	315	320
Thr Leu Pro Glu Glu Gln Ser Gly Met Ala Trp Glu Trp His Asp Lys			
325	330	335	
Asp Trp Met Leu Asp Leu Thr Asn Asp Gly Ile Ile Gln Leu Pro Ala			
340	345	350	
Ser Ala Ala Lys Thr Lys Val Lys Pro Gly Ala Asp Glu Gly Phe Ile			
355	360	365	
Tyr Tyr Asp Asn Thr Trp Asn Asn Pro Ser Ala Thr Asp Thr Tyr Lys			
370	375	380	
Lys Tyr Thr Arg Arg Arg Arg Trp Ile Arg Thr Ala Thr Val Thr Thr			
385	390	395	400
Thr Tyr Asp Asp Glu Pro Thr Val Glu Lys Ala Thr Pro Asn Ser His			
405	410	415	
Ala Leu Lys Ser Glu Glu Asn Asn Arg Val Arg Lys Arg Lys Val Ser			
420	425	430	
Phe Ser Thr Ala Asn Glu Val His Ile Ile Pro Ser Ser Asp Ser Ser			
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Lys Leu Ile Gln Ile Ser Asp Val Ser Met Ser Pro Ser Leu			

450

455

460

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<211> 3921

<212> DNA

<213> *Saccharomyces cerevisiae*

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Met Gln Phe Pro Phe Ala Cys Leu Leu Ser Thr Leu Val Ile Ser Gly

1 5 10 15

tca ttg gcc cgg gcc agc ccc ttc gac tat ata ttc ggc aat gga aag 96

Ser Leu Ala Arg Ala Ser Pro Phe Asp Phe Ile Phe Gly Asn Gly Thr

20 25 30

caa caa gct cag agc caa agc gag agt caa ggt caa gtt tct ttc acc 144

Gln Gln Ala Glu Ser Gln Ser Glu Ser Gln Gly Gln Val Ser Phe Thr

35 40 45

aat gaa gct tct cag gat agt tcc acc acc tct ttg gta acc gcc tat 192

Asn Glu Ala Ser Gln Asp Ser Ser Thr Thr Ser Leu Val Thr Ala Tyr

50 55 60

tct caa ggt gtt cat tgg caa cag tat gaa aaa ata gtg agt gcc acc 240

Ser Gln Gly Val His Ser His Gln Ser Ala Thr Ile Val Ser Ala Thr

65 70 75 80

atc tct tcc ctg cca tct act tgg tat gat gcg agc tcc act tcc cag 288

Ile Ser Ser Leu Pro Ser Thr Trp Tyr Asp Ala Ser Ser Thr Ser Gln

85 90 95

act tct gtg tca tat gcc agt caa gaa tcc gac tat gcc gtt aat caa 336

Thr Ser Val Ser Tyr Ala Ser Gln Glu Ser Asp Tyr Ala Val Asn Gln

100 105 110

aac tct tgg agc gag tct act aat caa atg cca tct acc agt acg aca	584
Asn Ser Trp Ser Ala Ser Thr Asn Gln Leu Pro Ser Thr Ser Thr Thr	
115 120 125	
agc tac tat gag cca acc ttc agt aca tgg gcc gat ttt gct gct tct	432
Ser Tyr Tyr Ala Pro Thr Phe Ser Thr Ser Ala Asp Phe Ala Ala Ser	
130 135 140	
agt gta aat gca gct tct gat gtc tcc act gcc agt gtt ccc att gat	480
Ser Val Asn Ala Ala Ser Asp Val Ser Thr Ala Ser Val Pro Ile Asp	
145 150 155 160	
acg agt gct aat tct atc cct ttc aca act aca agt aac ata gag act	528
Thr Ser Ala Asn Ser Ile Pro Phe Thr Thr Thr Ser Asn Ile Glu Thr	
165 170 175	
aca acg agt gca cct ctc act tgg gac act cca ctt att tcc act agt	576
Thr Thr Ser Ala Pro Leu Thr Ser Asp Thr Pro Leu Ile Ser Thr Ser	
180 185 190	
acg atg tcc gca gct gat aac gta tct tgg tca gca aac cct att tct	624
Thr Met Ser Ala Ala Asp Asn Val Phe Ser Ser Ala Asn Pro Ile Ser	
195 200 205	
gcc tcc cta aca acc acc gat agt tca gaa agt ttt gac caa acg tgg	672
Ala Ser Leu Thr Thr Thr Asp Ser Ser Gln Ser Phe Asp Gln Thr Ser	
210 215 220	
act gct ggt gcc att ccg gtc caa agt tca gcc gat ttt agt agt tct	720
Thr Ala Gly Ala Ile Pro Val Gln Ser Ser Ala Asp Phe Ser Ser Ser	
225 230 235 240	
agt gaa att tta gta caa agt tgg gag gat ttc agt agc cct agt tct	768
Ser Glu Ile Leu Val Gln Ser Ser Ala Asn Phe Ser Ser Pro Ser Ser	
245 250 255	
cda act act acc gat ata tgg cta tca gct gcc cca atg caa aca agt	816
Pro Thr Thr Thr Asp Ile Ser Leu Ser Ala Ala Pro Leu Gln Thr Ser	
260 265 270	
gaa tca agc agt ttt acc act gca tca gcc gct cta cca gta agt Leu	864
Glu Ser Ser Ser Phe Thr Thr Ala Ser Ala Ala Leu Pro Val Ser Ser	

275	280	285	
aca gac gtt gat ggc tca agc gcc tca acc gta gtg agc atg agc gcc			912
Thr Asp Val Asp Gly Ser Ser Ala Ser Pro Val Val Ser Met Ser Ala			
290	295	300	
gca gga caa ata gct agc tca agc agc aca gat aat cca aat atg tca			950
Ala Gly Gln Ile Ala Ser Ser Ser Ser Thr Asp Asn Pro Thr Met Ser			
305	310	315	320
gaa acc ttt tcg tta aca tct aca gaa gct gat ggt tcc gat gtt tca			1008
Glu Thr Phe Ser Leu Thr Ser Thr Glu Val Asp Gly Ser Asp Val Ser			
325	330	335	
tca aca gtg agc gca tta tta tcg gct cct ttt tta caa aca aat act			1056
Ser Thr Val Ser Ala Leu Leu Ser Ala Pro Phe Leu Gln Thr Ser Thr			
340	345	350	
tcc aac agt ttc agc att gtt agc cca tcg gta tct ttt gtt cca tca			1104
Ser Asn Ser Phe Ser Ile Val Ser Pro Ser Val Ser Phe Val Pro Ser			
355	360	365	
cag agt leu tca gac gtt gct agc tcc agt act gca aat gta gtt agt			1152
Gln Ser Ser Ser Asp Val Ala Ser Ser Ser Thr Ala Asn Val Val Ser			
370	375	380	
tca tcc ttt tct gat att cca cug caa act agt acc tca ggg agc gta			1200
Ser Ser Phe Ser Asp Ile Pro Pro Gln Thr Ser Thr Ser Gly Ser Val			
385	390	395	400
gtt tcg gta ggc caa tcc gaa tct gcc ctc gca ttt caa agt leu acc			1248
Val Ser Val Ala Gln Ser Ala Ser Ala Leu Ala Phe Gln Ser Ser Thr			
405	410	415	
gag gta tat ggt gcc agt gcc tcg agc aca atg agt tca tta ata tca			1296
Glu Val Tyr Gly Ala Ser Ala Ser Ser Thr Met Ser Ser Leu Leu Ser			
420	425	430	
act act tcg cta cag tct act act ttg gat agc tca agt tta gct agc			1344
Thr Thr Ser Leu Gln Ser Thr Thr Leu Asp Ser Ser Ser Leu Ala Ser			
435	440	445	

tcc tct gag tgg agt tca gac ctt aca gat tat ggc gtc tcc agt aca	1392
Ser Ser Ala Ser Ser Ser Asp Leu Thr Asp Tyr Gly Val Ser Ser Thr	
450 455 460	
gca agc ata cgg ctg ttg tca gcc tca gaa caa gca agt act tcc agc	1440
Ala Ser Ile Pro Leu Leu Ser Ala Ser Glu Gln Ala Ser Thr Ser Ser	
465 470 475 480	
agt ttt agc gtt gtt agc cct tgg gta tcc ttt gtt cca tca caa agt	1488
Ser Phe Ser Val Val Ser Pro Ser Val Ser Phe Val Pro Ser Gln Ser	
485 490 495	
tcc tca gat gtt gct acc acc agt gct cca agt gta gtt agt tca tcc	1536
Ser Ser Asp Val Ala Ser Thr Ser Ala Pro Ser Val Val Ser Ser Ser	
500 505 510	
ttt tct tat act tca ctg caa gca ggt ggc tct agc atg acc aat ccc	1584
Phe Ser Tyr Thr Ser Leu Gln Ala Gly Gly Ser Ser Met Thr Asn Pro	
515 520 525	
tct tca tca act ata gta tat tcc agt agt cct ggc agt tct gag gaa	1632
Ser Ser Ser Thr Phe Val Tyr Ser Ser Ser Thr Gly Ser Ser Glu Glu	
530 535 540	
tcc gct gca tct aca gcc tct gca aca ctg tgg ggc tcc tgg tct act	1680
Ser Ala Ala Ser Thr Ala Ser Ala Thr Leu Ser Gly Ser Ser Ser Thr	
545 550 555 560	
tat atg gca qga aat ttg caa tca cag cct cca tcc act tca agt ttg	1728
Tyr Met Ala Gly Asn Leu Gln Ser Gln Pro Pro Ser Thr Ser Ser Leu	
565 570 575	
ctt tgg gag tct caa gcc aca agc act tca gct gtg cta gct agc agt	1776
Leu Ser Glu Ser Gln Ala Thr Ser Thr Ser Ala Val Leu Ala Ser Ser	
580 585 590	
tct gtt tct aca act tca ccc tat acc act gca ggt ggt gca tct aca	1824
Ser Val Ser Thr Thr Ser Pro Tyr Thr Thr Ala Gly Gly Ala Ser Thr	
595 600 605	
gag gcc tca tcc ctc ata tca tct aca tct ggc gaa act tcc cag gta	1872
Glu Ala Ser Ser Leu Ile Ser Ser Thr Ser Ala Glu Thr Ser Gln Val	

610	615	620	
agt tat taa caa agc aca act gca ttg caa act taa taa ttc gca tgg			1920
Ser Tyr Ser Gln Ser Thr Thr Ala Leu Gln Thr Ser Ser Phe Ala Ser			
625	630	635	640
tct taa aca aca gaa gga agt gaa aca tct agt caa ggt ttt tct aac			1968
Ser Ser Thr Thr Glu Gly Ser Glu Thr Ser Ser Gln Gly Phe Ser Thr			
645	650	655	
agc tct gtt tta gtt caa atg cct tct tgg att tcc agc gaa ttc tca			2016
Ser Ser Val Leu Val Gln Met Pro Ser Ser Ile Ser Ser Glu Phe Ser			
660	665	670	
ccc tct cug aag aca act caa atg aat tct gca agc tca tca tct cag			2064
Pro Ser Gln Thr Thr Thr Gln Met Asn Ser Ala Ser Ser Ser Ser Gln			
675	680	685	
tac act ata tca tcc act ggt ata ctt tct cag gtt tca gac aca tgg			2112
Tyr Thr Ile Ser Ser Thr Gly Ile Leu Ser Gln Val Ser Asp Thr Ser			
690	695	700	
gtg tct tat aca act tca agt tgg tct gtt tct caa gtt tca gac aca			2160
Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp Thr			
705	710	715	720
cca gtt tct tat aca act tca agt tgg tct gtt tct caa gtt tca gac			2208
Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp			
725	730	735	
aca cgg gtt tct tat aca act tca agt tgg tct gtt tct caa gtt tca			2256
Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser			
740	745	750	
gac aca cca gtt tct tat aca act tca agt tca tct gtt tct caa gtt			2304
Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val			
755	760	765	
tca gac aca cgg gtt tct tat aca act tca agt tgg tcc gtt tct caa			2352
Ser Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln			
770	775	780	

gtt tca gac acg tca gta cct cct aca agt tcc aqa tgg tcc gtt tct	2400
Val Ser Asp Thr Ser Val Pro Ser Thr Ser Ser Arg Ser Ser Val Ser	
785 790 795 800	
caa gta tca gac act cgg gta cct tct aca agt tca agg tgg tcc gtt	2448
Gln Val Ser Asp Thr Pro Val Pro Ser Thr Ser Ser Arg Ser Ser Val	
805 810 815	
tct caa aca tct agc tca ata cag ccc acc act aca tcc tcc caa cgt	2496
Ser Gln Thr Ser Ser Ser Leu Gln Pro Thr Thr Thr Ser Ser Gln Arg	
820 825 830	
ttc acc att tcc act cat gga gag att tct gaa agt aqa tct gtt agc	2544
Phe Thr Ile Ser Thr His Gly Ala Leu Ser Glu Ser Ser Ser Val Ser	
835 840 845	
caa caa gct tct gag att act agc tca atc aat gca aca gct tcc gaa	2592
Gln Gln Ala Ser Glu Ile Thr Ser Ser Ile Asn Ala Thr Ala Ser Glu	
850 855 860	
tac cat agc atc cag aca acc gag gct act caa tcc aca act ata tct	2640
Tyr His Ser Ile Gln Thr Thr Ala Ala Thr Gln Ser Thr Thr Leu Ser	
865 870 875 880	
ttt acc gac gca aac agc agt tct gct tcc gct cca ttg gaa gta gca	2688
Phe Thr Asp Ala Asn Ser Ser Ser Ala Ser Ala Pro Leu Glu Val Ala	
885 890 895	
acg tct acg cca acc cca tct tca aag gca tcc tct ctg ttg ctt aca	2736
Thr Ser Thr Pro Thr Pro Ser Ser Lys Ala Ser Ser Leu Leu Leu Thr	
900 905 910	
cca tca aca tcc tct tta agt cag gtt gct cca aat acc aat gta cag	2784
Pro Ser Thr Ser Ser Leu Ser Gln Val Ala Thr Asn Thr Asn Val Gln	
915 920 925	
acg agt tta aca acg gaa tgg acg acc gtt tta gaa cca tca acg act	2832
Thr Ser Leu Thr Thr Glu Ser Thr Thr Val Leu Glu Pro Ser Thr Thr	
930 935 940	
aac agt tcc agt acg ttt agt ctg gtc act tca agt gac aac aat tgg	2880
Asn Ser Ser Ser Thr Phe Ser Leu Val Thr Ser Ser Asp Asn Asn Trp	

945	950	955	960	
tgg att cca act gag tta atc acg cag gca cca gaa gct gca tcc acc	2928			
Trp Ile Pro Thr Glu Leu Ile Thr Gln Ala Pro Glu Ala Ala Ser Thr				
965	970	975		
gca tct tct acc gtt gga gga aca caa acg atg act ttg ccc cat gca	2976			
Ala Ser Ser Thr Val Gly Gly Thr Gln Thr Met Thr Leu Pro His Ala				
980	985	990		
att gca gcc gag aca caa gtt ccc gag cct gag ggc tac acc cta atc	3024			
Ile Ala Ala Ala Thr Gln Val Pro Glu Pro Gln Gly Tyr Thr Leu Ile				
995	1000	1005		
aca ata ggg ttc caa aaa gct ttg aac tac gaa ttt gtt gta tca	3069			
Thr Ile Gly Phe Cys Lys Ala Leu Asn Tyr Gln Phe Val Val Ser				
1010	1015	1020		
gaa cca aca tca tgg gct caa atc ttc gga tac ttg cct gaa gct	3114			
Glu Pro Lys Ser Ser Ala Gln Ile Phe Gly Tyr Leu Pro Glu Ala				
1025	1030	1035		
ctg aac aca cct ttt aag aac gta ttc aca aac att acg gta cta	3159			
Leu Asn Thr Pro Phe Lys Asn Val Phe Thr Asn Ile Thr Val Leu				
1040	1045	1050		
caa ata gtg cca tta cag gat gac tca ctg aac tac tta gla agt	3204			
Gln Ile Val Pro Leu Gln Asp Asp Ser Leu Asn Tyr Leu Val Ser				
1055	1060	1065		
gtt gct gaa gta tac ttt cca act gca gaa ata gag gag ctg tca	3249			
Val Ala Glu Val Tyr Phe Pro Thr Ala Glu Ile Glu Glu Leu Ser				
1070	1075	1080		
aat cta att acc aac tct tca agc gct ttt tac acg gat gga atg	3294			
Asn Leu Ile Thr Asn Ser Ser Ser Ala Phe Tyr Thr Asp Gly Met				
1085	1090	1095		
ggc aca gca aca tct atg gct gca atg gtt gat tcc tca ata cgc	3339			
Gly Thr Ala Lys Ser Met Ala Ala Met Val Asp Ser Ser Ile Pro				
1100	1105	1110		

cta acg	ggc ctc tta cgc gat	agt aac agc aac tct	ggc gga tct	3384
Leu Thr	Gly Leu Leu His Asp	Ser Asn Ser Asn Ser	Gly Gly Ser	
1115	1120	1125		
tcg gac	qga tcc tcc tcc agt	aat tgg aac tca gga	tct tca ggt	3429
Ser Asp	Gly Ser Ser Ser Ser	Asn Ser Asn Ser Gly	Ser Ser Gly	
1130	1135	1140		
tca gga	tct aat tgg aac tcc	ggg gtg tct tca tct	tcc gga aat	3474
Ser Gly	Ser Asn Ser Asn Ser	Gly Val Ser Ser Ser	Ser Gly Asn	
1145	1150	1155		
tcc tac	caa gat gcc ggt acg	ttg gaa tat tca tcc	aaa tct aac	3519
Ser Tyr	Gln Asp Ala Gly Thr	Leu Glu Tyr Ser Ser	Lys Ser Asn	
1160	1165	1170		
tcc aac	gta tcc act tct agc	aaa tca aag aac aaa	atc aat ggt	3564
Ser Asn	Val Ser Thr Ser Ser	Lys Ser Lys Lys Lys	Ile Ile Gly	
1175	1180	1185		
tta gtt	atc ggc ggt ggt gtt	ggt gga tgc tta tct	att tta ttc	3609
Leu Val	Ile Gly Val Val Val	Gly Gly Cys Leu Tyr	Ile Leu Phe	
1190	1195	1200		
atg att	ttt gct ttc aag tct	atc atc aga agg cgg	att caa agt	3654
Met Ile	Phe Ala Phe Lys Tyr	Ile Ile Arg Arg Arg	Ile Gln Ser	
1205	1210	1215		
caa gaa	att atc aag aac cca	gaa att tcc agt atc	agt tca agt	3699
Gln Glu	Ile Ile Lys Asn Pro	Glu Ile Ser Ser Ile	Ser Ser Ser	
1220	1225	1230		
gaa ttt	ggt gga gag aaa aat	tac cat aat gaa aag	aga atg agc	3744
Glu Phe	Gly Gly Glu Lys Asn	Tyr Asn Asn Glu Lys	Arg Met Ser	
1235	1240	1245		
ggt caa	gaa tcc ata aca caa	tct atg cga att caa	aat tgg atg	3789
Val Gln	Glu Ser Ile Thr Gln	Ser Met Arg Ile Gln	Asn Trp Met	
1250	1255	1260		
gat gat	agt tac tat ggt cag	ggg ttg aca aat aat	gac tca act	3834
Arg Arg	Ser Tyr Tyr Gly His	Gly Leu Thr Asn Asn	Asp Ser Thr	

1265	1270	1275	
cca acc agg cac aat ada tgg	agt tcc ata cca aac	att tca aga	1280
Pro Thr Arg His Asn Thr Ser	Ser Ser Ile Pro Lys	Ile Ser Arg	
1280	1285	1290	
cca att gct agc caa aac tcc	ctg ggt tgg aac gaa	gtt tga	1295
Pro Ile Ala Ser Gln Asn Ser	Leu Gly Trp Asn Glu	Val	
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Ser Leu Ala Arg Ala Ser Pro Phe Asp Phe Ile Phe Gly Asn Gly Thr	
20	30
Gln Gln Ala Gln Ser Gln Ser Gln Gly Gln Val Ser Phe Thr	
35	45
Asn Glu Ala Ser Gln Asp Ser Ser Thr Thr Ser Leu Val Thr Ala Tyr	
50	60
Ser Gln Gly Val His Ser His Gln Ser Ala Thr Ile Val Ser Ala Thr	
65	80
Ile Ser Ser Leu Pro Ser Thr Trp Tyr Asp Ala Ser Ser Thr Ser Gln	
85	95
Thr Ser Val Ser Tyr Ala Ser Gln Gln Ser Asp Tyr Ala Val Asn Gln	
100	110
Asn Ser Trp Ser Ala Ser Thr Asn Gln Leu Pro Ser Thr Ser Thr Thr	
115	125

Ser Tyr Tyr Ala Pro Thr Phe Ser Thr Ser Ala Asp Phe Ala Ala Ser
 130 135 140

Ser Val Asn Ala Ala Ser Asp Val Ser Thr Ala Ser Val Pro Ile Asp
 145 150 155 160

Thr Ser Ala Asn Ser Ile Pro Phe Thr Thr Thr Ser Asn Ile Glu Thr
 165 170 175

Thr Thr Ser Ala Pro Leu Thr Ser Asp Thr Pro Leu Ile Ser Thr Ser
 180 185 190

Thr Met Ser Ala Ala Asp Asn Val Phe Ser Ser Ala Asn Pro Ile Ser
 195 200 205

Ala Ser Leu Thr Thr Thr Asp Ser Ser Glu Ser Phe Asp Gln Thr Ser
 210 215 220

Thr Ala Gly Ala Ile Pro Val Gln Ser Ser Ala Asp Phe Ser Ser Ser
 225 230 235 240

Ser Glu Ile Leu Val Gln Ser Ser Ala Asp Phe Ser Ser Pro Ser Ser
 245 250 255

Pro Thr Thr Thr Asp Ile Ser Leu Ser Ala Ala Pro Leu Gln Thr Ser
 260 265 270

Gln Ser Ser Ser Phe Thr Thr Ala Ser Ala Ala Leu Pro Val Ser Ser
 275 280 285

Thr Asp Val Asp Gly Ser Ser Ala Ser Pro Val Val Ser Met Ser Ala
 290 295 300

Ala Gly Gln Ile Ala Ser Ser Ser Ser Thr Asp Asn Pro Thr Met Ser
 305 310 315 320

Glu Thr Phe Ser Leu Thr Ser Thr Glu Val Asp Gly Ser Asp Val Ser
 325 330 335

Ser Thr Val Ser Ala Leu Leu Ser Ala Pro Phe Leu Gln Thr Ser Thr
 340 345 350

Ser Asn Ser Phe Ser Ile Val Ser Pro Ser Val Ser Phe Val Pro Ser
 355 360 365

Gln Ser Ser Ser Asn Val Ala Ser Ser Ser Thr Ala Asn Val Val Ser
 370 375 380

Ser Ser Phe Ser Asp Ile Pro Pro Gln Thr Ser Thr Ser Gly Ser Val
 385 390 395 400

Val Ser Val Ala Gln Ser Ala Ser Ala Leu Ala Phe Gln Ser Ser Thr
 405 410 415

Glu Val Tyr Gly Ala Ser Ala Ser Ser Thr Met Ser Ser Leu Leu Ser
 420 425 430

Thr Thr Ser Leu Gln Ser Thr Thr Leu Asp Ser Ser Ser Leu Ala Ser
 435 440 445

Ser Ser Ala Ser Ser Ser Asp Leu Thr Asp Tyr Gly Val Ser Ser Thr
 450 455 460

Ala Ser Ile Pro Leu Leu Ser Ala Ser Glu Gln Ala Ser Thr Ser Ser
 465 470 475 480

Ser Phe Ser Val Val Ser Pro Ser Val Ser Phe Val Pro Ser Gln Ser
 485 490 495

Ser Ser Asp Val Ala Ser Thr Ser Ala Pro Ser Val Val Ser Ser Ser
 500 505 510

Phe Ser Tyr Thr Ser Leu Gln Ala Gly Gly Ser Ser Met Thr Asn Pro
 515 520 525

Ser Ser Ser Thr Ile Val Tyr Ser Ser Ser Thr Gly Ser Ser Glu Glu
 530 535 540

Ser Ala Ala Ser Thr Ala Ser Ala Thr Leu Ser Gly Ser Ser Ser Thr
 545 550 555 560

Tyr Met Ala Gly Asn Leu Gln Ser Gln Pro Pro Ser Thr Ser Ser Leu
 565 570 575

Leu Ser Gln Ser Gln Ala Thr Ser Thr Ser Ala Val Leu Ala Ser Ser
 580 585 590

Ser Val Ser Thr Thr Ser Pro Tyr Thr Thr Ala Gly Gly Ala Ser Thr
 595 600 605

Glu Ala Ser Ser Leu Ile Ser Ser Thr Ser Ala Glu Thr Ser Gln Val
 610 615 620

Ser Tyr Ser Gln Ser Thr Thr Ala Leu Gln Thr Ser Ser Phe Ala Ser
 625 630 635 640

Ser Ser Thr Thr Glu Gly Ser Glu Thr Ser Ser Gln Gly Phe Ser Thr
 645 650 655

Ser Ser Val Leu Val Gln Met Pro Ser Ser Ile Ser Ser Glu Phe Ser
 660 665 670

Pro Ser Gln Thr Thr Thr Gln Met Asn Ser Ala Ser Ser Ser Ser Gln
 675 680 685

Tyr Thr Ile Ser Ser Thr Gly Ile Leu Ser Glu Val Ser Asp Thr Ser
 690 695 700

Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp Thr
 705 710 715 720

Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser Asp
 725 730 735

Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val Ser
 740 745 750

Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln Val
 755 760 765

Ser Asp Thr Pro Val Ser Tyr Thr Thr Ser Ser Ser Ser Val Ser Gln
 770 775 780

Val Ser Asp Thr Ser Val Pro Ser Thr Ser Ser Arg Ser Ser Val Ser
 785 790 795 800

Gln Val Ser Asp Thr Pro Val Pro Ser Thr Ser Ser Arg Ser Ser Val
 805 810 815

Ser Gln Thr Ser Ser Ser Leu Gln Pro Thr Thr Thr Ser Ser Gln Arg
 820 825 830

Phe Thr Ile Ser Thr His Gly Ala Leu Ser Glu Ser Ser Ser Val Ser
 835 840 845

Gln Gln Ala Ser Glu Ile Thr Ser Ser Ile Asn Ala Thr Ala Ser Glu
 850 855 860

Tyr His Ser Ile Gln Thr Thr Ala Ala Thr Cln Ser Thr Thr Leu Ser
 865 870 875 880

Phe Thr Asp Ala Asn Ser Ser Ser Ala Ser Ala Pro Leu Glu Val Ala
 885 890 895

Thr Ser Thr Pro Thr Pro Ser Ser Lys Ala Ser Ser Leu Leu Leu Thr
 900 905 910

Pro Ser Thr Ser Ser Leu Ser Cln Val Ala Thr Asn Thr Asn Val Gln
 915 920 925

Thr Ser Leu Thr Thr Glu Ser Thr Thr Val Leu Glu Pro Ser Thr Thr
 930 935 940

Asn Ser Ser Ser Thr Phe Ser Leu Val Thr Ser Ser Asp Asn Asn Asp
 945 950 955 960

Trp Ile Pro Thr Glu Leu Ile Thr Gln Ala Pro Glu Ala Ala Ser Thr
 965 970 975

Ala Ser Ser Thr Val Gly Gly Thr Gln Thr Met Thr Leu Pro His Ala
 980 985 990

Ile Ala Ala Ala Thr Gln Val Pro Glu Pro Glu Gly Tyr Thr Leu Ile
 995 1000 1005

Thr Ile Gly Phe Lys Lys Ala Leu Asn Tyr Glu Phe Val Val Ser
 1010 1015 1020

Gln Pro	Lys Ser Ser Ala Gln	Ile Phe Gly Tyr Leu	Pro Glu Ala
1025	1030	1035	
Leu Asn	Thr Pro Phe Lys Asn	Val Phe Thr Asn Ile	Thr Val Leu
1040	1045	1050	
Gln Ile	Val Pro Leu Gln Asp	Asp Ser Leu Asn Tyr	Leu Val Ser
1055	1060	1065	
Val Ala	Glu Val Tyr Phe Pro	Thr Ala Glu Ile Glu	Glu Leu Ser
1070	1075	1080	
Asn Leu	Ile Thr Asn Ser Ser	Ser Ala Phe Tyr Thr	Asp Gly Met
1085	1090	1095	
Gly Thr	Ala Lys Ser Met Ala	Ala Met Val Asp Ser	Ser Ile Pro
1100	1105	1110	
Leu Thr	Gly Leu Leu His Asp	Ser Asn Ser Asn Ser	Gly Gly Ser
1115	1120	1125	
Ser Asp	Gly Ser Ser Ser Ser	Asn Ser Asn Ser Gly	Ser Ser Gly
1130	1135	1140	
Ser Gly	Ser Asn Ser Asn Ser	Gly Val Ser Ser Ser	Ser Gly Asn
1145	1150	1155	
Ser Tyr	Gln Asp Ala Gly Thr	Leu Glu Tyr Ser Ser	Lys Ser Asn
1160	1165	1170	
Ser Asn	Val Ser Thr Ser Ser	Lys Ser Lys Lys Lys	Ile Ile Gly
1175	1180	1185	
Leu Val	Ile Gly Val Val Val	Gly Gly Cys Leu Tyr	Ile Leu Phe
1190	1195	1200	
Met Ile	Phe Ala Phe Lys Tyr	Ile Ile Arg Arg Arg	Ile Gln Ser
1205	1210	1215	
Gln Glu	Ile Ile Lys Asn Pro	Gln Ile Ser Ser Ile	Ser Ser Ser
1220	1225	1230	

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Glu Phe Gly Gly Glu Lys Asn Tyr Asn Asn Glu Iys Arg Met Ser
 1235 1240 1245

Val Gln Glu Ser Ile Thr Gln Ser Met Arg Ile Gln Asn Trp Met
 1250 1255 1260

Asp Asp Ser Tyr Tyr Gly His Gly Leu Thr Asn Asn Asp Ser Thr
 1265 1270 1275

Pro Thr Arg His Asn Thr Ser Ser Ser Ile Pro Lys Ile Ser Arg
 1280 1285 1290

Pro Ile Ala Ser Gln Asn Ser Leu Gly Trp Asn Glu Val
 1295 1300 1305

<210> 7

<211> 315

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(315)

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 Met Lys Phe Leu Lys Asn Lys Ala Pro Ala Asn Leu Val Asp Asn Gly
 1 5 10 15

agg ttt gtg gaa gca ata acg tgc aat aac gtt aac cog aat oca tct 36
 Arg Phe Val Gly Ala Ile Thr Cys Asn Lys Val Lys Pro Asn Pro Ser
 20 25 30

tgc gtc tcc aac tgc ctg aaa ttt ctt tcc gaa gtt tta gcg gta gaa 144
 Cys Val Ser Asn Cys Leu Lys Phe Leu Ser Glu Val Leu Ala Val Glu
 35 40 45

gca ata act gat tgg gcc aga aat tta gct acg gtt tcc aaa tgg gac 192
 Ala Ile Thr Asp Ser Ala Arg Asn Leu Ala Thr Val Ser Lys Ser Asp
 50 55 60

ald gaa gla ttt tct ctt cta caa ttg agt agc aat aaa cag agc ggg 240
 ile leu leu phe ser leu leu glu leu ser ser asn lys gln ser gly
 65 70 75 80

tcc tct ttg cca ctt ttt gat ctt gtg ttt ata cta ctt tca acc ttt 288
 ser ser leu pro leu phe asp leu val phe ile leu leu ser thr phe
 85 90 95

ttt tta ttc cat aat ccc tgc aat tga 315
 phe leu phe his asn pro cys asn
 100

<210> 8

<211> 104

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 8

Met Lys Phe leu lys asn lys ala pro ala asn leu val asp asn gly
 1 5 10 15

arg phe val glu ala ile thr cys asn lys val lys pro asn pro ser
 20 25 30

cys val ser asn cys leu lys phe leu ser glu val leu ala val glu
 35 40 45

ala ile thr asp ser ala arg asn leu ala thr val ser lys ser asp
 50 55 60

ile leu leu phe ser leu leu gln leu ser ser asn lys gln ser gly
 65 70 75 80

ser ser leu pro leu phe asp leu val phe ile leu leu ser thr phe
 85 90 95

Phe Leu Phe His Asn Pro Cys Asn
100

<210> 9

<211> 2064

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2064)

<400> 9

atg tgc gcc agt tta aac gag gta aca aag aat gac acc tat ggg gtc 48
Met Cys Ala Ser Ieu Asn Glu Val Lys Lys Asn Asp Thr Tyr Gly Val

1 5 10 15

tca caa aag ggc tac aat gac aat ttc agt gaa agt ggg ggc gtc ctt 96
Ser Gln Lys Gly Tyr Asn Asp Asn Phe Ser Glu Ser Gln Gly Val Ieu

20 25 30

cat ggt agt aag tgg atg ccc act agc atg aca aat atg cta cag tct 144
His Gly Ser Lys Ser Met Pro Thr Ser Met Lys Asn Met Leu Gln Ser

35 40 45

ccc acg atg gtc aac atg tgt gat att tta caa aac aag gaa gct gct 192
Pro Thr Met Val Asn Met Cys Asp Ile Leu Glu Asn Lys Gln Ala Ala

50 55 60

aat gac gaa aaa cct gtg ata cct acc acg gat acc gcc act ggc ggg 240
Asn Asp Glu Lys Pro Val Ile Pro Thr Thr Asp Thr Ala Thr Ala Gly

65 70 75 80

act ggt act gaa gat att agc tcc acc caa tcc gag gaa act gat cag 298
Thr Gly Thr Glu Asp Ile Ser Ser Thr Gln Ser Glu Glu Thr Asp Gln

85 90 95

aat agt cat ctt att gcc tca gag atc ttg gaa ggc act ttc aca gat 336
Asn Ser His Leu Ile Ala Ser Glu Ile Leu Glu Gly Thr Phe Lys Asp

100 105 110

gta tct tac aag qaa tat gca aat ttc lly gga aac qat aac aat aat	384
Val Ser Tyr Lys Glu Tyr Ala Asn Phe Leu Gly Asn Asp Asn Asn Asn	
115 120 125	
caa gtc ttg act gag ttt gta aag tta ttg agt cct ttg cag tog lea	432
Gln Val Leu Thr Glu Phe Val Tyr Leu Leu Ser Pro Leu Pro Ser Ser	
130 135 140	
cta tta gaa acg ctt ttc aat tta tog aaa agt ata tat ttc att gca	480
Leu Leu Glu Thr Leu Phe Asn Leu Ser Lys Ser Ile Tyr Phe Ile Ala	
145 150 155 160	
gaa gag caa aat atc gac cgg ala cta gag lyc lly agc ala gaa tgg	528
Glu Ala Gln Asn Ile Asp Arg Ile Leu Glu Cys Leu Ser Ile Glu Trp	
165 170 175	
ata gct tgc cac cag aac aca cct tgg aag tca ggc tat aag tca tgc	576
Ile Ala Cys His Pro Asn Thr His Trp Lys Ser Gly Tyr Lys Ser Cys	
180 185 190	
cct ata gtc tta ttt tcc ctg ttg atc ctt aat tgg gat ttg cac aac	624
His Ile Val Leu Phe Ser Leu Leu Ile Leu Asn Ser Asp Leu His Asn	
195 200 205	
aac ttt caa gtt gac cat aaa aag att aag ttt tcc ctg gtt gca ttt	672
Asn Phe Gln Val Asp His Lys Lys Ile Lys Phe Ser Met Val Ala Phe	
210 215 220	
atc aac aat aca ctg agg gca cta aga gag gau aat gaa tac gaa gaa	720
Ile Asn Asn Thr Leu Arg Ala Leu Arg Glu Glu Asn Glu Tyr Glu Glu	
225 230 235 240	
ttg aaa ata tac tcc cgc gaa cat lly atc atc gaa gaa ctt tcc gaa	768
Leu Lys Ile Tyr Ser Arg Glu His Leu Ile Ile Glu Glu Leu Ser Glu	
245 250 255	
tac tat aaa acg tta aat gaa acg cct tta ccg tta tgc aca gaa tct	816
Tyr Tyr Lys Thr Leu Asn Glu Thr Pro Leu Pro Leu Cys Thr Glu Ser	
260 265 270	

aga aca tca ata aat ata tca gat aac caa tct tcc ttg aaa agg ttc	864
Arg Thr Ser Ile Asn Ile Ser Asp Asn Gln Ser Ser Leu Lys Arg Phe	
275 280 285	
tct act cta gga tca cgg gaa ttt agt aca tca aat tta cgt agt gtt	912
Ser Thr Leu Gly Ser Arg Gln Phe Ser Thr Ser Asn Leu Arg Ser Val	
290 295 300	
aac tct aat tct act aca cta tat tca aga gat ggt caa gta tct gta	960
Asn Ser Asn Ser Thr Thr Leu Tyr Ser Arg Asp Gly Gln Val Ser Val	
305 310 315 320	
cga gaa atg agc gca aaa tca aat aaa aac ttt cac aat aat cac ccc	1008
Arg Glu Met For Ala Lys Ser Asn Lys Asn Phe His Asn Asn His Pro	
325 330 335	
atg gat gca ctc tac ctt aaa gag tct ttt gat gac ggt tta att acc	1056
Met Asp Ala Leu Tyr Leu Lys Glu Ser Phe Asp Asp Gly Leu Ile Thr	
340 345 350	
gaa aac ggc tcc agt tgg ttc atg gac gat tta att ctt ata agc aag	1104
Glu Asn Gly Ser Ser Trp Phe Met Asp Asp Leu Ile Leu Ile Ser Lys	
355 360 365	
aaa tct tta cca cgt aaa tat tct aaa aga gac aaa gat caa gtc ggc	1152
Lys Ser Leu Pro Arg Lys Tyr Ser Lys Arg Asp Lys Asp Gln Val Ala	
370 375 380	
gca cca aaa atg acc tct aag aga aac aaa tcc ttc ttc gga tgg cta	1200
Ala Pro Lys Met Thr Ser Lys Arg Asn Lys Ser Phe Phe Gly Trp Leu	
385 390 395 400	
aaa cca tct aaa acg act aca ctt att gag cac aca tct aga agg act	1248
Lys Pro Ser Lys Thr Thr Thr Leu Ile Glu His Thr Ser Arg Arg Thr	
405 410 415	
tct tta tcc tat ttg aat aag gat tct gaa tgg gag agg gtc aaa ata	1296
Ser Leu Ser Tyr Leu Asn Lys Asp Ser Glu Trp Glu Arg Val Lys Ile	
420 425 430	

cag gtc aag gag ggc aga att ttt att ttc aaa att aaa cca gat gtt	1344
Gln Val Lys Glu Gly Arg Ile Phe Ile Phe Tyr Ile Lys Pro Asp Val	
435 440 445	
aag gat atc atc caa tca agt gaa aca gac agt gct acc atc gac tat	1392
Lys Asp Ile Ile Gln Ser Ser Glu Thr Asp Ser Ala Thr Ile Asp Tyr	
450 455 460	
ttc aaa gat atc agt agc tct tat ttt gct tac tca ctg ctt gaa gct	1440
Phe Lys Asp Ile Ser Ser Ser Tyr Phe Ala Tyr Ser Leu Leu Glu Ala	
465 470 475 480	
gaa gca cat gtc gtg caa gat aat ata att ata ggt agt gga gca atg	1488
Glu Ala His Val Val Gln Asp Asn Ile Ile Ile Gly Ser Gly Ala Met	
485 490 495	
aaa tca aat gtg tgt aac aaa aac acc aag agg aaa agt ggc aac LL	1536
Lys Ser Asn Val Cys Asn Lys Asn Thr Lys Arg Lys Ser Gly Asn Phe	
500 505 510	
acc gtt agt ttt cca gag aat atc aac gga cca aag ctt gtt ctg gag	1584
Thr Val Ser Phe Pro Glu Asn Ile Asn Gly Pro Lys Leu Val Leu Glu	
515 520 525	
ttc cag acg aga agt gtt gaa gaa gcc cac aag ttt atg gac tgt atc	1632
Phe Gln Thr Arg Ser Val Glu Glu Ala His Lys Phe Met Asp Cys Ile	
530 535 540	
aac ttc tgg gca ggt agg att tct cca gtt cct tta acc caa ttc gaa	1680
Asn Phe Trp Ala Gly Arg Ile Ser Pro Val Pro Leu Thr Gln Phe Glu	
545 550 555 560	
gcc gta tct aac gca gaa tat gga tgg agt gac aag atc ttg aca gag	1728
Ala Val Ser Asn Ala Glu Tyr Gly Thr Ser Asp Lys Ile Asn Thr Glu	
565 570 575	
cac gct tcc ctg aat ctt aaa aat att gtt gta agt gaa tgg aag cca	1776
His Ala Ser Leu Asn Leu Lys Asn Ile Val Val Ser Glu Trp Lys Pro	
580 585 590	
cta ttg ggg cta gag cta cta tac gaa gat gcg aaa gat gta gag atg	1824

Leu Leu Gly Leu Glu Leu Leu Tyr Glu Asp Ala Lys Asp Val Glu Met
 595 600 605
 gtc gaa cta aaa gaa agg cta aag gaa ttg atg aac lle aac aga cag 1672
 Val Glu Leu Lys Glu Arg Leu Lys Glu Leu Met Asn Phe Thr Arg Gln
 610 615 620
 ott ggt ata tgg ata gac aaa cat aac gaa ata aag gat aag ctg gtc 1920
 Leu Gly Ile Trp Ile Asp Lys His Asn Glu Ile Lys Asp Lys Leu Val
 625 630 635 640
 gaa att tgg agc ttt gac gat aac cat ttt gaa gaa gtc atg aat aat 1968
 Glu Ile Trp Ser Phe Asp Asp Asn Tyr Phe Glu Ala Val Met Asn Asn
 645 650 655
 tgg aat tgg aga tat ttg tat atg aat aat caa tat aag aac aga ctg 2016
 Trp Asn Ser Arg Tyr Leu Tyr Met Asn Asn Gln Tyr Lys Lys Arg Leu
 660 665 670
 agc tac ttg aaa gct ttg caa aaa gcc atg ggt tct gtt cag ttc taa 2064
 Ser Tyr Leu Lys Ala Leu Gln Lys Ala Met Gly Ser Val Gln Phe
 675 680 685
 <210> 10
 <211> 687
 <212> PRT
 <213> *Saccharomyces cerevisiae*
 <400> 10
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 1 5 10 15
 Ser Gln Lys Gly Tyr Asn Asp Asn Phe Ser Glu Ser Glu Gly Val Leu
 20 25 30
 His Gly Ser Lys Ser Met Pro Thr Ser Met Lys Asn Met Asn Gln Ser
 35 40 45
 Pro Thr Met Val Asn Met Cys Asp Ile Leu Gln Asn Lys Glu Ala Ala

50	55	60
Asn Asp Glu Lys Pro Val Ile Pro Thr Thr Asp Thr Ala Thr Ala Gly		
65	70	75
Thr Gly Thr Glu Asp Ile Ser Ser Thr Glu Ser Glu Glu Thr Asp Gln		
	85	90
Asn Ser His Leu Ile Ala Ser Glu Ile Leu Glu Gly Thr Phe Lys Asp		
	100	110
Val Ser Tyr Lys Glu Tyr Ala Asn Phe Leu Gly Asn Asp Asn Asn Asn		
	115	120
Gln Val Leu Thr Glu Phe Val Lys Leu Leu Ser Pro Leu Pro Ser Ser		
	130	140
Leu Leu Glu Thr Leu Phe Asp Leu Ser Lys Ser Ile Tyr Phe Ile Ala		
145	150	155
Glu Ala Gln Asn Ile Asp Arg Ile Leu Glu Cys Leu Ser Ile Glu Trp		
	165	170
Ile Ala Cys His Pro Asn Thr His Trp Lys Ser Gly Tyr Lys Ser Cys		
	180	190
His Ile Val Leu Phe Ser Leu Leu Ile Leu Asn Ser Asp Leu His Asn		
	195	200
Asn Phe Gln Val Asp His Lys Lys Ile Lys Phe Ser Met Val Ala Phe		
210	215	220
Ile Asn Asn Thr Leu Arg Ala Leu Arg Glu Glu Asn Glu Tyr Glu Gln		
225	230	235
Leu Lys Ile Tyr Ser Arg Glu His Leu Ile Ile Glu Glu Leu Ser Gln		
	245	250
Tyr Tyr Lys Thr Leu Asn Glu Thr Pro Leu Pro Leu Cys Thr Glu Ser		
	260	270
Arg Thr Ser Ile Asn Ile Ser Asp Asn Gln Ser Ser Leu Lys Arg Phe		

275	280	285
Ser Thr Leu Gly Ser Arg Glu Phe Ser Thr Ser Asn Leu Arg Ser Val		
290	295	300
Asn Ser Asn Ser Thr Thr Leu Tyr Ser Arg Asp Gly Gln Val Ser Val		
305	310	315
Arg Glu Met Ser Ala Lys Ser Asn Lys Asn Phe His Asn Asn His Pro		
325	330	335
Met Asp Ala Leu Tyr Leu Lys Glu Ser Phe Asp Asp Gly Leu Ile Thr		
340	345	350
Glu Asn Gly Ser Ser Trp Phe Met Asp Asp Leu Ile Leu Ile Ser Lys		
355	360	365
Lys Ser Leu Pro Arg Lys Tyr Ser Lys Arg Asp Lys Asp Gln Val Ala		
370	375	380
Ala Pro Lys Met Thr Ser Lys Arg Asn Lys Ser Phe Phe Gly Trp Leu		
385	390	395
Lys Pro Ser Lys Thr Thr Thr Leu Ile Glu His Thr Ser Arg Arg Thr		
405	410	415
Ser Leu Ser Tyr Leu Asn Lys Asp Ser Glu Trp Glu Arg Val Lys Ile		
420	425	430
Gln Val Lys Glu Gly Arg Ile Phe Ile Phe Lys Ile Lys Pro Asp Val		
435	440	445
Lys Asp Ile Ile Gln Ser Ser Glu Thr Asp Ser Ala Thr Ile Asp Tyr		
450	455	460
Phe Lys Asp Ile Ser Ser Ser Tyr Phe Ala Tyr Ser Leu Leu Glu Ala		
465	470	475
Glu Ala His Val Val Gln Asp Asn Ile Ile Ile Gly Ser Gly Ala Met		
480	485	490
Lys Ser Asn Val Cys Asn Lys Asn Thr Lys Arg Lys Ser Gly Asn Phe		

500	505	510
Thr Val Ser Phe Pro Glu Asn Ile Asn Gly Pro Lys Leu Val Leu Glu		
515	520	525
Phe Gln Thr Arg Ser Val Glu Glu Ala His Lys Phe Met Asp Cys Ile		
530	535	540
Asn Phe Trp Ala Gly Arg Ile Ser Pro Val Pro Leu Thr Gln Phe Glu		
545	550	555
Ala Val Ser Asn Ala Glu Tyr Gly Trp Ser Asp Lys Ile Leu Thr Glu		
565	570	575
His Ala Ser Leu Asn Leu Lys Asn Ile Val Val Ser Glu Trp Lys Pro		
580	585	590
Leu Leu Gly Leu Glu Leu Leu Tyr Glu Asp Ala Lys Asp Val Glu Met		
595	600	605
Val Glu Leu Lys Glu Arg Leu Lys Glu Leu Met Asn Phe Thr Arg Gln		
610	615	620
Leu Gly Ile Trp Ile Asp Lys His Asn Glu Ile Lys Asp Lys Leu Val		
625	630	635
Glu Ile Trp Ser Phe Asp Asp Asn Tyr Phe Glu Ala Val Met Asn Asn		
645	650	655
Trp Asn Ser Arg Tyr Leu Tyr Met Asn Asn Gln Tyr Lys Lys Arg Leu		
660	665	670
Ser Tyr Leu Lys Ala Leu Gln Lys Ala Met Gly Ser Val Gln Phe		
675	680	685

<210> 11

<211> 678

<212> DNA

<213> *Saccharomyces cerevisiae*

<222> (1) .. (678)

GGC Gta aat ggt cgc tgc tgc gat gta gac atg aca acc aca tgc cgc 432
Gly Leu Asn Gly Arg Ser Ser Asp Val Asp Met Thr Thr Thr Leu Pro
120 130 140

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agt ttg aag cca cct ctg caa aac gga gaa att aag gcc gac agc att 480
 Ser Leu Lys Pro Pro Leu Gln Asn Gly Glu Ile Lys Ala Asp Ser Ile
 145 150 155 160

gac aat ctt gat ttg gct tcc ctg gat ccg ctt gag caa agc cct agt 528
 Asp Asn Leu Asp Leu Ala Ser Leu Asp Pro Leu Glu Gln Ser Pro Ser
 165 170 175

ata tct atg gaa cct gtt agt atc aat gaa aca gga agc gca tat aca 576
 Ile Ser Met Glu Pro Val Ser Ile Asn Glu Thr Gly Ser Ala Tyr Thr
 180 185 190

act acg aac aca gca cta aac gat att gac att cca ttc tcc atc aat 624
 Thr Thr Asn Thr Ala Leu Asn Asp Ile Asp Ile Pro Phe Ser Ile Asn
 195 200 205

gag ttg aac gag cta tac aaa caa gta tct tcg cat aac tca cat tca 672
 Glu Leu Asn Glu Leu Tyr Lys Gln Val Ser Ser His Asn Ser His Ser
 210 215 220

cca tca 678
 Gln
 225

<210> 12
 <211> 225
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 12

Met Val Val Ile Asn Gly Val Lys Tyr Ala Cys Glu Thr Cys Ile Arg
 1 5 10 15

Gly His Arg Ala Ala Gln Cys Thr His Thr Asp Gly Pro Leu Gln Met
 20 25 30

Ile Arg Arg Lys Gly Arg Pro Ser Thr Thr Cys Gly His Cys Lys Glu
 35 40 45

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Leu Arg Arg Thr Lys Asn Phe Asn Pro Ser Gly Gly Cys Met Cys Ala
 50 55 60

Ser Ala Arg Arg Pro Ala Val Gly Ser Lys Glu Asp Glu Thr Arg Cys
 65 70 75 80

Arg Cys Asp Glu Gly Glu Pro Cys Lys Lys His Thr Lys Arg Lys Ser
 85 90 95

Ser Arg Lys Ser Lys Gly Gly Ser Cys His Arg Arg Ala Asn Asp Glu
 100 105 110

Ala Ala His Val Asn Gly Leu Gly Ile Ala Asp Leu Asp Val Leu Leu
 115 120 125

Gly Leu Asn Gly Arg Ser Ser Asp Val Asp Met Thr Thr Thr Leu Pro
 130 135 140

Ser Leu Lys Pro Pro Leu Gln Asn Gly Glu Ile Lys Ala Asp Ser Ile
 145 150 155 160

Asp Asn Leu Asp Leu Ala Ser Leu Asp Pro Leu Glu Gln Ser Pro Ser
 165 170 175

Ile Ser Met Glu Pro Val Ser Ile Asn Glu Thr Gly Ser Ala Tyr Thr
 180 185 190

Thr Thr Asn Thr Ala Leu Asn Asp Ile Asp Ile Pro Phe Ser Ile Asn
 195 200 205

Glu Leu Asn Glu Leu Tyr Lys Gln Val Ser Ser His Asn Ser His Ser
 210 215 220

Gln

225

<210> 13

<211> 750

<212> n/a

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1) .. (750)

<400> 13

atg ttg cag cta agg ttt atg cct gga tgg gtc ccc aga aat ggt ttt 48

Met Leu Gln Leu Arg Phe Met Pro Gly Trp Val Pro Arg Asn Gly Phe

1 5 10 15

ttt ggt ttg aag gag aca atc ggt aca gta cat aag aga ttt tat gct 96

Phe Gly Leu Lys Gln Thr Ile Gly Thr Val His Lys Arg Phe Tyr Ala

20 25 30

ctg gct tct gaa caa ccc tca aga aag aca gta aag ccc ctg gac tag 144

Leu Ala Ser Glu Gln Pro Ser Arg Lys Thr Val Lys Pro Leu Asp Ser

35 40 45

agg aag aag ttt ctc atc gat aca tac aag cat tta atg gag aac agt 192

Arg Lys Thr Phe Leu Ile Asp Thr Tyr Lys His Leu Met Glu Asn Ser

50 55 60

tct atg att ttt ttt gtc cat tac aat aat ctt tcc aaa aca gaa gat 240

Ser Met Ile Phe Phe Val His Tyr Asn Asn Leu Ser Lys Thr Glu Asp

65 70 75 80

cac cat ttc aga ttc aag att aaa cag aca gga ggg aaa ctg aca aca 288

His His Phe Arg Phe Lys Ile Lys Gln Thr Gly Gly Lys Leu Thr Lys

85 90 95

cta aga aac aac ctg ttc gaa gtc tac ttg aga aat tgg cat ctg ccc 336

Val Arg Asn Asn Leu Phe Glu Val Tyr Leu Arg Asn Ser His Leu Pro

100 105 110

gac cca tgt gga ttc gtg aag cgt aaa gag caa aac tgg aaa cat cca 384

Asp Pro Cys Gly Phe Val Lys Arg Lys Glu Gln Asn Trp Lys His Pro

115 120 125

ctc ttg cca cta ctg aag ggt cat arg gcc aca att aca tac gaa gac 432

Leu Leu Pro Leu Leu Lys Gly Pro Thr Ala Thr Ile Thr Tyr Glu Asp

130 135 140

acc aac cct caa caa gta gcc aag cta ttg aag gtt ctg cag tca gca 480
 Thr Asn Pro Gln Gln Val Ala Lys Ileu Leu Lys Val Leu Gln Ser Ala
 145 150 155 160

cna gac aag ctg atg gtg att ggt gca aaa gta gaa aac gaa gtt ttg 528
 Gln Asp Lys Leu Met Val Ile Gly Ala Lys Val Glu Asn Glu Val Leu
 165 170 175

aat gtg gaa aaa ata aac act ttt aag act ctg ccc aca aag cag gaa 576
 Asn Val Glu Lys Ile Asn Thr Phe Lys Thr Leu Pro Thr Lys Pro Glu
 180 185 190

atg cag tgg caa tta gtc agc gtt ttg caa atg cta agt ggg ttg ggt 624
 Met Gln Ser Gln Leu Val Ser Val Ile Gln Met Leu Ser Gly Leu Gly
 195 200 205

ttg gtt agt aag ttg gaa aac agt tca aat gca ttg tat tta aca cta 672
 Leu Val Arg Thr Ileu Glu Asn Ser Ser Asn Ala Leu Tyr Leu Thr Ileu
 210 215 220

aaa tct cac aat gac aac cna aaa cct aaa gag gat gtg gag tca act 720
 Lys Ser His Asn Asp Asn Gln Lys Pro Lys Glu Asp Val Glu Ser Thr
 225 230 235 240

aca gat gca gaa tgg aag gga tca aag taa 750
 Thr Asp Ala Glu Ser Lys Gly Ser Lys
 245

<210> 14

<211> 249

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 14

Met Leu Gln Ileu Arg Phe Met Pro Gly Tyr Val Pro Arg Asn Gly Phe
 1 5 10 15

Phe Gly Leu Lys Glu Thr Ile Gly Thr Val His Lys Arg Phe Tyr Ala
 20 25 30

Leu Ala Ser Glu Gln Pro Ser Arg Lys Thr Val Lys Pro Leu Asp Ser
35 40 45

Arg Lys Thr Phe Leu Ile Asp Thr Tyr Lys His Leu Met Gln Asn Ser
50 55 60

Ser Met Ile Phe Phe Val His Tyr Asn Asn Leu Ser Lys Thr Glu Asp
65 70 75 80

His His Phe Arg Phe Lys Ile Lys Gln Thr Gly Gly Lys Leu Thr Lys
85 90 95

Val Arg Asn Asn Leu Phe Glu Val Tyr Leu Arg Asn Ser His Leu Pro
100 105 110

Asp Pro Cys Gly Phe Val Lys Arg Lys Glu Gln Asn Trp Lys His Pro
115 120 125

Leu Leu Pro Leu Leu Lys Gly Pro Thr Ala Thr Ile Thr Tyr Glu Asp
130 135 140

Thr Asn Pro Gln Gln Val Ala Lys Leu Leu Lys Val Leu Gln Ser Ala
145 150 155 160

Gln Asp Lys Leu Met Val Ile Gly Ala Lys Val Glu Asn Glu Val Leu
165 170 175

Asn Val Glu Lys Ile Asn Thr Phe Lys Thr Leu Pro Thr Lys Pro Glu
180 185 190

Met Gln Ser Gln Leu Val Ser Val Leu Gln Met Leu Ser Gly Leu Gly
195 200 205

Leu Val Arg Thr Leu Glu Asn Ser Ser Asn Ala Leu Tyr Leu Thr Leu
210 215 220

Lys Ser His Asn Asp Asn Gln Lys Pro Lys Glu Asp Val Glu Ser Thr
225 230 235 240

Thr Asp Ala Glu Ser Lys Gly Ser Lys

245

<210> 15
 <211> 357
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
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<400> 15
 atg aag ctc cca cag acc atg cta cgt tat ata tct gtg aag cat gtc 40
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 1 5 10 15

cgg tgg cca agg att ctg aag ggc tca aag ctt tgg tac tca acg cag 26
 Arg Trp Pro Arg Ile Leu Thr Gly Ser Lys Leu Trp Tyr Ser Thr Gln
 20 25 30

atg gaa atg act ccg gag gag aag atg atc acc gat aaa cta caa cag 144
 Met Ala Met Thr Pro Glu Glu Lys Met Ile Thr Asp Lys Leu Gln Gln
 35 40 45

gaa ctg gaa cct gaa gtg tgt aac gtg caa gag gtt tcc ggt ggc tgc 192
 Glu Leu Glu Pro Glu Val Cys Lys Val Gln Asp Val Ser Gly Gly Cys
 50 55 60

gga tcc atg ttt gct atc aac ata aca agc aag aag ttc aac gga ctc 240
 Gly Ser Met Phe Ala Ile Asn Ile Thr Ser Lys Lys Phe Asn Gly Leu
 65 70 75 80

agt ctg atc aag cag caa cag ctg gtg aac aga att ttg agg gac gat 288
 Ser Leu Ile Lys Gln His Gln Leu Val Asn Arg Ile Leu Arg Asp Asp
 85 90 95

att tcc aga tgg cat ggc cta caa ttg acc act aag aag tca act ggg 336
 Ile Ser Arg Trp His Gly Leu Gln Leu Thr Thr Lys Lys Ser Thr Gly
 100 105 110

aag ggt ccg gca tca tca tga

357

Lys Gly Pro Ala Ser Ser

115

<210> 16

<211> 116

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Met Lys Leu Pro Gln Thr Met Leu Arg Ser Ile Ser Val Lys His Val

1

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10

15

Arg Trp Pro Arg Ile Leu Thr Gly Ser Lys Leu Trp Tyr Ser Thr Gln

20

25

30

Met Ala Met Thr Pro Gln Glu Lys Met Ile Thr Asp Lys Leu Gln Gln

35

40

45

Glu Leu Glu Pro Glu Val Cys Lys Val Gln Asp Val Ser Gly Gly Cys

50

55

60

Gly Ser Met Phe Ala Ile Asn Ile Thr Ser Lys Lys Phe Asn Gly Leu

65

70

75

80

Ser Leu Ile Lys Gln His Gln Leu Val Asn Arg Ile Leu Arg Asp Asp

85

90

95

Ile Ser Arg Trp His Gly Leu Gln Leu Thr Thr Lys Lys Ser Thr Gly

100

105

110

Lys Gly Pro Ala Ser Ser

115

<210> 17
 <211> 1782
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
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 1 5 10 15
 aaa aat att cta cag gaa tgg gtc ttg aac aat tac aga aat ggt gga 96
 Lys Asn Ile Leu Gln Glu Ser Val Leu Asn Lys Tyr Arg Thr Ala Gly
 20 25 30
 cca atc gca caa aat gct ttg aat tat gtt act tct tgg atc aat gat 144
 Cln Ile Ala Gln Thr Ala Leu Lys Tyr Val Thr Ser Leu Ile Asn Asp
 35 40 45
 tca tat cac tct aag aac aca cag cgc caa tta acc gtg cca gag cta 192
 Ser Tyr His Ser Lys Thr Thr Gln Arg Cln Leu Thr Val Pro Glu Leu
 50 55 60
 tgt ttg ctt acc gat tct ttt att ttg acc cgg ttg gaa caa tat tat 240
 Cys Leu Leu Thr Asp Ser Phe Ile Leu Thr Arg Leu Glu Gln Tyr Tyr
 65 70 75 80
 aaa aac aaa gtc aat gaa aga ggt att gcc att cca acc aat att gat 288
 Lys Asn Lys Val Asn Glu Arg Gly Ile Ala Ile Pro Thr Thr Ile Asp
 85 90 95
 atc gac caa att tct ggt gga tgg tgc ccc gaa ata gat gat act caa 336
 Ile Asp Glu Ile Ser Gly Gly Trp Cys Pro Glu Ile Asp Asp Thr Gln
 100 105 110

44/762

aat ttg tta aac tgg aat aag ggg aau gaa tuc act ttt gca tca tct	384
Asn Leu Leu Asn Trp Asn Lys Gly Lys Asp Ser Thr Phe Ala Ser Ser	
115 120 125	
gtc act ggg act ttg aga cgg ggg gat tta gtc aag att aca cta ggt	432
Val Thr Gly Thr Leu Arg Pro Gly Asp Leu Val Lys Ile Thr Leu Gly	
130 135 140	
gtt cat att gat ggt tac aac tct gaa gtt tct cat act aig gtt att	480
Val His Ile Asp Gly Tyr Thr Ser Glu Val Ser His Thr Met Val Ile	
145 150 155 160	
tac ccc gtt gat gaa aac aca cct att ctt caa ccc act ggg cca cta	528
Tyr Pro Val Asp Glu Thr Lys Pro Ile Leu Gln Pro Thr Gly Pro Leu	
165 170 175	
cta ggt ggt aaa cgg gal gct gta gct gct gct cac att gct atg gaa	576
Leu Gly Gly Lys Ala Asp Ala Val Ala Ala Ala His Ile Ala Met Glu	
180 185 190	
aca gtt gtt gct tta tta gcc tct cct ctg act cca gaa aag ctt cct	624
Thr Val Val Ala Leu Leu Ala Cys Ala Leu Thr Pro Glu Lys Leu Pro	
195 200 205	
gcc tca ctg gga gga act tca agt ggt aca aca ggc caa ttg att aga	672
Ala Ser Leu Gly Gly Thr Ser Ser Gly Ile Thr Gly Gln Leu Ile Arg	
210 215 220	
act ata gtg gat act att gcc aga tct tat aac tgt gcc gtt gtt cct	720
Thr Ile Val Asp Thr Ile Ala Arg Ser Tyr Asn Cys Gly Val Val Pro	
225 230 235 240	
ggt tct cgt gta aga cgg att aga aga ttc ctg gca gcc caa aac gaa	768
Gly Ser Arg Val Arg Arg Ile Arg Arg Phe Leu Ala Gly Gln Asn Glu	
245 250 255	
ggt att gtt gcc gaa agg gaa tat aag ggt gtt gtt lgg aca gag tcc	816
Gly Ile Val Ala Glu Arg Glu Tyr Lys Gly Val Val Trp Thr Glu Ser	
260 265 270	
cat caa gaa gca gat ttg cta tct aat act gat gcc aag gat tta aca	864

His Gln Glu Ala Asp Leu Leu Ser Asn Thr Asp Ala Lys Asp Leu Thr	
275 280 285	
gtg gta gat cgt gga caa cca act cca ttc act aat ggt tct gct att	912
Val Val Asp Arg Gly Gln Ser Thr Pro Phe Thr Asn Val Ser Ala Ile	
290 295 300	
cca agt gat gat ttc gtt gtt caa tca ggt gaa gtc tat tta att gat	960
Pro Ser Asp Asp Phe Val Val Gln Ser Gly Glu Val Tyr Leu Ile Asp	
305 310 315 320	
ctg aaa atg gca tct ttg gag cat tgt acc aaa aag ggt tta gta act	1008
Leu Lys Met Ala Ser Leu Glu His Cys Thr Lys Lys Gly Leu Val Thr	
325 330 335	
tta gaa acc ggt gac tct tac aca ggt aaa tct cat aag gct gga gaa	1056
Leu Glu Thr Val Asp Ser Tyr Thr Gly Lys Ser His Lys Ala Gly Glu	
340 345 350	
ctg att gca aga ccc ggt gca tat gtc aga gat ttt gct caa acc cat	1104
Leu Ile Ala Arg Pro Gly Ala Tyr Val Arg Asp Phe Ala Gln Thr His	
355 360 365	
att ctt aag tta aaa act tct aga caa tta tta act aag atc gat aca	1152
Ile Leu Lys Leu Lys Thr Ser Arg Gln Leu Leu Thr Lys Ile Asp Lys	
370 375 380	
caa ggc gtt tat cca ttc aag tta tcc cat tta tct tct aac ttt act	1200
Gln Gly Val Tyr Pro Phe Lys Leu Ser His Leu Ser Ser Asn Phe Pro	
385 390 395 400	
ttc gtt caa gaa aat gaa gaa gaa ctc caa agc tta aag aag gat ttg	1248
Phe Val His Gln Asn Glu Glu Glu Leu Gln Ser Leu Lys Lys Asp Leu	
405 410 415	
aaa tca ttt aga ctt ggg atg agt gag att tcc aac aac tac tta tgt	1296
Lys Ser Phe Arg Leu Gly Met Ser Glu Ile Ser Asn Asn Tyr Leu Cys	
420 425 430	
gtg gaa agt cca ata caa att gct aga tgg gtt cca tgg gac cat att	1344

Val	Glu	Ser	Pro	Ile	Gln	Ile	Ala	Arg	Trp	Val	Pro	Trp	Asp	His	Ile		
				435					440							445	
tta	aag	gct	acc	aat	cca	aac	ggc	aac	tta	agt	cal	gal	gaa	acc	tcc		
Leu	Lys	Ala	Thr	Asn	Pro	Asn	Gly	Asn	Leu	Ser	Tyr	Asp	Ala	Thr	Ser		
				450					455							460	
aca	tta	aca	tta	cct	ggg	cat	cag	tta	cct	tta	cca	aaa	tig	ggc	gtt		
Thr	Leu	Thr	Leu	Pro	Gly	His	Gln	Leu	Pro	Leu	Pro	Lys	Leu	Gly	Val		
				465					470					475			480
tcc	gcc	atc	aag	ctt	aaa	tcc	tta	atg	aat	tca	acc	aag	gaa	tgc	att		
Ser	Ala	Ile	Lys	Leu	Lys	Ser	Leu	Met	Asn	Ser	Thr	Lys	Glu	Ser	Ile		
				485					490					495			
tcc	tta	cna	gtt	gct	agt	gaa	tgt	aal	acc	atc	glc	tta	tgt	gac	tct		
Ser	Leu	Pro	Val	Ala	Arg	Glu	Cys	Asn	Thr	Ile	Val	Leu	Cys	Asp	Ser		
				500					505					510			
agt	gta	agt	aca	acg	gac	aga	ccc	aaa	tta	tig	aga	tta	act	ggc	ggc		
Ser	Val	Ser	Thr	Thr	Asp	Arg	Pro	Glu	Leu	Leu	Arg	Leu	Thr	Gly	Gly		
				515					520					525			
tcu	aag	acc	tgt	caa	cgc	agg	att	cac	tct	cag	cac	gaa	tta	aat			
Ser	Lys	Thr	Cys	Gln	Pro	Ser	Trp	Ile	His	Ser	Gln	His	Gln	Leu	Asn		
				530					535					540			
cca	caa	gat	tca	att	gtt	caa	ggg	atc	ttt	caa	tta	gct	act	tig	gca		
Pro	Gln	Asp	Ser	Ile	Val	Gln	Gly	Ile	Phe	Gln	Leu	Ala	Thr	Leu	Ala		
				545					550					555			560
aag	gat	aag	agg	tto	ggc	cta	tta	tta	aag	gan	acg	cag	ccc	atg	aag		
Lys	Asp	Lys	Arg	Phe	Gly	Leu	Leu	Leu	Lys	Gln	Thr	Gln	Pro	Met	Lys		
				565					570					575			
cag	aag	agt	gtt	gag	aca	tca	aat	ggc	gga	gtt	gaa	gaa	acc	atg	aaa		
Gln	Lys	Ser	Val	Glu	Thr	Ser	Asn	Gly	Gly	Val	Gln	Gln	Thr	Met	Lys		
				580					585					590			
atg	tgg																
Met																	
															1392		
															1440		
															1488		
															1536		
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															1776		
															1782		

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<211> 593

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 18

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20 25 30

Gln Ile Ala Gln Thr Ala Leu Lys Tyr Val Thr Ser Leu Ile Asn Asp
35 40 45

Ser Tyr His Ser Lys Thr Thr Gln Arg Gln Leu Thr Val Pro Glu Leu
50 55 60

Cys Leu Leu Lir Asp Ser Phe Ile Leu Thr Arg Leu Gln Gln Tyr Tyr
65 70 75 80

Lys Asn Lys Val Asn Glu Arg Gly Ile Ala Ile Pro Thr Thr Ile Asp
85 90 95

Ile Asp Gln Ile Ser Gly Gly Trp Cys Pro Gln Ile Asp Asp Thr Gln
100 105 110

Asn Leu Leu Asn Trp Asn Lys Gly Lys Asp Ser Thr Phe Ala Ser Ser
115 120 125

Val Thr Gly Thr Leu Arg Pro Gly Asp Leu Val Lys Ile Thr Leu Gly
130 135 140

Val His Ile Asp Gly Tyr Thr Ser Glu Val Ser His Thr Met Val Ile
145 150 155 160

Tyr Pro Val Asp Glu Thr Lys Pro Ile Leu Gln Pro Thr Gly Pro Leu
165 170 175

Leu Gly Gly Lys Ala Asp Ala Val Ala Ala Ala His Ile Ala Met Gly
180 185 190

Thr Val Val Ala Leu Leu Ala Cys Ala Leu Thr Pro Glu Lys Leu Pro
195 200 205

Ala Ser Leu Gly Gly Thr Ser Ser Gly Ile Thr Gly Gln Leu Ile Arg
210 215 220

Thr Ile Val Asp Thr Ile Ala Arg Ser Tyr Asn Cys Gly Val Val Pro
225 230 235 240

Gly Ser Arg Val Arg Arg Ile Arg Arg Phe Leu Ala Gly Gln Asn Glu
245 250 255

Gly Ile Val Ala Glu Arg Glu Tyr Lys Gly Val Val Trp Thr Glu Ser
260 265 270

His Gln Glu Ala Asp Leu Leu Ser Asn Thr Asp Ala Lys Asp Leu Thr
275 280 285

Val Val Asp Arg Gly Gln Ser Thr Pro Phe Thr Asn Val Ser Ala Ile
290 295 300

Pro Ser Asp Asp Phe Val Val Gln Ser Gly Glu Val Tyr Leu Ile Asp
325 310 315 320

Leu Lys Met Ala Ser Leu Glu His Cys Thr Lys Lys Gly Leu Val Thr
325 330 335

Leu Glu Thr Val Asp Ser Tyr Thr Gly Lys Ser His Lys Ala Gly Glu
340 345 350

Leu Ile Ala Arg Pro Gly Ala Tyr Val Arg Asp Phe Ala Glu Thr His
355 360 365

Ile Leu Lys Leu Lys Thr Ser Arg Glu Leu Leu Thr Lys Ile Asp Lys
370 375 380

Gln Gly Val Tyr Pro Phe Lys Leu Ser His Met Ser Ser Asn Phe Pro
385 390 395 400

Phe Val His Glu Asn Glu Glu Glu Leu Gln Ser Leu Lys Lys Asp Leu
405 410 415

Lys Ser Phe Arg Leu Gly Met Ser Glu Ile Ser Asn Asn Tyr Leu Cys
420 425 430

Val Gln Ser Pro Ile Gln Ile Ala Arg Trp Val Pro Trp Asp His Ile
435 440 445

Leu Lys Ala Thr Asn Pro Asn Gly Asn Leu Ser Tyr Asp Ala Thr Ser
450 455 460

Thr Leu Thr Leu Pro Gly His Glu Leu Pro Leu Pro Lys Leu Gly Val
 465 470 475 480

Ser Ala Ile Lys Leu Lys Ser Leu Met Asn Ser Thr Lys Glu Ser Ile
 485 490 495

Ser Leu Pro Val Ala Arg Glu Cys Asn Thr Ile Val Leu Cys Asp Ser
 500 505 510

Ser Val Ser Thr Thr Asp Arg Pro Glu Leu Ser Arg Leu Thr Gly Gly
 515 520 525

Ser Lys Thr Cys Gln Pro Ser Trp Ile His Ser Gln His Glu Leu Asn
 530 535 540

Pro Gln Asp Ser Ile Val Gln Gly Ile Phe Gln Leu Ala Thr Leu Ala
 545 550 555 560

Lys Asp Lys Arg Phe Gly Leu Leu Leu Lys Glu Thr Gln Pro Met Lys
 565 570 575

Gln Lys Ser Val Glu Thr Ser Asn Gly Gly Val Glu Glu Thr Met Lys
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Met

<210> 19

<211> 2097

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> cds

<222> (1) .. (2097)

<400> 15

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Met	Val	Phe	Ser	Tyr	Glu	His	Tyr	Met	Asn	Leu	Leu	Phe	His	Leu	Asp	
1			5					10					15			

aac	agt	aaa	gaa	acg	gtg	cct	cca	gag	att	gca	aaa	aga	ata	att	tca	96
Asn	Ser	Lys	Glu	Thr	Val	Pro	Pro	Glu	Ile	Ala	Lys	Arg	Ile	Ile	Ser	
			20					25					30			

cat	gct	ata	gct	cct	gta	ata	aca	gtt	act	tca	act	cct	ctc	ttc	gac	144
Asn	Ala	Ile	Ala	Pro	Val	Ile	Thr	Val	Thr	Ser	Thr	Pro	Leu	Phe	Asp	
			35					40					45			

aaa	cat	att	caa	gaa	acg	tac	aaa	gta	gat	tct	ctc	tat	atg	ctg	ctg	192
Lys	His	Ile	Glu	Glu	Thr	Tyr	Lys	Val	Asp	Ser	Asn	Tyr	Met	Leu	Leu	
			50					55					60			

cga	ttc	tta	ggc	ggt	tgt	gtc	tct	gct	aga	gat	caa	guc	aat	gaa	gcg	240
Arg	Phe	Phe	Gly	Gly	Cys	Val	Ser	Asp	Arg	Asp	Gln	Ala	Asn	Glu	Ala	
65					70					75				80		

aag	gtt	gga	cag	cct	gag	cct	gag	gtt	tgt	gat	gca	agt	gac	tgg	acg	288
Lys	Val	Gly	Gln	His	Gln	His	Gln	Val	Cys	Asp	Ala	Ser	Asp	Ser	Thr	
					85					90				95		

gat	tca	att	ccc	aaa	aat	aaa	aat	ttg	gaa	gig	ccc	aat	tta	tca	aag	336
Asp	Ser	Ile	Pro	Lys	Asn	Lys	Asn	Leu	Glu	Val	Pro	Asn	Leu	Ser	Lys	
					100					105				110		

aaa	ggt	agt	cgc	agt	agg	tgg	aat	agt	ctt	ttc	cag	agg	gat	tca	aag	384
Lys	Gly	Ser	Arg	Ser	Arg	Ser	Asn	Ser	Leu	Phe	Gln	Arg	Asp	Ser	Thr	
			115						120					125		

caa	tct	caa	tat	atc	agg	ttt	cca	agg	cca	tta	ggt	gac	ttg	atc	gaa	432
Gln	Ser	Gln	Tyr	Ile	Arg	Phe	Thr	Arg	Pro	Leu	Gly	Asp	Leu	Ile	Glu	
			130					135						140		

aca aga gat gca aat gat atg tta ttc aat tac cat tct tta gag gta	480
Thr Arg Asp Ala Asn Asp Met Leu Phe Asn Tyr His Ser Leu Glu Val	
145 150 155 160	
ttc tta gat aat tat ttg aac ttg gtt gca gca aat act gat gaa atg	528
Phe Leu Asp Asn Tyr Leu Lys Leu Val Ala Ala Asn Thr Asp Glu Met	
165 170 175	
gtt cct cat aat ctt ctt aag aac tcc att tat cat agt ttc ttt tca	576
Val Pro His Asn Leu Leu Lys Lys Ser Ile Tyr His Ser Phe Phe Ser	
180 185 190	
cta gca att tca tcc aca aat aac tta tgg acc tat gaa act ttt aat	624
Leu Ala Ile Ser Ser Thr Asn Asn Leu Ser Pro Tyr Glu Thr Phe Asn	
195 200 205	
cac cct att ctt tcc tgg att gct tca gat ata tca aat ggc gaa gtt	672
His Pro Ile Leu Ser Leu Ile Ala Leu Asp Ile Ser Asn Gly Glu val	
210 215 220	
tat gag gat gca aga gat ctt tta gtc aat ttc aag aat ctt aat cat	720
Tyr Glu Asp Ala Arg Asp Leu Leu Val Asn Phe Lys Asn Leu Asn His	
225 230 235 240	
aat act gaa aac ttt cct atc ttc atg aat aca aat gaa atg ctt cca	768
Asn Thr Glu Asn Phe Pro Ile Phe Met Asn Thr Asn Glu Met Leu Pro	
245 250 255	
gtt ttc tta ctc tcc tac aat cac gat tcc caa gaa gaa ttc gaa aac	816
Val Phe Leu Leu Cys Tyr Asn Asp Asp Ser Gln Glu Glu Phe Glu Lys	
260 265 270	
tgc cag gcg tta gct aag aac cta aag aag cag ttg ttt gtt gag agt	864
Cys Gln Ala Leu Ala Lys Lys Leu Lys Lys Gln Leu Phe Val Glu Ser	
275 280 285	
atc tta cta gca ctc tgg aag gat tct ttt att tac gac gaa aat tca	912
Ile Leu Leu Ala Leu Trp Lys Asp Ser Phe Ile Tyr Asp Glu Asn Ser	
290 295 300	
gtc ata cag tta cac caa cca gta atg tca tgg ctt gaa gaa att ctc	960
Val Ile Gln Leu His Gln Pro Val Met Ser Ser Leu Glu Glu Ile Leu	

305	310	315	320	
ttc ttc ctt caa gct cca act caa aca aaa ctc tct atg gat ttg ata				1003
Phe Phe Leu Gln Ala Pro Thr Gln Thr Thr Leu Ser Leu Ala Leu Ile				
	325	330	335	
aac tcc atc tat gat atg cct gat tat ttg gtt tat gat tta atg ata				1053
Asn Ser Ile Tyr Asp Met Leu Asp Tyr Leu Val Tyr Asp Leu Met Ile				
	340	345	350	
cca ttc atg aaa aga aaa gtg tca ttc tgg gaa gag aca att tta cag				1104
Pro Phe Met Lys Arg Lys Val Ser Phe Trp Gln Glu Thr Ile Leu Gln				
	355	360	365	
cca aga aag tcc cta ttt aat ggt gca aag ttt ttc aaa aca ttt atg				1152
Pro Arg Lys Ser Leu Phe Asn Gly Ala Lys Phe Phe Lys Lys Phe Met				
	370	375	380	
aat aaa aat cct gtc aat ggt aat cac caa cat aat tct cta aag aga				1203
Asn Lys Asn Pro Val Asn Gly Asn His Gln His Asn Ser Leu Thr Arg				
	385	390	395	400
gac agc cag gga aat gaa taa tta gca tcc tca tct tct gag ttt ttg				1248
Asp Ser Gln Gly Asn Glu Tyr Phe Ala Ser Ser Ser Ser Glu Phe Ile				
	405	410	415	
atg aga aag tta gca gat tgg tct atg atg cta tcc gac ttc aaa act				1296
Met Arg Lys Leu Ala Asp Trp Ser Met Met Leu Ser Asp Phe Lys Thr				
	420	425	430	
gct tat tcc aca taa gaa tcc ctt atg gat gac cta gat gca ttt cca				1344
Ala Tyr Ser Thr Tyr Glu Ser Leu Met Asp Asp Leu Asp Ala Phe Pro				
	435	440	445	
aag taa cly gca tca tgc atc gaa tgg tgc gcg gta tca cta ttg atg				1392
Lys Tyr Leu Ala Ser Cys Ile Glu Trp Cys Ala Val Ser Leu Leu Met				
	450	455	460	
ggt gcg cag agc ata gtc acc gtg aaa atg atc aaa aac gat ata aat				1440
Gly Ala Gln Ser Ile Val Thr Val Lys Met Ile Lys Asn Asp Ile Asn				
	465	470	475	480

cct ctt atc gaa agg gca tta gcc aca tac gaa aac tgc tca cga ata	1488
Pro Leu Ile Glu Arg Ala Leu Ala Thr Tyr Glu Asn Cys Ser Arg Ile	
485 490 495	
caa cgt ggt aaa ggc aaa gaa tca aac tct ttg gat gtt aca gag cca	1526
Gln Arg Gly Lys Gly Lys Glu Ser Asn Ser Leu Asp Val Thr Glu Pro	
500 505 510	
gtg cgt tgg tat gag aca cgt tgt atg att ttg gca tct gaa ttg ttt	1584
Val Arg Ser Tyr Glu Thr Arg Cys Met Ile Leu Ala Ser Gln Leu Phe	
515 520 525	
tta tct tta agc aat aag tgg aca tct aca cca tac ggt atc caa tat	1632
Leu Ser Leu Ser Asn Thr Trp Thr Ser Thr Pro Tyr Ala Ile Gln Tyr	
530 535 540	
lta gaa aca att cta gac gag tgc aag ttg gga cct tgt tca cag ata	1680
Leu Glu Thr Ile Leu Asp Glu Cys Lys Leu Gly Pro Cys Ser Gln Ile	
545 550 555 560	
atg gtt tgg gaa agg ctt agt gac tgc tat aat ttg aga gtt gac cct	1728
Met Val Trp Glu Arg Leu Ser Asp Cys Tyr Asn Leu Arg Val Asp Pro	
565 570 575	
aga atc aaa cat aga gtt ggc gca atg cag cag gac gct aac gac aac	1776
Arg Ile Lys His Arg Val Gly Ala Met Lys Lys Asp Ala Lys Asp Thr	
580 585 590	
gaa gat ctc cga ggt gag cat aag tat agc aca gat cat ttc aca gac	1824
Glu Asp Leu Arg Gly Glu His Lys Tyr Ser Thr Asn His Phe Thr Asp	
595 600 605	
gag gac ata tta tgg gaa ggg tta aca aga aga cgc aag gca gct ttt	1872
Glu Asp Ile Leu Ser Glu Gly Leu Thr Arg Arg Arg Lys Ala Ala Phe	
610 615 620	
ttt agg tta ata gca gct aag aag tgg gca gag caa aaa caa tgg aga	1920
Phe Arg Leu Ile Ala Ala Lys Lys Trp Ala Glu Gln Lys Glu Trp Arg	
625 630 635 640	

cag gtt tct tgg tgc tta aaa gat att gaa agt acc tat tca gag atc 1968
 Gln Val Ser Trp Cys Leu Lys Asp Ile Glu Ser Thr Tyr Ser Glu Ile
 645 650 655

aaa ttt ttg cat ggt aac ggt tta att tta agc aaa cta aaa aat cca 2016
 Lys Phe Leu His Gly Asn Gly Leu Ile Leu Ser Lys Leu Lys Asn Glu
 660 665 670

ctc aat tta aag gac ggc gat tct gca cca cgg ccc tcc gaa aag aat 2064
 Leu Asn Leu Lys Asp Val Asp Ser Ala Pro Arg Pro Ser Glu Lys Asn
 675 680 685

ctt acc aga aca agt gtt agc ttt att gca lga 2097
 Leu Thr Arg Thr Ser Val Ser Phe Ile Gly
 690 695

<210> 20

<211> 698

<212> PRT

<213> Saccharomyces cerevisiae

<400> 20

Met Val Phe Ser Tyr Glu His Tyr Met Asn Leu Leu Phe His Leu Asp
 1 5 10 15

Asn Ser Lys Glu Thr Val Pro Pro Glu Ile Ala Lys Arg Ile Ile Ser
 20 25 30

Asn Ala Ile Ala Pro Val Ile Thr Val Thr Ser Thr Pro Leu Phe Asp
 35 40 45

Lys His Ile Gln Glu Thr Tyr Lys Val Asp Ser Leu Tyr Met Leu Leu
 50 55 60

Arg Phe Phe Gly Gly Cys Val Ser Asp Arg Asp Gln Ala Asn Glu Ala

65		70		75		80
Lys Val Gly Gln His Glu His Glu Val Cys Asp Ala Ser Asp Ser Thr						
	85		90		95	
Asp Ser Ile Pro Lys Asn Lys Asn Leu Glu Val Pro Asn Leu Ser Lys						
	100		105		110	
Lys Gly Ser Arg Ser Arg Ser Asn Ser Leu Phe Gln Arg Asp Ser Thr						
	115		120		125	
Gln Ser Gln Tyr Ile Arg Phe Thr Arg Pro Leu Gly Asp Leu Ile Glu						
	130		135		140	
Thr Arg Asp Ala Asn Asp Met Leu Phe Asn Tyr His Ser Leu Glu Val						
145		150		155		160
Phe Leu Asp Asn Tyr Leu Lys Leu Val Ala Ala Asn Thr Asp Glu Met						
	165		170		175	
Val Pro His Asn Leu Leu Lys Lys Ser Ile Tyr His Ser Phe Phe Ser						
	180		185		190	
Leu Ala Ile Ser Ser Thr Asn Asn Leu Ser Pro Tyr Glu Thr Phe Asn						
	195		200		205	
His Pro Ile Leu Ser Leu Ile Ala Leu Asp Ile Ser Asn Gly Glu Val						
	210		215		220	
Tyr Glu Asp Ala Arg Asp Leu Leu Val Asn Phe Lys Asn Leu Asn His						
225		230		235		240

Asn Thr Glu Asn Phe Pro Ile Phe Met Asn Thr Asn Glu Met Leu Pro
245 250 255

Val Phe Leu Leu Cys Tyr Asn Asp Asp Ser Gln Glu Glu Phe Glu Lys
260 265 270

Cys Gln Ala Leu Ala Lys Lys Leu Lys Lys Ser Leu Phe Val Glu Ser
275 280 285

Ile Leu Leu Ala Leu Trp Lys Asp Ser Phe Ile Tyr Asp Glu Asn Ser
290 295 300

Val Ile Gln Leu His Gln Pro Val Met Ser Ser Leu Glu Glu Ile Leu
305 310 315 320

Phe Phe Leu Gln Ala Pro Thr Gln Thr Thr Leu Ser Leu Ala Leu Ile
325 330 335

Asn Ser Ile Tyr Asp Met Leu Asp Tyr Leu Val Tyr Asp Leu Met Ile
340 345 350

Pro Phe Met Lys Arg Lys Val Ser Phe Trp Gln Glu Thr Phe Leu Gln
355 360 365

Pro Arg Lys Ser Leu Phe Asn Gly Ala Lys Phe Phe Lys Lys Phe Met
370 375 380

Asn Lys Asn Pro Val Asn Gly Asn His Gln His Asn Ser Leu Thr Arg
385 390 395 400

Asp Ser Gln Gly Asn Glu Tyr Phe Ala Ser Ser Ser Ser Glu Phe Leu

605 410 415

Met Arg Lys Leu Ala Asp Thr Ser Met Met Leu Ser Asp Phe Tyr Thr
420 425 430

Ala Tyr Ser Thr Tyr Glu Ser Leu Met Asp Asp Leu Asp Ala Phe Pro
435 440 445

Lys Tyr Leu Ala Ser Cys Ile Glu Trp Cys Ala Val Ser Leu Leu Met
450 455 460

Gly Ala Gln Ser Ile Val Thr Val Tyr Met Ile Lys Asn Asp Ile Asn
465 470 475 480

Pro Leu Ile Glu Arg Ala Leu Ala Thr Tyr Glu Asn Cys Ser Arg Ile
485 490 495

Gln Arg Gly Lys Gly Lys Glu Ser Asn Ser Leu Asp Val Thr Glu Pro
500 505 510

Val Arg Ser Tyr Glu Thr Arg Cys Met Ile Ser Ala Ser Glu Leu Phe
515 520 525

Leu Ser Leu Ser Asn Thr Trp Thr Ser Thr Pro Tyr Ala Ile Gln Tyr
530 535 540

Leu Glu Thr Ile Leu Asp Glu Cys Tyr Leu Gly Pro Cys Ser Glu Ile
545 550 555 560

Met Val Trp Glu Arg Leu Ser Asp Cys Tyr Asn Leu Arg Val Asp Pro
565 570 575

Arg Ile Lys His Arg Val Gly Ala Met Lys Lys Asp Ala Lys Asp Thr
580 585 590

Glu Asp Leu Arg Gly Gln His Lys Tyr Ser Thr Asp His Phe Thr Asp
595 600 605

Gln Asp Ile Leu Ser Glu Gly Leu Thr Arg Arg Arg Lys Ala Ala Phe
610 615 620

Phe Arg Leu Ile Ala Ala Lys Lys Trp Ala Glu Gln Lys Gln Trp Arg
625 630 635 640

Gln Val Ser Trp Cys Leu Lys Asp Ile Glu Ser Thr Tyr Ser Glu Ile
645 650 655

Lys Phe Leu His Gly Asn Gly Leu Ile Leu Ser Lys Ser Lys Asn Gln
660 665 670

Leu Asn Leu Lys Asp Val Asp Ser Ala Pro Arg Pro Ser Glu Lys Asn
675 680 685

Leu Thr Arg Thr Ser Val Ser Phe Ile Gly
690 695

<210> 21

<211> 327

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(327)

<400> 21

atg cga tat act gca act ttt cgg cct ttg caa cga ttt gta atg aat 18
Met Arg Tyr Thr Ala Thr Phe Arg Pro Leu Gln Arg Phe Val Met Asn
1 5 10 15

cct ttt gca tgg cta gaa gga caa gat aat att tct tct gtt ttt ttc 36
Pro Phe Ala Ser Leu Glu Gly Gln Asp Asn Ile Ser Ser Val Phe Phe
20 25 30

tta cat atg caa caa ttt gaa agt cag gtc aaa gac aga ttc cgg ttc 144
Leu His Met Gln Gln Phe Glu Ser Gln Val Lys Asp Arg Phe Arg Phe
35 40 45

ccc ata ttc aga ttg gag aga aaa act ttt ggc aac tca tgt tac caa 192
Pro Ile Phe Arg Leu Glu Arg Lys Thr Phe Gly Asn Ser Cys Tyr Gln
50 55 60

gtc gag acg ctt aaa gtt aag tgt cgg cca aaa cac gca aaa tct tgc 240
Val Glu Thr Leu Lys Val Lys Cys Arg Pro Arg His Ala Lys Ser Cys
65 70 75 80

zat ctt tta acg ctg ctc ttc aaa tca cgg acg caa tca gta ctt gca 288
Asn Leu Leu Thr Leu Leu Phe Lys Ser Arg Thr Gln Ser Val Leu Val
85 90 95

cct aat ttt ggt ttt cta ata ttg aat agc gaa cca tag 327
Pro Asn Phe Gly Phe Leu Ile Leu Asn Ser Glu Pro
100 105

<210> 22

<211> 108

<212> PRT

<213> Saccharomyces cerevisiae

<400> 22

Met Arg Tyr Thr Ala Thr Phe Arg Pro Leu Gln Arg Phe Val Met Asn
1 5 10 15

Pro Phe Ala Ser Leu Glu Gly Gln Asp Asn Ile Ser Ser Val Phe Phe
 20 25 30

Leu His Met Gln Gln Phe Glu Ser Gln Val Lys Asp Arg Phe Arg Phe
 35 40 45

Pro Ile Phe Arg Leu Glu Arg Lys Thr Phe Gly Asn Ser Cys Tyr Gln
 50 55 60

Val Glu Thr Leu Lys Val Lys Cys Arg Pro Arg His Ala Lys Ser Cys
 65 70 75 80

Asn Leu Leu Thr Leu Leu Phe Lys Ser Arg Thr Gln Ser Val Leu Val
 85 90 95

Pro Asn Phe Gly Phe Leu Ile Leu Asn Ser Glu Pro
 100 105

<210> 23
 <211> 411
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(411)

<400> 23
 atg caa ttc tct acc gtc gct tct acc gct gct att gcc gct gtt gcc 48
 Met Gln Phe Ser Thr Val Ala Ser Ile Ala Ala Ile Ala Ala Val Ala
 1 5 10 15
 tcc gcc gct tct aac att acc act gct act gtc aca gaa gaa tct acc 96
 Ser Ala Ala Ser Asn Ile Thr Thr Ala Thr Val Thr Glu Glu Ser Thr

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[illegible]

63/762

Ser Ala Ala Ser Asn Ile Thr Thr Ala Thr Val Thr Glu Gln Ser Thr
 20 25 30

Thr Leu Val Thr Ile Thr Ser Cys Glu Asp His Val Cys Ser Glu Thr
 35 40 45

Val Ser Pro Ala Leu Val Ser Thr Ala Thr Val Thr Val Asn Asp Val
 50 55 60

Gln Thr
 65

<210> 25
 <211> 69
 <212> FRT
 <213> *Saccharomyces cerevisiae*

<400> 25

Tyr Thr Thr Trp Cys Pro Leu Pro Thr Thr Glu Ala Pro Lys Asn Thr
 1 5 10 15

Thr Ser Pro Ala Pro Thr Glu Lys Pro Thr Gln Lys Pro Thr Glu Lys
 20 25 30

Pro Thr Gln Gln Gly Ser Ser Thr Gln Thr Val Thr Ser Tyr Thr Gly
 35 40 45

Ala Ala Val Lys Ala Leu Pro Ala Ala Gly Ala Leu Leu Ala Gly Ala
 50 55 60

Ala Ala Leu Leu Leu
 65

<210> 26
 <211> 693
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (693)

<400> 26
 atg qaa atg act gat ttt gaa cta act agt aat tog caa tog aac ttg 48
 Met Glu Met Thr Asp Phe Glu Leu Thr Ser Asn Ser Gln Ser Asn Leu
 1 5 10 15
 gct atc cct acc aac ttc aag tog act ctg cct cca agg aaa aga gcc 96
 Ala Ile Pro Thr Asn Phe Lys Ser Thr Leu Pro Pro Arg Lys Arg Ala
 20 25 30
 aag acc aaa gag gaa aag gaa cag cga agg atc gag cgt att ttg aga 144
 Lys Thr Lys Glu Glu Lys Glu Gln Arg Arg Ile Glu Arg Ile Leu Arg
 35 40 45
 aac aga aga gct gct ccc cag agc aga gag aaa aaa aga cta cat ctg 192
 Asn Arg Arg Ala Ala His Gln Ser Arg Glu Lys Lys Arg Leu His Leu
 50 55 60
 caq tat ctc gag aga aaa tgt tct ctt ctg gaa aat tta ctg aac agc 240
 Gln Tyr Leu Glu Arg Lys Cys Ser Leu Leu Glu Asn Leu Leu Asn Ser
 65 70 75 80
 gtc aac ctt gaa aaa ctg got gac cac gaa gac gag ttg act tgc agc 288
 Val Asn Leu Glu Lys Leu Ala Asp His Glu Asp Ala Leu Thr Cys Ser
 85 90 95
 caa gaa got ttt gtc got tct ctt gac gag tac agg gat ttc cag agc 336
 His Asp Ala Phe Val Ala Ser Leu Asp Glu Tyr Arg Asp Phe Gln Ser
 100 105 110
 aag agg ggu got tca ctg gac acc agg gcc agt tog caa tog tog tct 384
 Thr Arg Gly Ala Ser Leu Asp Thr Arg Ala Ser Ser His Ser Ser Ser

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115	120	125	
gat aag ttc aca cct tca cct ctg aac tgt aca atg gag cct gog act 432			
Asp Thr Phe Thr Pro Ser Pro Leu Asn Cys Thr Met Glu Pro Ala Thr			
130	135	140	
ttg tgg ccc aag agc atg cgc gat tcc gog tgg gac caa gag act tca 480			
Leu Ser Pro Lys Ser Met Arg Asp Ser Ala Ser Asp Gln Glu Thr Ser			
145	150	155	160
tgg gag cgg cag atg ttt aag acg gaa aat gla cca gag tgg acg acg 520			
Trp Glu Leu Gln Met Phe Lys Thr Glu Asn Val Pro Gln Ser Thr Thr			
	165	170	175
cta cct gcc gta gac aac aac aat ttg ttt gat gcg gtg gcc tgg cgg 576			
Leu Pro Ala Val Asp Asn Asn Asn Leu Phe Asp Ala Val Ala Ser Pro			
	180	185	190
ttg gca gcc cca ctg tgc gac gat ata gcg gga aac agt cta ccc ttt 624			
Leu Ala Asp Pro Leu Cys Asp Asp Ile Ala Gly Asn Ser Leu Pro Phe			
	195	200	205
gac aat tca att gat ctt gac aat tgg cgt aat cca gcc gtg att acg 672			
Asp Asn Ser Ile Asp Leu Asp Asn Trp Arg Asn Pro Ala Val Ile Thr			
	210	215	220
atg acc agg aaa cta cag tga 693			
Met Thr Arg Lys Leu Gln			
225	230		

<210> 27

<211> 230

<212> PRT

<213> Saccharomyces cerevisiae

<400> 27

Met Glu Met Thr Asp Phe Glu Leu Thr Ser Asn Ser Glu Ser Asn Leu

1

5

10

15

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Ala Ile Pro Thr Asn Phe Lys Ser Thr Leu Pro Pro Arg Lys Arg Ala
20 25 30

Lys Thr Lys Glu Glu Lys Glu Glu Arg Arg Ile Glu Arg Ile Leu Arg
35 40 45

Asn Arg Arg Ala Ala His Glu Ser Arg Glu Lys Lys Arg Leu His Leu
50 55 60

Glu Tyr Leu Glu Arg Lys Cys Ser Leu Leu Glu Asn Leu Leu Asn Ser
65 70 75 80

Val Asn Leu Glu Lys Leu Ala Asp His Glu Asp Ala Leu Thr Cys Ser
85 90 95

His Asp Ala Phe Val Ala Ser Leu Asp Glu Tyr Arg Asp Phe Glu Ser
100 105 110

Thr Arg Gly Ala Ser Leu Asp Thr Arg Ala Ser Ser His Ser Ser Ser
115 120 125

Asp Thr Phe Thr Pro Ser Pro Leu Asn Cys Thr Met Glu Pro Ala Thr
130 135 140

Leu Ser Pro Lys Ser Met Arg Asp Ser Ala Ser Asp Gln Glu Thr Ser
145 150 155 160

Trp Glu Leu Gln Met Phe Lys Thr Glu Asn Val Pro Glu Ser Thr Thr
165 170 175

Leu Pro Ala Val Asp Asn Asn Asn Leu Phe Asp Ala Val Ala Ser Pro
180 185 190

Leu Ala Asp Pro Leu Cys Asp Asp Ile Ala Gly Asn Ser Leu Pro Phe
 195 200 205

Asp Asn Ser Ile Asp Leu Asp Asn Trp Arg Asn Pro Ala Val Ile Thr
 210 215 220

Met Thr Arg Tyr Leu Gln
 225 230

<213> 28
 <211> 1398
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1398)

<400> 28
 atg gcc cgc aat aga caa gag tgc gac tgt tgt tgc att cgt cga gta 48
 Met Ala Arg Asn Arg Gln Ala Cys Asp Cys Cys Cys Ile Arg Arg Val
 1 5 10 15

aag tgt gat cgt aaa aaa cca tgt aaa tgt tgt ctt caa cac aat ctg 96
 Lys Cys Asp Arg Lys Lys Pro Cys Lys Cys Cys Leu Gln His Asn Leu
 20 25 30

caa tgt aca tat ctt cga cct ttg aag aaa aga ggt cca aaa ccc gtc 144
 Cln Cys Thr Tyr Leu Arg Pro Leu Lys Lys Arg Gly Pro Lys Pro Val
 35 40 45

aag gag aga aat tta aag aaa gta gat gat gta cag gta ttt agt aaa 192
 Lys Val Arg Asn Leu Lys Lys Val Asp Asp Val Gln Val Phe Ser Lys
 50 55 60

agt agt agt ggt ggc ata atg aag gtt cca aag gca cta att gat cag 240

Ser	Ser	Ser	Gly	Gly	Ile	Met	Lys	Val	Pro	Lys	Ala	Leu	Ile	Asp	Gln		
65					70				75					80			
tgt	ctg	egg	ctc	tai	aal	gal	aag	ttg	tat	gtg	alc	tgg	cct	ttg	ctg	288	
Cys	Leu	Arg	Leu	Tyr	Asn	Asp	Lys	Leu	Tyr	Val	Ile	Trp	Pro	Leu	Leu		
			85					90					95				
tgt	tat	gat	gat	ctt	tac	gaa	ctt	tta	gag	aaa	aga	tat	gac	gaa	acc	336	
Cys	Tyr	Asp	Asp	Leu	Tyr	Glu	Leu	Leu	Glu	Lys	Arg	Tyr	Asp	Glu	Tar		
			100					105					110				
tgt	ggg	tat	tgg	ttc	ctg	gta	tct	ctt	tct	gcc	gcc	acg	ctt	agc	gat	384	
Cys	Val	Tyr	Trp	Phe	Leu	Val	Ser	Leu	Ser	Ala	Ala	Thr	Leu	Ser	Asp		
			115				120						125				
ttg	cag	act	gaa	att	gag	tcc	gaa	gga	ggg	gtt	acc	ttt	act	ggg	ata	432	
Leu	Gln	Thr	Glu	Ile	Glu	Ser	Glu	Gly	Gly	Val	Thr	Phe	Thr	Gly	Ile		
			130			135					140						
cag	tta	tcc	agt	ttc	tgc	atg	tca	tca	cgc	caa	gaa	ttt	gac	gat	ttc	480	
Gln	Leu	Ser	Ser	Phe	Cys	Met	Ser	Ser	Arg	Gln	Glu	Phe	Asp	Asp	Phe		
145				150					155				160				
aac	ggt	agt	gat	ata	ttc	aag	att	atg	acg	tac	tat	tgt	cca	aac	cgc	528	
Asn	Gly	Ser	Asp	Ile	Phe	Lys	Ile	Met	Thr	Tyr	Tyr	Cys	Leu	Asn	Arg		
				165				170					175				
tgc	tac	gca	cag	atg	ccc	aac	tca	aga	act	tgg	tat	cgg	ctt	tct	tgt	576	
Cys	Tyr	Ala	Gln	Met	Ser	Asn	Ser	Arg	Thr	Ser	Tyr	Arg	Leu	Ser	Cys		
			180					185					190				
gaa	gac	gtg	ggg	ctc	att	aag	ttg	ggg	ggg	tcc	cac	cgc	gag	gaa	act	624	
Glu	Ala	Val	Gly	Leu	Ile	Lys	Leu	Ala	Gly	Phe	His	Arg	Glu	Glu	Thr		
			195				200					205					
ttg	aaa	ctt	ctt	cct	ttc	gat	gag	cag	cag	ctt	gga	agg	aaa	gtt	tat	672	
Leu	Lys	Leu	Leu	Pro	Phe	Asp	Glu	Gln	Gln	Leu	Gly	Arg	Lys	Val	Tyr		
			210			215					220						
tat	ttg	ctt	ctc	tta	acg	gaa	aga	tac	ttt	tct	gtg	tat	acg	cac	tcc	720	
Tyr	Leu	Leu	Leu	Leu	Thr	Glu	Arg	Tyr	Phe	Ser	Val	Tyr	Thr	His	Cys		
225				230						235				240			

gac aac agc ctg gat acc aac att gct cca cca caa cag gag aac gla	768
Ala Thr Ser Leu Asp Thr Thr Ile Ala Pro Pro Gln Pro Glu Asn Val	
245 250 255	
aac gac ccc cga cta tct ctc gac agc ttc ttg gag atg att agc gta	816
Thr Asp Pro Arg Leu Ser Leu Asp Ser Phe Leu Glu Met Ile Arg Val	
260 265 270	
ttt act gta cag gga aaa tgc ttc ttt gat gct cta gct acc gac tct	864
Phe Thr Val Pro Gly Lys Cys Phe Phe Asp Ala Leu Ala Thr Asp Ser	
275 280 285	
gct aat gta acc tgc act gaa gac tcc ctt aca aag ata tgg agc gaa	912
Ala Asn Val Thr Cys Thr Glu Asp Ser Leu Lys Lys Ile Trp Arg Glu	
290 295 300	
ctt cct aac gtc cca ctt gag ata gaa cca tgg tct tac ggc tct gta	960
Leu His Thr Val Pro Leu Glu Ile Glu Pro Trp Ser Tyr Gly Tyr Val	
305 310 315 320	
gac ata tct ctt tca cgg cct tgg att aga acc ctt gct tgg aag cta	1008
Asp Ile Ser Phe Ser Arg His Trp Ile Arg Thr Leu Ala Trp Lys Leu	
325 330 335	
gtg ctt caa aca agc ggc atg cga atc agt ttc ctt tca aat agc aag	1056
Val Leu Gln Ile Ser Gly Met Arg Ile Ser Phe Leu Ser Asn Ser Lys	
340 345 350	
aat aac cat att cca gta gaa att gct aga gac atg tta gaa gac aca	1104
Asn Thr His Ile Pro Val Glu Ile Ala Arg Asp Met Leu Glu Asp Thr	
355 360 365	
ttt tta atc cca aaa aat ctt tat gca gtt cac ggt cca gag ala tca	1152
Phe Leu Ile Pro Lys Asn Leu Tyr Ala Val His Gly Pro Gly Ile Ser	
370 375 380	
gtg aaa gca cta gaa ata gcc gac gca ttg gta gat gtt gtg aat cag	1200
Val Lys Ala Leu Glu Ile Ala Asp Ala Leu Val Asp Val Val Asn Gln	
385 390 395 400	
tac gat caa aat gca gag tgg gag gct tgg aat ttt ttg ttc gat ata	1248

Tyr Asp Gln Asn Ala Glu Ser Glu Ala Trp Asn Phe Leu Phe Asp Ile
 405 410 415

tcc aaa ttt gtc ttc tct ctt aag cat tgt gat agc aca tta gtt gat 1296
 Ser Lys Phe Val Phe Ser Leu Lys His Cys Asp Ser Thr Leu Val Asp
 420 425 430

aag ttt acg aca aag tgt cag tgt gag ctt atc acg ctt cct ctt tct 1344
 Lys Phe Thr Thr Lys Cys Gln Cys Ala Leu Ile Thr Asn Pro Leu Ser
 435 440 445

aat ccg ctt gaa tcg aca gat ggt cct aaa gaa gal gln gat gag ctt 1392
 Asn Pro Leu Glu Ser Thr Asp Gly Ser Lys Glu Asp Val Asp Ala Leu
 450 455 460

cct taa 1398
 Pro
 465

<210> 29

<211> 465

<212> PRT

<213> Saccharomyces cerevisiae

<400> 29

Met Ala Arg Asn Arg Glu Ala Cys Asp Cys Cys Cys Ile Arg Arg Val
 1 5 10 15

Lys Cys Asp Arg Lys Lys Pro Cys Lys Cys Cys Leu Gln His Asn Leu
 20 25 30

Gln Cys Thr Tyr Leu Arg Pro Leu Lys Lys Arg Gly Pro Lys Pro Val
 35 40 45

Lys Val Arg Asn Leu Lys Lys Val Asp Asp Val Gln Val Phe Ser Lys
 50 55 60

Ser Ser Ser Gly Gly Ile Met Lys Val Pro Lys Ala Leu Ile Asp Gln
65 70 75 80

Cys Leu Arg Leu Tyr Asn Asp Lys Leu Tyr Val Ile Trp Pro Leu Leu
85 90 95

Cys Tyr Asp Asp Leu Tyr Glu Leu Leu Glu Lys Arg Tyr Asp Glu Thr
100 105 110

Cys Val Tyr Trp Phe Leu Val Ser Leu Ser Ala Ala Thr Leu Ser Asp
115 120 125

Leu Gln Thr Glu Ile Glu Ser Glu Gly Gly Val Thr Phe Thr Gly Ile
130 135 140

Gln Leu Ser Ser Phe Cys Met Ser Ser Arg Gln Glu Phe Asp Asp Phe
145 150 155 160

Asn Gly Ser Asp Ile Thr Lys Ile Met Thr Tyr Tyr Cys Leu Asn Arg
165 170 175

Cys Tyr Ala Glu Met Ser Asn Ser Arg Thr Ser Tyr Arg Leu Ser Cys
180 185 190

Glu Ala Val Gly Leu Ile Lys Leu Ala Gly Phe His Arg Glu Glu Thr
195 200 205

Leu Lys Leu Leu Pro Phe Asp Glu Gln Gln Leu Gly Arg Lys Val Tyr
210 215 220

Tyr Leu Leu Leu Leu Thr Glu Arg Tyr Phe Ser Val Tyr Thr His Cys

225	230	235	240
Ala Thr Ser Leu Asp Thr Thr Ile Ala Pro Pro Gln Pro Glu Asn Val			
245	250	255	
Thr Asp Pro Arg Leu Ser Leu Asp Ser Phe Leu Glu Met Ile Arg Val			
260	265	270	
Phe Thr Val Pro Gly Lys Cys Phe Phe Asp Ala Leu Ala Thr Asp Ser			
275	280	285	
Ala Asn Val Thr Cys Thr Glu Asp Ser Leu Lys Lys Ile Trp Arg Glu			
290	295	300	
Leu His Thr Val Pro Leu Glu Ile Glu Pro Trp Ser Tyr Gly Tyr Val			
305	310	315	320
Asp Ile Ser Phe Ser Arg His Trp Ile Arg Thr Leu Ala Trp Lys Leu			
325	330	335	
Val Leu Gln Ile Ser Gly Met Arg Ile Ser Phe Leu Ser Asn Ser Lys			
340	345	350	
Asn Thr His Ile Pro Val Glu Ile Ala Arg Asp Met Leu Glu Asp Thr			
355	360	365	
Phe Leu Ile Pro Lys Asn Leu Tyr Ala Val His Gly Pro Gly Ile Ser			
370	375	380	
Val Lys Ala Leu Glu Ile Ala Asp Ala Leu Val Asp Val Val Asn Gln			
385	390	395	400

Tyr Asp Cln Asn Ala Glu Ser Glu Ala Trp Asn Phe Leu Phe Asp Ile
 405 410 415

Ser Lys Phe Val Phe Ser Leu Lys His Cys Asp Ser Thr Leu Val Asp
 420 425 430

Lys Phe Thr Thr Lys Cys Gln Cys Ala Leu Ile Thr Leu Pro Leu Ser
 435 440 445

Asn Pro Leu Glu Ser Thr Asp Gly Ser Lys Glu Asp Val Asp Ala Leu
 450 455 460

Pro
 465

<210> 30
 <211> 2025
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(2025)

<400> 30
 atg tog gat gta gat aac tgg gaa ccc gta tca gat aat gag gac agt 45
 Met Ser Asp Val Asp Asn Trp Glu Pro Val Ser Asp Asn Glu Asp Ser
 1 5 10 15
 act gat tct gtg aaa caa ttg ggt ccc ccc ttt gag cat gca agt aac 96
 Thr Asp Ser Val Lys Gln Leu Gly Pro Pro Phe Glu His Ala Ser Asn
 20 25 30
 aat gac aat gcc ggc gat aat gaa gat gag tca ctg caa gaa gly ccc 144

Asn Asp Asn Ala Gly Asp Thr Glu Ala Glu Ser Leu Gln Glu Val Pro	
35 40 45	
cta aat aca gag acc aac gac gta cgc aag aat tta gta gtg att aca	192
Leu Asn Thr Glu Thr Asn Asp Val Arg Tyr Asn Leu Val Val Ile Thr	
50 55 60	
aac caa agt gcc gcc gat gaa cac cct aca gag atc aag cac gat caa	240
Asn Gln Ser Ala Ala Asp Glu His Pro Thr Glu Ile Lys His Asp Gln	
65 70 75 80	
tca agg act tct tgg acg tcc tgg ttc ttc agt gga atg atc tct tgg	288
Ser Arg Thr Ser Ser Thr Ser Ser Phe Phe Ser Gly Met Ile Ser Ser	
85 90 95	
ttt aag tca aac gtg cca tca cca gtt tct aga tca act acg cca act	336
Phe Lys Ser Asn Val Pro Ser Pro Val Ser Arg Ser Thr Thr Pro Thr	
100 105 110	
tgg cca gtt tgg cca cca agc att ata tca cat aga agg gag cct tcc	384
Ser Pro Val Ser Gln Pro Ser Ile Ile Ser His Arg Arg Glu Pro Ser	
115 120 125	
atg gag tcc aaa aga aga tca agc cgc cgt atc agt aat gcc aca att	432
Met Gly Ser Lys Arg Arg Ser Ser Arg Arg Ile Ser Asn Ala Thr Ile	
130 135 140	
gct gaa ata ggc tct ccc ttg cca cag gtg gaa aag cct gat gag gtc	480
Ala Glu Ile Gly Ser Pro Leu Gln Gln Val Gln Lys Pro Asp Glu Val	
145 150 155 160	
aag aca aga ctg act cct tcc caa atg aaa gaa gac aat tac gat cat	528
Lys Thr Arg Leu Thr Pro Ser Gln Met Lys Glu Asp Asn Tyr Asp His	
165 170 175	
aga cga ttc gtg gaa gaa cgt tac atg gac aca cct tat cac tat gcg	576
Arg Arg Phe Val Glu Glu Arg Tyr Met Asp Thr Pro Tyr His Tyr Ala	
180 185 190	
cct gag cca aga aat aaa gac ttt cat gag aca ttc aag tcc gtt cct	624
Ser Glu Gln Arg Asn Lys Asp Phe His Glu Thr Phe Lys Ser Val Pro	
195 200 205	

aaa gat gac aga cca ctg gat gat ttt aat tgt ggg ctg aat aga gag	672
Lys Asp Asp Arg Leu Leu Asp Asp Phe Asn Cys Gly Leu Asn Arg Glu	
210 215 220	
ctg att tac cag ggg aaa cta tac ata aca gaa acg cat ctc tgc ttc	720
Leu Leu Tyr Gln Gly Lys Leu Tyr Ile Thr Glu Thr His Leu Cys Phe	
225 230 235 240	
aac tcc aat gtt ctt ggt tgg att gct aaa gta ctg att gag ttc gaa	768
Asn Ser Asn Val Leu Gly Trp Ile Ala Lys Val Leu Ile Ala Phe Glu	
245 250 255	
gat gtc acg ttt atg gaa aaa act tct gct gct ggg ttg ttc ccc agc	816
Asp Val Thr Phe Met Glu Lys Thr Ser Ala Ala Gly Leu Phe Pro Ser	
260 265 270	
gca ata tcc atc gaa acc aag atg ggc aaa act ctc ttt aat ggt ttt	864
Ala Ile Ser Ile Glu Thr Lys Met Gly Lys Thr Leu Phe Asn Gly Phe	
275 280 285	
ata tcc agg gat gct gca ttt gca tta atg aaa gaa gtg tgg tca agc	912
Ile Ser Arg Asp Ala Ala Phe Gly Asn Met Lys Glu Val Trp Ser Arg	
290 295 300	
acc tta ttg cag aag gac atg gcc agc gaa aac atc aat acc aaa gca	960
Thr Leu Leu Gln Lys Asp Met Ala Ser Glu Asn Ile Asn Thr Lys Ala	
305 310 315 320	
gaa aag tca gga aat ggc aaa gag att gat gat gca ata aac tcc atc	1008
Glu Lys Ser Gly Asn Gly Lys Glu Ile Asp Asp Ala Ile Asn Ser Ile	
325 330 335	
gat gag gaa aac aat gat aaa gac gcc aat gat aat gac act aat gaa	1056
Asp Glu Glu Asn Asn Asp Lys Asp Ala Asn Asp Asn Asp Thr Asn Glu	
340 345 350	
aat gac gat gaa aat atc tct aca aat gag act acc ccc aat agt acg	1104
Asn Asp Asp Glu Asn Ile Ser Thr Asn Glu Thr Thr Pro Asn Ser Thr	
355 360 365	
agt tcc tgg ccg gat aaa gaa aaa gag aaa gcg tat aaa ctg cgt gcc	1152

Ser Ser Ser Pro Asp Lys Glu Lys Glu Lys Ala Tyr Lys Leu Arg Ala	
370 375 380	
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Asp Ser Ser Tyr Gln Tyr Asp Gly Pro Ile Tyr His His Ser Thr Ser	
385 390 395 400	
ttt ccc gct gaa cct atg gcc aat aac gag ttt gtt ctc aag gag tta	1240
Phe Pro Ala Glu Pro Met Ala Asn Asn Glu Phe Val Leu Lys Glu Leu	
405 410 415	
cca ttc gat tgt gca cct ggt ata ctt ttt gag atc atg ttc aac tca	1296
Pro Phe Asp Cys Ala Pro Gly Ile Leu Phe Glu Ile Met Phe Asn Ser	
420 425 430	
gag caa aac gaa ttt ctt cta gat ttt tta cgg ggt caa gaa ggt cca	1344
Glu Gln Asn Gln Phe Leu Leu Asp Phe Leu Arg Gly Gln Glu Gly Ser	
435 440 445	
caa att acc acc att cca aat ttc acc agc agc att gac gga tct tcc atg	1392
Gln Ile Thr Thr Ile Pro Asn Phe Thr Ser Ile Asp Gly Ser Ser Met	
450 455 460	
act ttg aag cgt gag tat tca tac gag aaa gca ttg cac ttt cct gag	1440
Thr Leu Lys Arg Glu Tyr Ser Tyr Glu Lys Ala Leu His Phe Pro Ala	
465 470 475 480	
ggg ccc aag tcc acc aca tgt tat ggt gct gag gta ata aag aga aaa	1488
Gly Pro Lys Ser Thr Thr Cys Tyr Val Ala Glu Val Ile Lys Arg Lys	
485 490 495	
gat cct gat act tac tat gag gtt abc agt agc ata cgc act ccg aac	1536
Asp Pro Asp Thr Tyr Tyr Glu Val Ile Ser Ser Ile Arg Thr Pro Asn	
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gtg ccc agt ggt ggt agt ltc tca act aag aca agg tat cta atc cgt	1584
Val Pro Ser Gly Gly Ser Phe Ser Thr Lys Thr Arg Tyr Leu Ile Arg	
515 520 525	
tgg aat gac gaa ata acc tgt ctg tta cgg gta tcc ttt tgg gtc gaa	1632
Trp Asn Asp Glu Ile Thr Cys Leu Leu Arg Val Ser Phe Trp Val Glu	
530 535 540	

tgg act ggt tcc aqt tgg atc aaa ggt atg gtt gaa aat gga tgc aag Trp Thr Gly Ser Ser Trp Ile Lys Gly Met Val Glu Asn Gly Cys Lys 545 550 555 560	1680
aat ggt caa tgg gag gct ggc caa tta atg gag cgt att ctt tcc aag Asn Gly Gln Leu Glu Ala Ala Gln Leu Met Glu Arg Ile Leu Ser Lys 565 570 575	1728
ttc atc aag aac aat gtc gaa gag tgc caa att act atc agc aag gag Phe Ile Lys Asn Asn Val Glu Glu Cys Gln Ile Thr Ile Ser Lys Glu 580 585 590	1776
gaa gag gag caa gat gat aac gaa gaa aaa aat aag ttg aaa gag gtt Glu Glu Glu Gln Asp Asp Lys Glu Val Lys Asn Lys Leu Lys Glu Val 595 600 605	1824
gac ctt gaa caa caa aga gaa gag gtt gtt acg gct ccc gca att gca Asp Leu Glu Gln Pro Arg Glu Ala Val Val Thr Ala Pro Ala Ile Ala 610 615 620	1872
gag atg caa ggt ctc aag gtc acc atg gaa acc tgg ttg ttc tta tac Glu Gln Gln Gly Leu Lys Val Thr Met Glu Thr Trp Leu Phe Leu Tyr 625 630 635 640	1920
ttg att gtg gtc gtc ttg cta ttg ttt aat atg ttc tac ata agt tca Leu Ile Val Val Val Leu Leu Leu Phe Asn Leu Phe Tyr Ile Arg Ser 645 650 655	1968
att gct gtc tca tta cat caa atg gtg aag atg caa ttg gta gaa atg Ile Ala Val Ser Leu His Gln Leu Val Lys Leu Gln Leu Val Glu Leu 660 665 670	2016
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<211> 674

<212> PPT

<213> Saccharomyces cerevisiae

<406> 31

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Asn Asp Asn Ala Gly Asp Thr Glu Ala Glu Ser Leu Glu Glu Val Pro
35 40 45

Leu Asn Thr Glu Thr Asn Asp Val Arg Lys Asn Leu Val Val Ile Thr
50 55 60

Asn Glu Ser Ala Ala Asp Glu His Pro Thr Glu Ile Lys His Asp Glu
65 70 75 80

Ser Arg Thr Ser Ser Thr Ser Ser Phe Phe Ser Gly Met Ile Ser Ser
85 90 95

Phe Lys Ser Asn Val Pro Ser Pro Val Ser Arg Ser Thr Thr Pro Thr
100 105 110

Ser Pro Val Ser Glu Pro Ser Ile Ile Ser His Arg Arg Glu Pro Ser
115 120 125

Met Gly Ser Lys Arg Arg Ser Ser Arg Arg Ile Ser Asn Ala Thr Ile
130 135 140

Ala Glu Ile Gly Ser Pro Leu Glu Glu Val Glu Lys Pro Asp Glu Val
145 150 155 160

Lys Thr Arg Leu Thr Pro Ser Gln Met Lys Glu Asp Asn Tyr Asp His
165 170 175

Arg Arg Phe Val Glu Glu Arg Tyr Met Asp Thr Pro Tyr His Tyr Ala
180 185 190

Ser Glu Gln Arg Asn Lys Asp Phe His Glu Thr Phe Lys Ser Val Pro
195 200 205

Lys Asp Asp Arg Leu Leu Asp Asp Phe Asn Cys Gly Leu Asn Arg Gln
210 215 220

Leu Leu Tyr Gln Gly Lys Leu Tyr Ile Thr Gln Thr His Leu Cys Phe
225 230 235 240

Asn Ser Asn Val Leu Gly Trp Ile Ala Lys Val Leu Ile Ala Phe Glu
245 250 255

Asp Val Thr Phe Met Glu Lys Thr Ser Ala Ala Gly Leu Phe Pro Ser
260 265 270

Ala Ile Ser Ile Glu Thr Lys Met Gly Lys Thr Leu Phe Asn Gly Phe
275 280 285

Ile Ser Arg Asp Ala Ala Phe Gly Leu Met Lys Glu Val Trp Ser Arg
290 295 300

Thr Leu Leu Cln Lys Asp Met Ala Ser Glu Asn Ile Asn Thr Lys Ala
305 310 315 320

Glu Lys Ser Gly Asn Gly Lys Glu Ile Asp Asp Ala Ile Asn Ser Ile
325 330 335

Asp Glu Glu Asn Asn Asp Lys Asp Ala Asn Asp Asn Asp Thr Asn Glu
340 345 350

Asn Asp Asp Glu Asn Ile Ser Thr Asn Glu Thr Thr Pro Asn Ser Thr
355 360 365

Ser Ser Ser Pro Asp Lys Glu Gln Glu Lys Ala Tyr Lys Leu Arg Ala
370 375 380

Asp Ser Ser Tyr Gln Tyr Asp Gly Pro Ile Tyr His His Ser Thr Ser
385 390 395 400

Phe Pro Ala Glu Pro Met Ala Asn Asn Glu Phe Val Leu Lys Glu Leu
405 410 415

Pro Phe Asp Cys Ala Pro Gly Ile Leu Phe Glu Ile Met Phe Asn Ser
420 425 430

Glu Gln Asn Glu Phe Leu Leu Asp Phe Leu Arg Gly Gln Glu Gly Ser
435 440 445

Gln Ile Thr Thr Ile Pro Asn Phe Thr Ser Ile Asp Gly Ser Ser Met
450 455 460

Thr Leu Lys Arg Glu Tyr Ser Tyr Glu Lys Ala Leu His Phe Pro Ala
465 470 475 480

Gly Pro Lys Ser Thr Thr Cys Tyr Val Ala Glu Val Ile Lys Arg Lys
485 490 495

Asp Pro Asp Thr Tyr Tyr Glu Val Ile Ser Ser Ile Arg Thr Pro Asn
500 505 510

Val Pro Ser Gly Gly Ser Phe Ser Thr Lys Thr Arg Tyr Leu Ile Arg
515 520 525

Trp Asn Asp Glu Ile Thr Cys Leu Leu Arg Val Ser Phe Trp Val Glu
530 535 540

Trp Thr Gly Ser Ser Trp Ile Lys Gly Met Val Glu Asn Gly Cys Lys
545 550 555 560

Asn Gly Gln Leu Glu Ala Ala Gln Leu Met Glu Arg Ile Leu Ser Lys
565 570 575

Phe Ile Lys Asn Asn Val Glu Glu Cys Gln Ile Thr Ile Ser Lys Glu
580 585 590

Glu Glu Glu Gln Asp Asp Lys Glu Val Lys Asn Lys Leu Lys Glu Val
595 600 605

Asp Leu Glu Gln Pro Arg Glu Ala Val Val Thr Ala Pro Ala Ile Ala
610 615 620

Glu Gln Gln Gly Leu Lys Val Thr Met Glu Thr Trp Leu Phe Leu Tyr
625 630 635 640

Leu Ile Val Val Val Leu Leu Leu Phe Asn Leu Phe Tyr Ile Arg Ser
645 650 655

Ile Ala Val Ser Leu His Gln Leu Val Lys Ile Gln Leu Val Gln Leu
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Lys Leu

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<211> 1185

<212> DNA

<213> *Saccharomyces cerevisiae*

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cca ggt aat aac ttg aca gcc ggt att gtc ggt ttg gcc aat gtt ggt 96
 Pro Gly Asn Asn Leu Lys Ala Gly Ile Val Gly Leu Ala Asn Val Gly
 20 25 30

aag tct acc ttt ttc cca gcc atc act aga tgt cca ttg ggt aac cca 144
 Lys Ser Thr Phe Phe Gln Ala Ile Thr Arg Cys Pro Leu Gly Asn Pro
 35 40 45

gct aac tat cca ttc gct aac att gat cca gaa gaa gcc cgt gtt att 192
 Ala Asn Tyr Pro Phe Ala Thr Ile Asp Pro Glu Glu Ala Arg Val Ile
 50 55 60

gtc cca tct cca aga ttt gat aag ttg tgt gaa atc tac aag aag aca 240
 Val Pro Ser Pro Arg Phe Asp Lys Leu Cys Glu Ile Tyr Lys Lys Thr
 65 70 75 80

gct tgg gaa gtt cca gct cat ttg aac gtt tac gat att gct ggt ttg 288
 Ala Ser Glu Val Pro Ala His Leu Thr Val Tyr Asp Ile Ala Gly Leu

83/762

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	Thr Lys Gly Ala Ser Ala Gly Glu Gly Leu Gly Asn Ala Phe Leu Ser			
	100	105	110	
	cac atc aga tca gtc gat tct atc tac caa gtc gtt cgt tgt ttc gat			384
	His Ile Arg Ser Val Asp Ser Ile Tyr Gln Val Val Arg Cys Phe Asp			
	115	120	125	
	gat gct gaa att atc cac gtt gag ggt gac gtt gat cca gtt cgt gat			432
	Asp Ala Glu Ile Ile His Val Glu Gly Asp Val Asp Pro Val Arg Asp			
	130	135	140	
	tta gaa att atc aac caa gaa cta aga ttg aaa gat att gaa ttc gca			480
	Leu Glu Ile Ile Asn Gln Gln Leu Arg Leu Lys Asp Ile Glu Phe Ala			
	145	150	155	160
	caa aag gct ttg gaa ggt gct gaa aag att gcc aaa aga ggt ggt caa			528
	Gln Lys Ala Leu Glu Gly Ala Glu Lys Ile Ala Lys Arg Gly Gly Gln			
	165	170	175	
	tct ttg gaa gtc aaa caa aag aag gaa gaa atg gat ttg att acg aaa			576
	Ser Leu Glu Val Lys Gln Lys Lys Glu Glu Met Asp Leu Ile Thr Lys			
	180	185	190	
	atc att aaa ttg cta gag agt ggt caa aga gtt gct aat cac tcc tgg			624
	Ile Ile Lys Leu Leu Glu Ser Gly Gln Arg Val Ala Asn His Ser Trp			
	195	200	205	
	act tca aaa gaa gtt gaa att atc aac tcc atg tcc ttg tag act gct			672
	Thr Ser Lys Glu Val Glu Ile Ile Asn Ser Met Phe Leu Ser Thr Ala			
	210	215	220	
	aag cca tgt atc tat ttg att aat tta tct gaa aga gat tac atc aga			720
	Lys Pro Cys Ile Tyr Leu Ile Asn Leu Ser Glu Arg Asp Tyr Ile Arg			
	225	230	235	240
	aag aaa aac aag cat ctg cta aga atc aag gaa tgg gta gac aag tac			768
	Lys Lys Asn Lys His Leu Leu Arg Ile Lys Glu Trp Val Asp Lys Tyr			
	245	250	255	

tct cca ggt gac ttg atc att cca ttc agt gtt tct cta gaa gaa aga 816
 Ser Pro Gly Asp Leu Ile Ile Pro Phe Ser Val Ser Leu Glu Glu Arg
 260 265 270

cta tct cat atc tcc cca gaa gat gct gaa gaa gaa ttg aag aac ctg 864
 Leu Ser His Met Ser Pro Glu Asp Ala Glu Glu Glu Leu Lys Lys Leu
 275 280 285

cag aca ata tct gcc ttg cca aag att atc act acc atg aga caa aag 912
 Gln Thr Ile Ser Ala Leu Pro Lys Ile Ile Thr Thr Met Arg Gln Tyr
 290 295 300

tta gat ttg att tcc ttt ttc acc tgc ggt cca gat gaa gtt cgt gaa 960
 Leu Asp Leu Ile Ser Phe Phe Thr Cys Gly Pro Asp Glu Val Arg Gln
 305 310 315 320

ttg acc atc aga aga ggt act aaa gct cca caa gct gct ggt gtt att 1008
 Trp Thr Ile Arg Arg Gly Thr Lys Ala Pro Gln Ala Ala Gly Val Ile
 325 330 335

cat aac gat tta atg aat acc ttt att ttg gct caa gtt atg aaa tgt 1056
 His Asn Asp Leu Met Asn Thr Phe Ile Leu Ala Gln Val Met Lys Cys
 340 345 350

gaa gat gtc ttc gaa tac aag gac gat tct gcc atc aag gcc gct ggt 1104
 Glu Asp Val Phe Glu Tyr Lys Asp Asp Ser Ala Ile Lys Ala Ala Gly
 355 360 365

aag ttg atg caa aag ggt aaa gac tat gtc gtc gaa gac ggt gat atc 1152
 Lys Leu Met Gln Lys Gly Lys Asp Tyr Val Val Glu Asp Gly Asp Ile
 370 375 380

att tac ttc aga gct ggt gct ggt aag aat tga 1185
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 385 390

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<211> 394

<212> PRO

<213> *Saccharomyces cerevisiae*

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 20 25 30

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 35 40 45

Ala Asn Tyr Pro Phe Ala Thr Ile Asp Pro Glu Glu Ala Arg Val Ile
 50 55 60

Val Pro Ser Pro Arg Phe Asp Lys Leu Cys Glu Ile Tyr Lys Lys Thr
 65 70 75 80

Ala Ser Glu Val Pro Ala His Leu Thr Val Tyr Asp Ile Ala Gly Leu
 85 90 95

Thr Lys Gly Ala Ser Ala Gly Glu Gly Leu Gly Asn Ala Phe Leu Ser
 100 105 110

His Ile Arg Ser Val Asp Ser Ile Tyr Gln Val Val Arg Cys Phe Asp
 115 120 125

Asp Ala Glu Ile Ile His Val Glu Gly Asp Val Asp Pro Val Arg Asp
 130 135 140

Leu Glu Ile Ile Asn Gln Glu Leu Arg Leu Lys Asp Ile Glu Phe Ala
 145 150 155 160

Gln Lys Ala Leu Glu Gly Ala Glu Lys Ile Ala Lys Arg Gly Gly Gln
165 170 175

Ser Leu Glu Val Lys Gln Lys Lys Gln Glu Met Asp Leu Ile Thr Lys
180 185 190

Ile Ile Lys Leu Leu Glu Ser Gly Gln Arg Val Ala Asn His Ser Thr
195 200 205

Thr Ser Lys Glu Val Glu Ile Ile Asn Ser Met Phe Leu Leu Thr Ala
210 215 220

Lys Pro Cys Ile Tyr Val Ile Asn Leu Ser Glu Arg Asp Tyr Ile Arg
225 230 235 240

Lys Lys Asn Lys His Leu Leu Arg Ile Lys Glu Trp Val Asp Lys Tyr
245 250 255

Ser Pro Gly Asp Leu Ile Ile Pro Phe Ser Val Ser Leu Glu Glu Arg
260 265 270

Leu Ser His Met Ser Pro Glu Asp Ala Glu Glu Glu Leu Lys Lys Leu
275 280 285

Gln Thr Ile Ser Ala Leu Pro Lys Ile Ile Thr Thr Met Arg Gln Lys
290 295 300

Leu Asp Leu Ile Ser Phe Phe Thr Cys Gly Pro Asp Glu Val Arg Glu
305 310 315 320

Trp Thr Ile Arg Arg Gly Thr Lys Ala Pro Gln Ala Ala Gly Val Ile

325

330

335

His Asn Asp Leu Met Asn Thr Phe Ile Leu Ala Gln Val Met Lys Cys

340

345

350

Glu Asp Val Phe Glu Tyr Lys Asp Asp Ser Ala Ile Lys Ala Ala Gly

355

360

365

Lys Leu Met Gln Lys Gly Lys Asp Tyr Val Val Glu Asp Gly Asp Ile

370

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Ile Tyr Phe Arg Ala Gly Ala Gly Lys Asn

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<212> DNA

<213> *Saccharomyces cerevisiae*

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10

15

act aca aac gct gct aat aaa ctc att gtc tta tat ttt aaa gct caa 96

Thr Thr Asn Ala Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln

20

25

30

tgg gct gat cct tgc aaa act atg agc cag gtg cta gaa gct gtt agt 144

Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser

35

40

45

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gaa aaa gtt agg caa gag gat gtc cgg ttt tta tca ata gat gca gac	132
Glu Lys Val Arg Glu Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp	
50 55 60	
gaa cat cca gaa ata tca gac ctt ttt gag att gca gcc gta cca tac	240
Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr	
65 70 75 80	
llu gtc ttc att caa aat ggt act att gta aaa gaa ata tca gcc gca	288
Phe Val Phe Ile Glu Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala	
85 90 95	
gat cct aag gag lll gtg aaa agc tta gaa att ctt tcc aat gct tct	336
Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser	
100 105 110	
gcc tca cta gcc aac aat gcc aag ggt cct aaa tct acg tct gat gag	384
Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu	
115 120 125	
gaa agc agc ggg tct tcc gat gat gaa gag gac gaa act gaa gaa gaa	432
Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu	
130 135 140	
ata aat gct agg ctg gtg aag cta gta caa gct gca cct gtg atg ctg	480
Ile Asn Ala Arg Leu Val Lys Leu Val Glu Ala Ala Pro Val Met Leu	
145 150 155 160	
ttc atg aaa gga agc cca tca gaa cct aaa tgc gga ttt tct aca cag	528
Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Glu	
165 170 175	
tta gtt ggt atc ctg aga gaa cac caa ata agg ttc gga ttt ttt gat	576
Leu Val Gly Ile Leu Arg Glu His Glu Ile Arg Phe Gly Phe Phe Asp	
180 185 190	
ata tta aga gac gaa aac gtt aga caa agc ttg aag aag ttt tct gat	624
Ile Leu Arg Asp Glu Asn Val Arg Glu Ser Leu Lys Lys Phe Ser Asp	
195 200 205	
cgg cct act ttt cct cag tta tat atc aat ggg gag ttc cag gga gga	672
Tyr Pro Thr Phe Pro Glu Leu Tyr Ile Asn Gly Glu Phe Glu Gly Gly	

210	215	220	
ttg gat att atc aag gaa tct ata gaa gaa gat oot gaa tat ttc caa			720
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His Ala Leu Gln			

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<210> 35
<211> 241
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<213> Saccharomyces cerevisiae
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4002 35

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Thr Thr Asp Ala Ala Asn Lys Leu Ile Val Leu Tyr Phe Lys Ala Gln
20 25 30

Trp Ala Asp Pro Cys Lys Thr Met Ser Gln Val Leu Glu Ala Val Ser
35 40 45

Glu Lys Val Arg Gln Glu Asp Val Arg Phe Leu Ser Ile Asp Ala Asp
50 55 60

Glu His Pro Glu Ile Ser Asp Leu Phe Glu Ile Ala Ala Val Pro Tyr
65 70 75 80

Phe Val Phe Ile Gln Asn Gly Thr Ile Val Lys Glu Ile Ser Ala Ala
85 90 95

Asp Pro Lys Glu Phe Val Lys Ser Leu Glu Ile Leu Ser Asn Ala Ser
100 105 110

Ala Ser Leu Ala Asn Asn Ala Lys Gly Pro Lys Ser Thr Ser Asp Glu
115 120 125

Glu Ser Ser Gly Ser Ser Asp Asp Glu Glu Asp Glu Thr Glu Glu Glu
130 135 140

Ile Asn Ala Arg Leu Val Lys Leu Val Gln Ala Ala Pro Val Met Leu
145 150 155 160

Phe Met Lys Gly Ser Pro Ser Glu Pro Lys Cys Gly Phe Ser Arg Gln
165 170 175

Leu Val Gly Ile Leu Arg Glu His Gln Ile Arg Phe Gly Phe Phe Asp
180 185 190

Ile Leu Arg Asp Glu Asn Val Arg Gln Ser Leu Lys Lys Phe Ser Asp
195 200 205

Trp Pro Thr Phe Pro Gln Leu Tyr Ile Asn Gly Glu Phe Gln Gly Gly
210 215 220

Leu Asp Ile Ile Lys Glu Ser Ile Gln Glu Asp Pro Glu Tyr Phe Gln
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His Ala Leu Gln

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212 INA

<213> *Saccharomyces cerevisiae*

€2203

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tbg att ttt ttt aag cna tac gta cca ttt gca gcg gcg gga gga tat 96
 Leu Ile Phe Phe Lys Gln Tyr Val Pro Phe Ala Ala Ala Gly Gly Tyr
 20 25 30

ccc ata tog ttt cta atc atc aaa gtt ctg acc gcc tca aag aat tta 144
Pro Ile Ser Phe Leu Phe Ile Lys Val Leu Thr Ala Ser Thr Asn Leu
35 40 45

cta ctt tct tct kcc tct gga ggg tcc tgg aat aag tta tcc aaa gag 192
Leu Leu Ser Ser Ser Ser Gly Gly Ser Trp Asn Lys Leu Ser Lys Glu
50 55 60

teg aea tta ctc aaa gtc att ctc aca can tti ott gtt cct att ttt 240
 Ser Gln Leu Leu Lys Val Ile Leu Thr His Phe Leu Val Pro Ile Phe
 65 70 75 80

Utt ttc tta ttc caa tat att att tta tca gaa gac aga cag caa gaa 289
Phe Phe Leu Phe Gln Tyr Ile Ile Leu Ser Glu Asp Arg Gln Gln Glu
35 90 95

cga cag cct aag ttt cga gac aac gct aaa ttt gac gga cat gcg aag 106
 Arg Gln Pro Lys Phe Arg Asp Asn Ala Lys Phe Asp Gly His Ala Lys
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aca tgc cat ata taa 351
Thr Cys His Ile
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<210> 37

<211> 116

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<213> *Saccharomyces cerevisiae*

<400> 37

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Leu Ile Phe Phe Tyr Gln Tyr Val Pro Phe Ala Ala Ala Gly Gly Tyr

20

25

30

Pro Ile Ser Phe Leu Phe Ile Lys Val Leu Thr Ala Ser Thr Asn Leu

35

40

45

Leu Leu Ser Ser Ser Ser Gly Gly Ser Trp Asn Lys Leu Ser Lys Glu

50

55

60

Ser Gln Leu Leu Lys Val Ile Leu Thr His Phe Leu Val Pro Ile Phe

65

70

75

80

Phe Phe Leu Phe Gln Tyr Ile Ile Leu Ser Glu Asp Arg Gln Gln Glu

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100

105

110

Thr Cys His Ile

115

<210> 38

<211> 900

<212> DNA

<213> *Saccharomyces cerevisiae*

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<221> CDS

<222> (1)..(900)

<400> 38

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tca	aga	cct	tct	tat	ccc	tcc	gat	ttt	tac	aag	atg	att	gat	gaa	tac	96
Ser	Arg	Pro	Ser	Tyr	Pro	Ser	Asp	Phe	Tyr	Lys	Met	Ile	Asp	Glu	Tyr	
			20					25					30			

cac	gac	gga	gac	agg	caa	tta	ctc	gta	gat	gtt	ggc	tgt	gga	cca	ggc	144
His	Asp	Gly	Glu	Arg	Lys	Leu	Val	Asp	Val	Gly	Cys	Gly	Pro	Gly		
		35					40				45					

act	gcc	act	tta	caa	atg	gct	cag	gag	tta	aaa	cca	ttc	gan	caa	att	192
Thr	Ala	Thr	Leu	Gln	Met	Ala	Gln	Glu	Leu	Lys	Pro	Phe	Gln	Gln	Ile	
		50					55				60					

atc	ggg	agc	gat	ctc	tcc	gct	acc	atg	att	aag	act	gca	gaa	gta	ata	240
Ile	Gly	Ser	Asp	Leu	Ser	Ala	Thr	Met	Ile	Lys	Thr	Ala	Glu	Val	Ile	
65				70						75				80		

aag	gaa	gga	agt	cct	gat	aca	tac	aaa	aac	gtt	tca	ttt	aaq	att	tct	288
Lys	Glu	Gly	Ser	Pro	Asp	Thr	Tyr	Lys	Asn	Val	Ser	Phe	Lys	Ile	Ser	
			85					90					95			

tca	agt	gat	gat	ttt	aaa	ttc	cta	ggg	ggg	gat	tca	gta	gac	aaa	cag	336
Ser	Ser	Asp	Asp	Phe	Lys	Phe	Leu	Gly	Ala	Asp	Ser	Val	Asp	Lys	Gln	
			100					105					110			

aaa	att	gat	atg	att	acc	gca	gla	gaa	tgt	ggt	cat	tgg	ttc	gat	ttc	384
Lys	Ile	Asp	Met	Ile	Thr	Ala	Val	Glu	Cys	Ala	His	Trp	Phe	Asp	Phe	
			115					120					125			

gaa aaa ttt cag cga tct gct tat gcc aac ttg aga aaa gat ggt act	432
Glu Lys Phe Gln Arg Ser Ala Tyr Ala Asn Leu Arg Lys Asp Gly Thr	
130 135 140	
atc gct att tgg ggt tat gcg gac cca att ttc cag gac tac cct gaa	460
Ile Ala Ile Trp Gly Tyr Ala Asp Pro Ile Phe Pro Asp Tyr Pro Glu	
145 150 155 160	
ttt gac gat ctg atg att gaa gtt cct tac ggg aag caa gga ctg gga	528
Phe Asp Asp Leu Met Ile Glu Val Pro Tyr Gly Lys Gln Gly Leu Gly	
165 170 175	
ccc tat tgg gaa caa ccg ggg aga tct cgc att cgt aat atg ctg aaa	576
Pro Tyr Trp Glu Gln Pro Gly Arg Ser Arg Leu Arg Asn Met Leu Lys	
180 185 190	
gac tct cac tta gac cca gaa ctt ttc cat gat ata caa gtt tca tac	624
Asp Ser His Leu Asp Pro Glu Leu Phe His Asp Ile Gln Val Ser Tyr	
195 200 205	
ttt tgt gca gca gat gtg aga gac aac gta aaa ctg cac cag cat aca	672
Phe Cys Ala Glu Asp Val Arg Asp Lys Val Lys Leu His Gln His Thr	
210 215 220	
aag aag cca tgg cta atc aga aag cag gtc acc cta gtg gag ttt gca	720
Lys Lys Pro Leu Leu Ile Arg Lys Gln Val Thr Leu Val Glu Phe Ala	
225 230 235 240	
gat tat qtc aqa acc tgg aac gct tac cat cag tgg aag caq gat cca	768
Asp Tyr Val Arg Thr Trp Ser Ala Tyr His Gln Trp Lys Gln Asp Pro	
245 250 255	
aag aac aaa gat aaa gaa gat gta gca gat tgg ttt att aaa gag tca	816
Lys Asn Lys Asp Lys Glu Asp Val Ala Asp Trp Phe Ile Lys Glu Ser	
260 265 270	
cta agg agg agg ccg gaa ctt tcc acc aac acc aaa att gaa gtt gtt	864
Leu Arg Arg Arg Pro Glu Leu Ser Thr Asn Thr Iys Ile Glu Val Val	
275 280 285	
tgg aat act ttt taa aaa ctt ggc aaa agg gtc tga	900
Trp Asn Thr Phe Tyr Lys Leu Gly Lys Arg Val	

290

295

<210> 39

<211> 299

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 39

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Ser Arg Pro Ser Tyr Pro Ser Asp Phe Tyr Lys Met Ile Asp Glu Tyr
20 25 30

His Asp Gly Glu Arg Lys Leu Leu Val Asp Val Gly Cys Gly Pro Gly
35 40 45

Thr Ala Thr Leu Gln Met Ala Gln Glu Ser Lys Pro Phe Gln Gln Ile
50 55 60

Ile Gly Ser Asp Leu Ser Ala Thr Met Ile Lys Thr Ala Glu Val Ile
65 70 75 80

Lys Glu Gly Ser Pro Asp Thr Tyr Lys Asn Val Ser Phe Lys Ile Ser
85 90 95

Ser Ser Asp Asp Phe Lys Phe Leu Gly Ala Asp Ser Val Asp Lys Gln
100 105 110

Lys Ile Asp Met Ile Thr Ala Val Glu Cys Ala His Trp Phe Asp Phe
115 120 125

Glu Lys Phe Gln Arg Ser Ala Tyr Ala Asn Leu Arg Lys Asp Gly Thr
130 135 140

Ile Ala Ile Trp Gly Tyr Ala Asp Pro Ile Phe Pro Asp Tyr Pro Glu
145 150 155 160

Phe Asp Asp Leu Met Ile Glu Val Pro Tyr Gly Lys Gln Gly Leu Gly
165 170 175

Pro Tyr Trp Glu Gln Pro Gly Arg Ser Arg Leu Arg Asn Met Leu Lys
180 185 190

Asp Ser His Leu Asp Pro Glu Leu Phe His Asp Ile Gln Val Ser Tyr
195 200 205

Phe Cys Ala Glu Asp Val Arg Asp Lys Val Lys Leu His Gln His Thr
210 215 220

Lys Lys Pro Leu Leu Ile Arg Lys Gln Val Thr Leu Val Glu Phe Asn
225 230 235 240

Asp Tyr Val Arg Thr Trp Ser Ala Tyr His Gln Trp Lys Gln Asp Pro
245 250 255

Lys Asn Lys Asp Lys Glu Asp Val Ala Asp Trp Phe Ile Lys Glu Ser
260 265 270

Leu Arg Arg Arg Pro Glu Leu Ser Thr Asn Thr Lys Ile Glu Val Val
275 280 285

Trp Asn Thr Phe Tyr Lys Leu Gly Lys Arg Val
290 295

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 <213> *Saccharomyces cerevisiae*

<220>
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 <222> (1) .. (336)

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 Met Lys Gly Ser Lys Ser His Leu Val Phe Thr Leu Leu Gln Val Ser
 1 5 10 15
 caa cta aat gtt ttt ctt ttc tct cta ggt ttt ctg ttg cca tta ttc 96
 Gln Leu Asn Val Phe Leu Phe Phe Leu Gly Phe Leu Leu Pro Leu Phe
 20 25 30
 tta gga ctg ttc gtt tca ctg cga tct ttg gct att gca cta tcc tct 114
 Leu Gly Leu Phe Val Ser Leu Arg Ser Leu Ala Leu Ala Leu Ser Ser
 35 40 45
 ggg tgg ttt att atg gat ctg ata cta ttt cga acc att cca gaa gca 192
 Gly Trp Phe Ile Met Asp Leu Ile Leu Phe Arg Thr Phe Pro Glu Ala
 50 55 60
 gaa tta tat cca gca ctc atc ggt aaa cca tct ggt ctg ggg att aat 240
 Glu Leu Tyr Pro Ala Val Ile Gly Lys Pro Ser Gly Leu Gly Leu Thr
 65 70 75 80
 gag gca ttt gag ttt ata tcc att ttt ttc cct gat gtt cag caa acc 288
 Glu Ala Phe Glu Phe Ile Ser Ile Phe Phe Pro Asp Val Gln Gln Thr
 85 90 95
 gaa aga aat ala aua taa aac tgg gaa aga tgt ttt aat ggt gag taa 336
 Glu Arg Asn Ile Lys Tyr Asn Trp Glu Arg Cys Phe Asn Gly Glu
 100 105 110

<210> 41
<211> 111
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 41

Met Lys Gly Ser Lys Ser His Leu Val Phe Thr Leu Leu Gln Val Ser
1 5 10 15

Gln Leu Asn Val Phe Leu Phe Phe Leu Gly Phe Leu Leu Pro Leu Phe
20 25 30

Leu Gly Leu Phe Val Ser Leu Arg Ser Leu Ala Leu Ala Leu Ser Ser
35 40 45

Gly Arg Phe Ile Met Asp Leu Ile Leu Phe Arg Thr Phe Pro Glu Ala
50 55 60

Glu Leu Tyr Pro Ala Val Ile Gly Lys Pro Ser Gly Leu Gly Leu Thr
65 70 75 80

Glu Ala Phe Glu Phe Ile Ser Ile Phe Phe Pro Asp Val Gln Glu Thr
85 90 95

Glu Arg Asn Ile Lys Tyr Asn Trp Glu Arg Cys Phe Asn Gly Glu
100 105 110

<210> 42
<211> 2556
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (2555)

<400> 42

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Met	Pro	Lys	Asn	Ser	His	His	His	His	Arg	Ser	Ser	Ser	Val	Asn	Ser	Thr	
1				5					10					15			

aag	agt	cgt	tct	acg	gaa	tct	acg	aat	aaa	tgg	aaa	att	ccg	cac	tat	96
Lys	Ser	Arg	Ser	Thr	Glu	Ser	Thr	Asn	Lys	Trp	Lys	Ile	Pro	His	Tyr	
				20				25					30			

tat	cgc	aga	ccc	gct	agc	ggc	agc	aca	caa	gct	tgc	ccg	gac	agg	aac	144
Tyr	Arg	Arg	Ser	Ala	Ser	Gly	Ser	Thr	Gln	Ala	Ser	Pro	Asp	Arg	Asn	
				35				40					45			

ccc	tca	aca	ggc	cca	cgt	agc	act	cca	gta	ata	cct	act	atg	aat	ggt	192
Ser	Ser	Thr	Gly	Ser	Cys	Ser	Thr	Pro	Val	Leu	Pro	Thr	Met	Asn	Val	
				50				55					60			

atg	tct	agc	ccg	aaa	aaa	gtt	ttg	cta	gag	gat	ccc	aga	gac	aac	cac	240
Met	Ser	Ser	Pro	Lys	Lys	Val	Leu	Leu	Glu	Asp	Pro	Arg	Asp	Asn	Ile	
65						70					75				80	

act	aag	ggc	aag	aag	agt	agt	aga	aag	aaa	cca	ggc	gaa	atg	gtc	ttc	288
Thr	Lys	Ala	Lys	Lys	Ser	Ser	Arg	Lys	Lys	Ser	Gly	Glu	Met	Val	Phe	

gtc	aat	tat	act	gta	cag	gac	acg	gct	aac	gaa	aat	gat	act	gac	ttg	336
Val	Asn	Tyr	Thr	Val	Gln	Asp	Thr	Ala	Asn	Glu	Asn	Asp	Thr	Asp	Leu	

caa	acc	cag	ccg	gtt	tct	gtg	ccc	gca	cca	aag	ggc	aaa	tta	aag	aag	384
Gln	Thr	Gln	Iro	Val	Ser	Val	Pro	Ala	Pro	Lys	Ala	Lys	Leu	Lys	Lys	

aaa	ccc	ccc	aaa	agg	aga	atg	ctg	aag	ata	ttt	gga	tgc	cca	aag	aac	432
Lys	Ser	Ser	Lys	Arg	Arg	Met	Leu	Lys	Ile	Phe	Gly	Ser	Ser	Lys	Asn	

gaa	cac	ata	gag	gac	atc	gtt	gaa	gag	caa	cca	atg	gtg	cct	caa	atg	480
Glu	His	Ile	Gln	Asp	Ile	Val	Glu	Glu	Gln	Pro	Met	Val	Leu	Gln	Met	

145	150	155	160	
gat tca gaa tct aaa ccc ctt tgg gga acc cct acc tca gaa agc gga				528
Asp Ser Gln Ser Lys Pro Leu Ser Gly Thr Pro Ile Ser Glu Ser Gly				
165	170	175		
atc gac gcc tgg tca cta aca acc aaa aga tct tat aac tgg ttc tta				576
Ile Asp Ala Ser Ser Leu Thr Thr Lys Arg Ser Tyr Asn Ser Phe Leu				
180	185	190		
aaa cac aat agg cta aac ggt aaa act cgg ttc tct gga aac ttg tcc				624
Lys His Asn Arg Leu Asn Gly Lys Thr Pro Phe Ser Gly Asn Leu Ser				
195	200	205		
ttt cca tca cta aac atg atg ggt aac act act gat ctg cct att gac				672
Phe Pro Ser Leu Asn Met Met Gly Asn Thr Thr Asp Leu Pro Phe Asp				
210	215	220		
aat aac gat ttt tgt tcc gag aaa gaa gtc gtt cgg aaa tca acc cat				720
Asn Asn Asp Phe Cys Ser Glu Lys Glu Val Val Pro Lys Ser Thr His				
225	230	235	240	
gat cct tca cta gca aaa cgg aaa tca agg ttc act gaa agc gaa aca				768
Asp Pro Ser Leu Ala Lys Pro Pro Ser Arg Phe Thr Glu Ser Glu Thr				
245	250	255		
aat tct act ccc aac tta tca agt aca cct ctc atg aac aca aaa aat				816
Asn Ser Thr Pro Asn Leu Ser Ser Ile Pro Leu Met Asn Thr Lys Asn				
260	265	270		
aca aga ttg aag tac aat aaa gtg ggg cct cag agt leu gac cga caa				864
Thr Arg Leu Lys Tyr Asn Lys Val Ala Pro Gln Ser Ser Asn Arg Gln				
275	280	285		
acg tca cag gaa agt ggg cta tat cat tct acc gaa tca ttc aac ttc				912
Lys Ser Gln Glu Ser Gly Leu Tyr His Ser Thr Glu Ser Phe Asn Phe				
290	295	300		
aaa gat caa aac tac agt aac aat aaa tcc tct tta agt ctg aac tcc				960
Lys Asp Gln Asn Tyr Ser Asn Asn Lys Ser Ser Leu Ser Leu Asn Ser				
305	310	315	320	

gat tta agt aca ccc cac ttt gca aag cat tca cct gat tca cca aga	1008
Asp Leu Ser Thr Pro His Phe Ala Lys His Ser Pro Asp Ser Pro Arg	
335 350 335	
act tca aga tct ttc aac tgc gga gac tca caa agt aaa gtt aaa tta	1056
Thr Ser Arg Ser Phe Asn Cys Gly Asp Ser Gln Ser Lys Val Lys Leu	
340 345 350	
cag gaa gaa aat gac ggt tct att gca ttt agt aag atg ttt act aga	1104
Pro Glu Glu Asn Asp Ala Ser Ile Ala Phe Ser Lys Met Phe Thr Arg	
355 360 365	
aaa aga gcc aac act ggc ggg tcc aag tgt teg cca gcc tca ccc act	1152
Lys Arg Ala Asn Thr Gly Gly Ser Thr Cys Ser Leu Ala Ser Pro Thr	
370 375 380	
att gca caa act act cag caa tca aat ata aaa gtt aat aaa ttg cca	1200
Ile Ala Gln Thr Ile Gln Gln Ser Asn Ile Lys Val Asn Lys Leu Pro	
385 390 395 400	
act cag cga acc act tca gtt ggc tca tta tca tcc atg tca aat cgt	1248
Thr Gln Arg Thr Thr Ser Val Gly Ser Leu Ser Ser Met Ser Asn Arg	
405 410 415	
tat tca cca ata aga gtt gca tgg cca gga aga gca aga tcc gca act	1296
Tyr Ser Pro Ile Arg Val Ala Ser Pro Gly Arg Ala Arg Ser Ala Thr	
420 425 430	
cgt ggg tct tcc ctt tat aga tta tcc aga gac ctt aat tct tta cca	1344
Arg Gly Ser Ser Leu Tyr Arg Leu Ser Arg Asp Leu Asn Ser Leu Pro	
435 440 445	
agc gtc act gat cta cca gaa atg gat agt aca acc cca gtt aac gaa	1392
Ser Val Thr Asp Leu Pro Gln Met Asp Ser Thr Thr Pro Val Asn Gln	
450 455 460	
ata ttc ttg gat ggc caa cca cag cat aaa agt ggc agt gtc aaa gga	1440
Ile Phe Leu Asp Gly Gln Pro Gln His Lys Ser Gly Ser Val Lys Gly	
465 470 475 480	
ggg cat agg aag aaa caa gaa tct acc tct gat gct caa aga att caa	1488
Gly His Arg Lys Lys Gln Glu Ser Ile Ser Asp Ala Gln Arg Ile Gln	

485	490	495	
cat tct aat tcy tac att aca aca cct tca tct tct ctg gtg act cct			1536
His Ser Asn Ser Tyr Ile Thr Thr Pro Ser Ser Ser Leu Val Thr Pro			
500	505	510	
cct tac tac atg aca ggt tac aca tta cca agt tct gca tct gct tct			1584
Pro Tyr Tyr Met Thr Gly Tyr Thr Leu Pro Ser Ser Ala Ser Ala Ser			
515	520	525	
tca aat cca aat ghg ctt gaa aca cac aat atg aac ttt gtt cca agt			1632
Ser Thr Pro Asn Val Leu Glu Thr His Asn Met Asn Phe Val Pro Ser			
530	535	540	
acc agt act gtt aca agt tat cgc cca tct agc aat ttt tcc tca ttt			1680
Thr Ser Thr Val Thr Ser Tyr Arg Pro Ser Ser Asn Phe Ser Ser Phe			
545	550	555	560
gac aax gac tac agt sac gaa aac gac gct agt ggg gaa ttc tct gct			1728
Asp Lys Glu Tyr Ser Asn Glu Asn Asp Ala Ser Gly Glu Phe Ser Ala			
565	570	575	
ttc aat act cca atg gag aat ata ccg gca cta aau ggt abu cct agu			1776
Phe Asn Thr Pro Met Glu Asn Ile Pro Ala Leu Lys Gly Ile Pro Arg			
580	585	590	
tcc acc tta gaa gaa aat gaa gaa gag gat gtc cta gta caa gat att			1824
Ser Thr Leu Glu Glu Asn Glu Glu Asp Val Leu Val Gln Asp Ile			
595	600	605	
ccg aat acg gca cac ttc caa aga agg gat att atc ggg atg cat act			1872
Pro Asn Thr Ala His Phe Gln Arg Arg Asp Ile Met Gly Met Asp Thr			
610	615	620	
cac aga aag gat gac agt tta gat ttt aac tct ttg atg cca cac ggt			1920
His Arg Lys Asp Asp Ser Leu Asp Phe Asn Ser Leu Met Pro His Gly			
625	630	635	640
agt aca act agt agc agu abc gta gat tct gtt atg acg aac tca ata			1968
Ser Thr Thr Ser Ser Ile Val Asp Ser Val Met Thr Asn Ser Ile			
645	650	655	

<p> tcc acg aca aca agc aac gag aac gga aac tac ttt caa gat caa gat Ser Thr Thr Thr Ser Asn Ala Thr Gly Asn Tyr Phe Gln Asp Gln Asp 660 665 670 </p>	2016
<p> aag tat aca ttg gta aat acg gga ttg gga ttg agt gat gca aac ctg Lys Tyr Thr Leu Val Asn Thr Gly Leu Gly Leu Ser Asp Ala Asn Leu 675 680 685 </p>	2064
<p> gat cat ttt att aga tct caa tgg aaa cac gcc tct cga tca gaa tcc Asp His Phe Ile Arg Ser Gln Trp Lys His Ala Ser Arg Ser Glu Ser 690 695 700 </p>	2112
<p> aat aat aat aac qqa aat cgc gtt tct tac agt ggc tca aca cca aac Asn Asn Asn Thr Gly Asn Arg Val Ser Tyr Ser Gly Ser Thr Pro Asn 705 710 715 720 </p>	2160
<p> aat gtt gat aca aca aag act aat ttg caa gtg tat acc gag ttc gat Asn Val Asp Thr Thr Lys Thr Asn Leu Gln Val Tyr Thr Glu Phe Asp 725 730 735 </p>	2208
<p> ttc gaa aac cca gag tgg ttt ttc cat gag caa tgg aag cta cta ggt Phe Glu Asn Pro Gln Ser Phe Phe His Glu Gln Ser Lys Leu Leu Gly 740 745 750 </p>	2256
<p> gag atg ggc caa agc aat aat aac agc aac agc ggc atc aac atg aat Glu Met Gly His Ser Asn Asn Asn Ser Asn Ser Ala Ile Asn Met Asn 755 760 765 </p>	2304
<p> gaa ccc aag tct gcg gat aca tac att gga aat ala tct ccg gat act Glu Pro Lys Ser Ala Asp Thr Tyr Ile Gly Asn Ile Ser Pro Asp Thr 770 775 780 </p>	2352
<p> tca gca act gtt tca tta ggc gac ctg atg ggc tca aac gtt tca aac Ser Ala Thr Val Ser Leu Gly Asp Leu Met Gly Ser Asn Val Ser Asn 785 790 795 800 </p>	2400
<p> aac agt gaa aga aat ttt tac gat ggt cat act ttc gct cca caa tat Asn Ser Glu Arg Asn Phe Tyr Asp Gly His Thr Phe val Pro Gln Tyr 805 810 815 </p>	2448
<p> cag ggc aac tca tct gtg gaa aac tca aat aat caa aat gca gca cca Gln Ala Asn Ser Ser Val Gln Asn Ser Asn Asn Gln Asn Ala Ala Pro 820 825 830 </p>	2496

820	825	830	
att gca att aac gac att gat aat aat tta cag tct ttt tat ttt gal	2544		
Ile Ala Asn Asn Asp Ile Asp Asn Asn Leu Gln Ser Phe Tyr Phe Asp			
835	840	845	
aat agc aac taa			2556
Asn Ser Asn			
850			
<210> 43			
<211> 851			
<212> PRT			
<213> <i>Saccharomyces cerevisiae</i>			
<400> 43			
Met Pro Lys Asn Ser His His His Arg Ser Ser Ser Val Asn Ser Thr			
1	5	10	15
Lys Ser Arg Ser Thr Glu Ser Thr Asn Lys Arg Lys Ile Pro His Tyr			
20	25	30	
Tyr Arg Arg Ser Ala Ser Gly Ser Thr Cln Ala Ser Pro Asp Arg Asn			
35	40	45	
Ser Ser Thr Gly Ser Cys Ser Thr Pro Val Leu Pro Thr Met Asn Val			
50	55	60	
Met Ser Ser Pro Lys Lys Val Leu Leu Glu Asp Pro Arg Asp Asn His			
65	70	75	80
Thr Lys Ala Lys Lys Ser Ser Arg Lys Lys Ser Gly Glu Met Val Phe			
85	90	95	

Val Asn Tyr Thr Val Gln Asp Thr Ala Asn Glu Asn Asp Thr Asp Leu
100 105 110

Gln Thr Gln Pro Val Ser Val Pro Ala Pro Lys Ala Lys Leu Lys Lys
115 120 125

Lys Ser Ser Lys Arg Arg Met Leu Lys Ile Phe Gly Ser Ser Lys Asn
130 135 140

Glu His Ile Glu Asp Ile Val Glu Glu Gln Pro Met Val Leu Gln Met
145 150 155 160

Asp Ser Glu Ser Lys Pro Leu Ser Gly Thr Pro Ile Ser Glu Ser Gly
165 170 175

Ile Asp Ala Ser Ser Leu Thr Thr Lys Arg Ser Tyr Asn Ser Phe Leu
180 185 190

Lys His Asn Arg Leu Asn Gly Lys Thr Pro Phe Ser Gly Asn Leu Ser
195 200 205

Phe Pro Ser Leu Asn Met Met Gly Asn Thr Thr Asp Leu Pro Ile Asp
210 215 220

Asn Asn Asp Phe Cys Ser Glu Lys Glu Val Val Pro Lys Ser Thr His
225 230 235 240

Asp Pro Ser Leu Ala Lys Pro Pro Ser Arg Phe Thr Glu Ser Glu Thr
245 250 255

Asn Ser Thr Pro Asn Leu Ser Ser Ile Pro Leu Met Asn Thr Lys Asn

260	265	270
Thr Arg Leu Lys Tyr Asn Lys Val Ala Pro Gln Ser Ser Asp Arg Gln		
275	280	285
Lys Ser Gln Glu Ser Gly Leu Tyr His Ser Thr Glu Ser Phe Asn Phe		
290	295	300
Lys Asp Gln Asn Tyr Ser Asn Asn Lys Ser Ser Leu Ser Leu Asn Ser		
305	310	315 320
Asp Leu Ser Thr Pro His Phe Ala Lys His Ser Pro Asp Ser Pro Arg		
325	330	335
Thr Ser Arg Ser Phe Asn Cys Gly Asp Ser Gln Ser Lys Val Lys Leu		
340	345	350
Pro Glu Glu Asn Asp Ala Ser Ile Ala Phe Ser Lys Met Phe Thr Arg		
355	360	365
Lys Arg Ala Asn Thr Gly Gly Ser Thr Cys Ser Leu Ala Ser Pro Thr		
370	375	380
Ile Ala Gln Thr Ile Gln Gln Ser Asn Ile Lys Val Asn Lys Leu Pro		
385	390	395 400
Thr Gln Arg Thr Thr Ser Val Gly Ser Leu Ser Ser Met Ser Asn Arg		
405	410	415
Tyr Ser Pro Ile Arg Val Ala Ser Pro Gly Arg Ala Arg Ser Ala Thr		
420	425	430

Arg Gly Ser Ser Leu Tyr Arg Leu Ser Arg Asp Ser Asn Ser Leu Pro
435 440 445

Ser Val Thr Asp Leu Pro Glu Met Asp Ser Thr Thr Pro Val Asn Glu
450 455 460

Ile Phe Leu Asp Gly Gln Pro Gln His Lys Ser Gly Ser Val Lys Gly
465 470 475 480

Gly His Arg Lys Lys Gln Glu Ser Ile Ser Asp Ala Gln Arg Ile Gln
485 490 495

His Ser Asn Ser Tyr Ile Thr Thr Pro Ser Ser Ser Leu Val Thr Pro
500 505 510

Pro Tyr Tyr Met Thr Gly Tyr Thr Leu Pro Ser Ser Ala Ser Ala Ser
515 520 525

Ser Thr Pro Asn Val Leu Glu Thr His Asn Met Asn Phe Val Pro Ser
530 535 540

Thr Ser Thr Val Thr Ser Tyr Arg Pro Ser Ser Asn Phe Ser Ser Phe
545 550 555 560

Asp Lys Glu Tyr Ser Asn Glu Asn Asp Ala Ser Gly Glu Phe Ser Ala
565 570 575

Phe Asn Thr Pro Met Glu Asn Ile Pro Ala Leu Lys Gly Ile Pro Arg
580 585 590

Ser Thr Leu Glu Glu Asn Glu Glu Glu Asp Val Leu Val Gln Asp Ile

535 600 605

Pro Asn Thr Ala His Phe Gln Arg Arg Asp Ile Met Gly Met Asp Thr
610 615 620

His Arg Lys Asp Asp Ser Leu Asp Phe Asn Ser Leu Met Pro His Gly
625 630 635 640

Ser Thr Thr Ser Ser Ser Ile Val Asp Ser Val Met Thr Asn Ser Ile
645 650 655

Ser Thr Thr Thr Ser Asn Ala Thr Gly Asn Tyr Phe Gln Asp Gln Asp
660 665 670

Lys Tyr Thr Leu Val Asn Thr Gly Leu Gly Leu Ser Asp Ala Asn Leu
675 680 685

Asp His Phe Ile Arg Ser Gln Thr Lys His Ala Ser Arg Ser Glu Ser
690 695 700

Asn Asn Asn Thr Gly Asn Arg Val Ser Tyr Ser Gly Ser Thr Pro Asn
705 710 715 720

Asn Val Asp Thr Thr Lys Thr Asn Leu Gln Val Tyr Thr Glu Phe Asp
725 730 735

Phe Glu Asn Pro Glu Ser Phe Phe His Glu Gln Ser Lys Leu Leu Gly
740 745 750

Glu Met Gly His Ser Asn Asn Asn Ser Asn Ser Ala Ile Asn Met Asn
755 760 765

Glu Pro Tyr Ser Ala Asp Thr Tyr Ile Gly Asn Ile Ser Pro Asp Thr
 770 775 780

Ser Ala Thr Val Ser Leu Gly Asp Leu Met Gly Ser Asn Val Ser Asn
 785 790 795 800

Asn Ser Glu Arg Asn Phe Tyr Asp Gly His Thr Phe Val Pro Gln Tyr
 805 810 815

Glu Ala Asn Ser Ser Val Glu Asn Ser Asn Asn Gln Asn Ala Ala Pro
 820 825 830

Ile Ala Asn Asn Asp Ile Asp Asn Asn Leu Glu Ser Phe Tyr Phe Asp
 835 840 845

Asn Ser Asn
 850

<210> 44
 <211> 1575
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
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 Met Ser Glu Arg Ser Ser Gln His Ile Val Gly Ile His Tyr Ala Val
 1 5 10 15
 gga cct aag att ggc gaa ggg tct ttc gga gta ata ttt gag gga gag 96

110/762

Gly Pro Lys Ile Gly Glu Gly Ser Phe Gly Val Ile Phe Glu Gly Glu	
20 25 30	
aac att att cat ccc cgt caa gag cag acc ggt agc aag aag gac tct	144
Asn Ile Leu His Ser Cys Gln Ala Gln Thr Gly Ser Lys Arg Asp Ser	
35 40 45	
agt ata ata atg gag aac gag cca gtc gca att aaa ttc gaa ccg cga	192
Ser Ile Ile Met Ala Asn Gln Pro Val Ala Ile Lys Phe Glu Pro Arg	
50 55 60	
cat tcg gac gca ccc cag ttg cgt gac gca ttt aga gcc tat agg ata	240
His Ser Asp Ala Pro Gln Leu Arg Asp Gln Phe Arg Ala Tyr Arg Ile	
65 70 75 80	
ttg aat ggc tgc gtt gga att ccc cca gcc tat tat ttt ggt caa gaa	288
Leu Asn Gly Cys Val Gly Ile Pro His Ala Tyr Tyr Phe Gly Gln Glu	
85 90 95	
ggt atg cac aac atc ttg att atc gat cta cta ggg cca tca ttg gaa	336
Gly Met His Asn Ile Leu Ile Ile Asp Leu Leu Gly Pro Ser Leu Glu	
100 105 110	
gat ctc ttc gag tgg tgt ggt aga aaa ttt cca gly aaa aca acc tgt	384
Asp Leu Phe Glu Trp Cys Gly Arg Lys Phe Ser Val Tyr Thr Thr Cys	
115 120 125	
atg gct gcc aag cca atg att gat aga gtt aga gca att cat gat cac	432
Met Val Ala Lys Gln Met Ile Asp Arg Val Arg Ala Ile His Asp His	
130 135 140	
gac tta atc tat cgc gat att aaa ccc gat aac ttt tca att tct caa	480
Asp Leu Ile Tyr Arg Asp Ile Lys Pro Asp Asn Phe Leu Ile Ser Gln	
145 150 155 160	
tat caa aga att tca cct gaa gga aaa gtc att aaa tca tgt gcc tcc	528
Tyr Gln Arg Ile Ser Pro Glu Gly Lys Val Ile Tyr Ser Cys Ala Ser	
165 170 175	
tct tct aat aat gat ccc aat tta ata tac atg gtt gac tcc ggt atg	576
Ser Ser Asn Asn Asp Pro Asn Leu Ile Tyr Met Val Asp Phe Gly Met	
180 185 190	

gca aaa caa tat aga gat cca aga acg aaa caa cat ata cca tac cgt	624
Ala Lys Gln Tyr Arg Asp Pro Arg Thr Lys Gln His Ile Pro Tyr Arg	
195 200 205	
gaa cga aaa tca ttg agc ggt acc gcc aga tat atg tct att aat act	672
Glu Arg Lys Ser Leu Ser Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr	
210 215 220	
cat ttt gga aga gaa cag tca cgt agg gat gat tta gaa tgg cta ggt	720
His Phe Gly Arg Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly	
225 230 235 240	
cac gtt ttt ttt tat ttc ttg agg gga tcc ttg cca tgg caa ggt ttg	768
His Val Phe Phe Tyr Phe Leu Arg Gly Ser Leu Pro Thr Gln Gly Leu	
245 250 255	
aaa gca cca aac aac aaa ctg aag tat gaa aag att ggt atg act aaa	816
Lys Ala Pro Asn Asn Lys Leu Lys Tyr Glu Lys Ile Gly Met Thr Lys	
260 265 270	
cag aaa ttg aat cct gat cat ctt tta ttc aat aat gct att cct tac	864
Gln Lys Leu Asn Pro Asp Asp Leu Leu Leu Asn Asn Ala Ile Pro Tyr	
275 280 285	
cag ttt gcc aca tat tta aaa tat gca cgt tcc ttg aag ttc gac gaa	912
Gln Phe Ala Thr Tyr Leu Lys Tyr Ala Arg Ser Leu Lys Phe Asp Glu	
290 295 300	
gat ccg gat tat gac tat tta atc tgg tta atg gat gac gct ttg aga	960
Asp Pro Asp Tyr Asp Tyr Leu Ile Ser Leu Met Asp Asp Ala Leu Arg	
305 310 315 320	
tta aac gac tta aag gat gat gga cgc tat gac tgg atg gat ttg aat	1008
Leu Asn Asp Leu Lys Asp Asp Gly His Tyr Asp Trp Met Asp Leu Asn	
325 330 335	
ggt ggt aaa ggc tgg aat atc aag att aat aga aga gct aac ttg cat	1056
Gly Gly Lys Gly Trp Asn Ile Lys Ile Asn Arg Arg Ala Asn Leu His	
340 345 350	
ggt tac gga aat cca aat cca aga gtc aat ggc aat act gca aga aac	1104

Gly Tyr Gly Asn Pro Asn Pro Arg Val Asn Gly Asn Thr Ala Arg Asn	
355	360
aat glg aat acg aal loa ung aca cga aat aca acg cca gtt gca ada	1152
Asn Val Asn Thr Asn Ser Lys Thr Arg Asn Thr Thr Pro Val Ala Thr	
370	380
act aag caa caa gct caa aac agt tat aac aag gac aat tog aaa tcc	1200
Pro Lys Gln Gln Ala Gln Asn Ser Tyr Asn Lys Asp Asn Ser Lys Ser	
385	400
aga att tct tog aac cag cag agc ttt act aaa cca cca cgc ttc	1240
Arg Ile Ser Ser Asn Pro Gln Ser Phe Thr Lys Gln Gln His Val Leu	
405	415
aaa aaa atc gaa ccc aat agt aaa tat att cct gaa aca cct tcc aat	1296
Lys Lys Ile Glu Pro Asn Ser Lys Tyr Ile Pro Glu Thr His Ser Asn	
420	430
ctt caa cgg cca att aaa agt caa agt caa acg tac gac tcc atc agt	1344
Leu Gln Arg Pro Ile Lys Ser Gln Ser Gln Thr Tyr Asp Ser Ile Ser	
435	445
cct aca caa aat tca cca ttt gta cca tat tca agt cct aaa gct aac	1392
His Thr Gln Asn Ser Pro Phe Val Pro Tyr Ser Ser Ser Lys Ala Asn	
450	460
cct aaa aga agt aat aat gag cca aac tta cca aac cca tac aca aac	1440
Pro Lys Arg Ser Asn Asn Glu His Asn Leu Pro Asn His Tyr Thr Asn	
465	480
gll gca aat aag aat atc aat tat caa agt cca cga aat tac gaa caa	1488
Leu Ala Asn Lys Asn Ile Asn Tyr Gln Ser Gln Arg Asn Tyr Glu Gln	
485	495
gaa aat gat gct tat tct gat gac gag aat gat aca ttt tgt tct aaa	1536
Glu Asn Asp Ala Tyr Ser Asp Asp Glu Asn Asp Thr Phe Cys Ser Lys	
500	510
ata tac aaa tat tgt tgt tgc tgt ttt tgt tgc tgt tga	1575
Ile Tyr Lys Tyr Cys Cys Cys Cys Phe Cys Cys Cys	
515	520

<210> 45

<211> 524

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 45

Met Ser Gln Arg Ser Ser Gln His Ile Val Gly Ile His Tyr Ala Val
1 5 10 15

Gly Pro Lys Ile Gly Glu Gly Ser Phe Gly Val Ile Phe Glu Gly Glu
20 25 30

Asn Ile Leu His Ser Cys Gln Ala Gln Thr Gly Ser Lys Arg Asp Ser
35 40 45

Ser Ile Ile Met Ala Asn Glu Pro Val Ala Ile Lys Phe Glu Pro Arg
50 55 60

His Ser Asp Ala Pro Gln Leu Arg Asp Glu Phe Arg Ala Tyr Arg Ile
65 70 75 80

Leu Asn Gly Cys Val Gly Ile Pro His Ala Tyr Tyr Phe Gly Gln Glu
85 90 95

Gly Met His Asn Ile Leu Ile Ile Asp Leu Leu Gly Pro Ser Leu Glu
100 105 110

Asp Leu Phe Glu Trp Cys Gly Arg Lys Phe Ser Val Lys Thr Thr Cys
115 120 125

Met Val Ala Lys Gln Met Phe Asp Arg Val Arg Ala Ile His Asp His
130 135 140

Asp Leu Ile Tyr Arg Asp Ile Lys Pro Asp Asn Phe Leu Ile Ser Gln
145 150 155 160

Tyr Glu Arg Ile Ser Pro Glu Gly Lys Val Ile Lys Ser Cys Ala Ser
165 170 175

Ser Ser Asn Asn Asp Pro Asn Leu Ile Tyr Met Val Asp Phe Gly Met
180 185 190

Ala Lys Gln Tyr Arg Asp Pro Arg Thr Lys Cln His Ile Pro Tyr Arg
195 200 205

Glu Arg Lys Ser Leu Ser Gly Thr Ala Arg Tyr Met Ser Ile Asn Thr
210 215 220

His Phe Gly Arg Glu Gln Ser Arg Arg Asp Asp Leu Glu Ser Leu Gly
225 230 235 240

His Val Phe Phe Tyr Phe Leu Arg Gly Ser Leu Pro Trp Gln Gly Leu
245 250 255

Lys Ala Pro Asn Asn Lys Leu Lys Tyr Glu Lys Ile Gly Met Thr Lys
260 265 270

Gln Lys Leu Asn Pro Asp Asp Leu Leu Leu Asn Asn Ala Ile Pro Tyr
275 280 285

Gln Phe Ala Thr Tyr Leu Lys Tyr Ala Arg Ser Leu Lys Phe Asp Glu

290 295 300
Asp Pro Asp Tyr Asp Tyr Leu Ile Ser Leu Met Asp Asp Ala Leu Arg
305 310 315 320
Leu Asn Asp Leu Lys Asp Asp Gly His Tyr Asp Trp Met Asp Leu Asn
325 330 335
Gly Gly Lys Gly Trp Asn Ile Lys Ile Asn Arg Arg Ala Asn Leu His
340 345 350
Gly Tyr Gly Asn Pro Asn Pro Arg Val Asn Gly Asn Thr Ala Arg Asn
355 360 365
Asn Val Asn Thr Asn Ser Lys Thr Arg Asn Thr Thr Pro Val Ala Thr
370 375 380
Pro Lys Gln Gln Ala Gln Asn Ser Tyr Asn Lys Asp Asn Ser Lys Ser
385 390 395 400
Arg Ile Ser Ser Asn Pro Gln Ser Phe Thr Lys Gln Gln His Val Leu
405 410 415
Lys Lys Ile Glu Pro Asn Ser Lys Tyr Ile Pro Glu Thr His Ser Asn
420 425 430
Leu Gln Arg Pro Ile Lys Ser Gln Ser Gln Thr Tyr Asp Ser Ile Ser
435 440 445
His Thr Gln Asn Ser Pro Phe Val Pro Tyr Ser Ser Ser Lys Ala Asn
450 455 460

Pro Lys Arg Ser Asn Asn Glu His Asn Leu Pro Asn His Tyr Thr Asn
465 470 475 480

Leu Ala Asn Lys Asn Ile Asn Tyr Gln Ser Gln Arg Asn Tyr Glu Gln
485 490 495

Glu Asn Asp Ala Tyr Ser Asp Asp Gln Asn Asp Thr Phe Cys Ser Lys
500 505 510

Ile Tyr Lys Tyr Cys Cys Cys Cys Phe Cys Cys Cys
515 520

<210> 48

<211> 1125

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1125)

<400> 46

atg agg ata cag tgg ctt att gtt tta ttt aat gtt gcc atc atc gca 48
Met Arg Ile Gln Ser Leu Phe Val Leu Phe Asn Val Ala Ile Ile Ala
1 5 10 15

tgg tca tat cca tat gag cct tta agg gtt tta caa gta gga gag aat 96
Tyr Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
20 25 30

gag gta atg gag gtt ccc gaa tca gaa aag cta aac tta cga aga aga 144
Glu Val Met Glu Val Pro Glu Ser Glu Lys Leu Asn Leu Arg Arg Arg
35 40 45

ggg gtc aac ttc ttt gat gtg ccc aac cgc act tct ttc tta cct ttc 192

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Gly Val Lys Phe Phe Asp Val Thr Lys His Thr Ser Phe Leu Pro Phe	
50 55 60	
ttt aac aag gag gaa gag cca aca gta cca acg tat aac tat cct cct	240
Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro	
65 70 75 80	
gag ata tcg aac aaa gaa gta gtg gat gat tcg att aag aat ata gac	288
Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp	
85 90 95	
aag ggc tct atc cac aag aac tly gca aag ttt aca agt ttt tac aac	316
Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr	
100 105 110	
cgt tac tac aag tcc gat cac ggc ttt gaa tct ggc gag tgg tta gct	384
Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Trp Leu Ala	
115 120 125	
gca acc atc gct aat att aca aca gct att ccg caa gat acg tly aat	432
Ala Thr Ile Ala Asn Ile Thr Lys Asp Ile Pro Glu Asp Thr Leu Thr	
130 135 140	
att gaa cat ttt gat cac aca gaa tgg aag caa tat tca att ata gtc	480
Ile Glu His Phe Asp His Lys Glu Trp Lys Glu Tyr Ser Ile Ile Val	
145 150 155 160	
cgt gtc acg gga tct acc aag cca gaa gat att ata ata att ggt tcc	528
Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser	
165 170 175	
cat caa gat tct atc aat ctg cta ctg cca tcc ata atg gca gct cca	576
His Glu Asp Ser Ile Asn Ileu Leu Leu Pro Ser Ile Met Ala Ala Pro	
180 185 190	
ggc gag gac gac aat ggg tca ggc acg gtg acc aat atg gag gct ctc	624
Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu	
195 200 205	
aga tca tat acg gaa aat ttt ttg aag aga gga ttt aga cct aac aac	672
Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Asn Asn	
210 215 220	

76A

316

၉၆၁

912

460

002

1055

1128

1125

ggg tca tgg tcc gct tgg taa
Gly Ser Trp Ser Ala Trp
370

<210> 47

<211> 374

<212> PRT

<213> Saccharomyces cerevisiae

<400> 47

Met Arg Ile Gln Ser Leu Phe Val Leu Phe Asn Val Ala Ile Ile Ala
1 5 10 15

Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
20 25 30

Glu Val Met Glu Val Pro Glu Ser Glu Lys Leu Asn Leu Arg Arg Arg
35 40 45

Gly Val Lys Phe Phe Asp Val Thr Lys His Thr Ser Phe Leu Pro Phe
50 55 60

Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro
65 70 75 80

Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp
85 90 95

Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr
100 105 110

Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Trp Leu Ala
115 120 125

Ala Thr Ile Ala Asn Ile Thr Lys Asp Ile Pro Gln Asp Thr Leu Thr
130 135 140

Ile Glu His Phe Asp His Lys Glu Trp Lys Glu Tyr Ser Ile Ile Val
145 150 155 160

Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser
165 170 175

His Glu Asp Ser Ile Asn Leu Leu Asn Pro Ser Ile Met Ala Ala Pro
180 185 190

Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu
195 200 205

Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Ser Asn
210 215 220

Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Leu Gly
225 230 235 240

Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Glu Lys Lys His Val Arg
245 250 255

Ala Met Leu Gln Gln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp
260 265 270

Glu His Val Gly Ile Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp
275 280 285

Phe Ile Lys Leu Ile Ile Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp
290 295 300

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Thr Gln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn
 305 310 315 320

Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn
 325 330 335

Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala
 340 345 350

His Met Ala Glu His Thr Lys Ile Val Leu Gly Val Ile Ile Glu Leu
 355 360 365

Gly Ser Trp Ser Ala Trp
 370

<210> 48

<211> 1530

<212> DNA

<213> *Saccharomyces cerevisiae*

<320>

<321> CDS

<322> (1)..(1530)

<400> 48

atg atc gct ttg aag ccc aat gct gtt cga acc ttc cca caa gtg cag 48
 Met Ile Ala Leu Lys Pro Asn Ala Val Arg Thr Phe Arg Gln Val Gln
 1 5 10 15

cat tgc agc ttt cgc att tgt cgg tat caa tct acg aag tca aat aag 96
 His Cys Ser Phe Arg Ile Cys Arg Tyr Gln Ser Thr Lys Ser Asn Lys
 20 25 30

tgt ctg acg ccc ttg caa gag tac gac aga ctg gtg aag ttg ggg aag 144
 Cys Leu Thr Pro Leu Gln Glu Tyr Asp Arg Leu Val Lys Leu Gly Lys
 35 40 45

cta cgg gat gat aca tat cag cgt ggt acb atc tct tcc tta ggg gat	192
Leu Arg Asp Asp Thr Tyr Gln Arg Gly Ile Ile Ser Ser Leu Gly Asp	
50 55 60	
ttg tat gat tca ctg gtt aau tat gta cct ccg gtt gtc aag aca ccc	240
Leu Tyr Asp Ser Leu Val Lys Tyr Val Pro Pro Val Val Lys Thr Pro	
65 70 75 80	
aat gct gtc gac caa gtt ggc cgt tgg ctg aat ggt ctt aaa tcc gta	288
Asn Ala Val Asp Gln Val Gly Gly Trp Leu Asn Gly Leu Lys Ser Val	
85 90 95	
ttt agc cgt ggc aaa cct aag aac att ggg gag tat gtc gat gta tcc	336
Phe Ser Arg Gly Lys Pro Lys Asn Ile Gly Ala Tyr Val Asp Val Ser	
100 105 110	
aaa att ggt aac tcg ata cct cga gga gtt tcc cta tat gga gat gtt	384
Lys Ile Gly Asn Ser Ile Pro Arg Gly Val Tyr Leu Tyr Gly Asp Val	
115 120 125	
ggc tgc gga aag aca atg ttg atg gac ctt ttt tat act aca att ccc	432
Gly Cys Gly Lys Thr Met Leu Met Asp Leu Phe Tyr Thr Thr Ile Pro	
130 135 140	
act cat tta aca aac cag cga ata cat ttt cac cag ttt arg caa tat	480
Asn His Leu Thr Lys Lys Arg Ile His Phe His Gln Phe Met Gln Tyr	
145 150 155 160	
gtt cac aaa agg tcg cat gaa att gtt aga gag cca aat ttg aaa gaa	528
Val His Lys Arg Ser His Glu Ile Val Arg Glu Gln Asn Leu Lys Glu	
165 170 175	
cta ggt gat gca aaa cga aaa gag atc gat acg gtt cca ttt ttg gcc	576
Leu Gly Asp Ala Lys Gly Lys Glu Ile Asp Thr Val Pro Phe Leu Ala	
180 185 190	
gca gag att gca aat aat tcg cat gtt ctt tgt ttt cac gag ttt caa	624
Ala Glu Ile Ala Asn Asn Ser His Val Leu Cys Phe Asp Glu Phe Gln	
195 200 205	
gtc act gaa gtg gca gat gaa atg ata ttg aga agg ctg atg act gcc	672

Val Thr Asp Val Ala Asp Ala Met Ile Leu Arg Arg Leu Met Thr Ala	
210 215 220	
tta cta tcc gat gat tat ggt gtc gta ctt ttc gca acc tgg aat aga	720
Leu Leu Ser Asp Asp Tyr Gly Val Val Leu Phe Ala Thr Ser Asn Arg	
225 230 235 240	
cat cca gat gag tgg tat atc aac ggt gtt caa aga caa tca ttt att	768
His Pro Asp Glu Leu Tyr Ile Asn Gly Val Gln Arg Gln Ser Phe Ile	
245 250 255	
cct tgt att gaa cgg ata aag cat aga act aag gtt atc ttc ttg aat	816
Pro Cys Ile Glu Leu Ile Lys His Arg Thr Lys Val Ile Phe Leu Asn	
260 265 270	
tgg cca aca gat tac cgt aag att cca aga cct gtc tcc tca gtt tac	864
Ser Pro Thr Asp Tyr Arg Lys Ile Pro Arg Pro Val Ser Ser Val Tyr	
275 280 285	
tat ttc cca tcc gat acg agc ata aaa tac gca tca aag gaa tgt aaa	912
Tyr Phe Pro Ser Asp Thr Ser Ile Lys Tyr Ala Ser Lys Glu Cys Lys	
290 295 300	
acc cgt cga gaa act cat att aag gaa tgg tat aac tat ttc gca cag	960
Thr Arg Arg Glu Thr His Ile Lys Glu Trp Tyr Asn Tyr Phe Ala Glu	
305 310 315 320	
ggt tcc cac acc gat gat tcc act gat tca cac aag gtc cat aag aca	1008
Ala Ser His Thr Asp Asp Ser Thr Asp Ser His Thr Val His Lys Thr	
325 330 335	
ttt tac gat tat cca tta act att tgg ggg aga gag ttc aaa gtc cct	1056
Phe Tyr Asp Tyr Pro Leu Thr Ile Trp Gly Arg Glu Phe Lys Val Pro	
340 345 350	
aag tgt acc cca cct cga gtc ggc cag ttt act ttc aag cag ttg tgt	1104
Lys Cys Thr Pro Pro Arg Val Ala Gln Phe Thr Phe Lys Gln Leu Cys	
355 360 365	
ggc gag cct ttg gcc gca gga gat tac ttg acg ttg gca aaa aat ttt	1152
Gly Glu Pro Leu Ala Ala Gly Asp Tyr Leu Thr Leu Ala Lys Asn Phe	
370 375 380	

gaa gaa ttt ata gtg acc gat att oaa tac ttg taa att tac gtt ogt 1200
 Glu Ala Phe Ile Val Thr Asp Ile Pro Tyr Leu Ser Ile Tyr Val Arg
 395 390 395 400

gat gaa gtg aga aga ttt att aca ttt tta gat gct gta tat gac agt 1248
 Asp Glu Val Arg Arg Phe Ile Thr Phe Leu Asp Ala Val Tyr Asp Ser
 405 410 415

ggc ggg aaa ctg gac act acg ggt gca gcg gac ttt tct taa ctg ttt 1296
 Gly Gly Lys Leu Ala Thr Thr Gly Ala Ala Asp Phe Ser Ser Leu Phe
 420 425 430

gtg gaa cct gaa cag ata ctt aat gat ttt gag tta cgc oaa aca acc 1344
 Val Glu Pro Glu Gln Ile Leu Asn Asp Phe Glu Leu Arg Pro Thr Thr
 435 440 445

aaa gaa cct gat agc gtc gat act ggt atg gla gat gag atg gtt gag 1392
 Lys Glu Pro Asp Ser Val Asp Thr Gly Met Val Asp Glu Met Val Glu
 450 455 460

caa caa ggt ttt tog aca gag att gac aag aca tog cag atg ttt gct 1440
 Lys His Gly Phe Ser Lys Gln Ile Ala Lys Lys Ser Gln Met Phe Ala
 465 470 475 480

ctt gat gaa gaa aga ttt gac ttt gac ogt gac tta agc agg ctg taa 1488
 Leu Asp Glu Glu Arg Phe Ala Phe Ala Arg Ala Leu Ser Arg Leu Ser
 485 490 495

cag atg agc taa aac gat tgg gtt act aag cct oaa taa taa 1530
 Gln Met Ser Ser Thr Asp Trp Val Thr Lys Pro Thr Tyr
 500 505

<210> 49

<211> 509

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 49

Met Ile Ala Leu Lys Pro Asn Ala Val Arg Thr Phe Arg Gln Val Gln

1				5						10					15				
His	Cys	Ser	Phe	Arg	Ile	Cys	Arg	Tyr	Gln	Ser	Thr	Lys	Ser	Asn	Lys				
			20					25						30					
Cys	Leu	Thr	Pro	Leu	Gln	Glu	Tyr	Asp	Arg	Leu	Val	Lys	Leu	Gly	Lys				
		35					40						45						
Leu	Arg	Asp	Asp	Thr	Tyr	Gln	Arg	Gly	Ile	Ile	Ser	Ser	Leu	Gly	Asp				
	50					55						60							
Leu	Tyr	Asp	Ser	Leu	Val	Lys	Lys	Val	Pro	Pro	Val	Val	Lys	Thr	Pro				
65					70					75					80				
Asn	Ala	Val	Asp	Gln	Val	Gly	Gly	Trp	Leu	Asn	Gly	Leu	Lys	Ser	Val				
			85					90						95					
Phe	Ser	Arg	Gly	Lys	Pro	Lys	Asn	Ile	Gly	Ala	Tyr	Val	Asp	Val	Ser				
			100					105						110					
Lys	Ile	Gly	Asn	Ser	Ile	Pro	Arg	Gly	Val	Tyr	Leu	Tyr	Gly	Asp	Val				
		115					120						125						
Gly	Cys	Gly	Lys	Thr	Met	Leu	Met	Asp	Leu	Phe	Tyr	Thr	Thr	Ile	Pro				
		130				135						140							
Asn	His	Leu	Thr	Lys	Lys	Arg	Ile	His	Phe	His	Gln	Phe	Met	Gln	Tyr				
145					150					155					160				
Val	His	Lys	Arg	Ser	His	Gln	Ile	Val	Arg	Glu	Gln	Asn	Leu	Lys	Gln				
					165				170						175				

Leu Gly Asp Ala Lys Gly Lys Glu Ile Asp Thr Val Pro Phe Leu Ala
180 185 190

Ala Glu Ile Ala Asn Asn Ser His Val Leu Cys Phe Asp Glu Phe Glu
195 200 205

Val Thr Asp Val Ala Asp Ala Met Ile Leu Arg Arg Leu Met Thr Ala
210 215 220

Leu Leu Ser Asp Asp Tyr Gly Val Val Leu Phe Ala Thr Ser Asn Arg
225 230 235 240

His Pro Asp Glu Leu Tyr Ile Asn Gly Val Glu Arg Glu Ser Phe Ile
245 250 255

Pro Cys Ile Glu Leu Ile Lys His Arg Thr Lys Val Ile Phe Leu Asn
260 265 270

Ser Pro Thr Asp Tyr Arg Lys Ile Pro Arg Pro Val Ser Ser Val Tyr
275 280 285

Tyr Phe Pro Ser Asp Thr Ser Ile Lys Tyr Ala Ser Lys Glu Cys Lys
290 295 300

Thr Arg Arg Glu Thr His Ile Lys Glu Trp Tyr Asn Tyr Phe Ala Glu
305 310 315 320

Ala Ser His Thr Asp Asp Ser Thr Asp Ser His Thr Val His Lys Thr
325 330 335

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Phe Tyr Asp Tyr Pro Leu Thr Ile Trp Gly Arg Glu Phe Lys Val Pro
340 345 350

Lys Cys Thr Pro Pro Arg Val Ala Glu Phe Thr Phe Lys Glu Leu Cys
355 360 365

Gly Glu Pro Leu Ala Ala Gly Asp Tyr Leu Thr Leu Ala Lys Asp Phe
370 375 380

Glu Ala Phe Ile Val Thr Asp Ile Pro Tyr Leu Ser Ile Tyr Val Arg
385 390 395 400

Asp Glu Val Arg Arg Phe Ile Thr Phe Leu Asp Ala Val Tyr Asp Ser
405 410 415

Gly Gly Lys Leu Ala Thr Thr Gly Ala Ala Asp Phe Ser Ser Leu Phe
420 425 430

Val Glu Pro Glu Glu Ile Leu Asn Asp Phe Glu Leu Arg Pro Thr Thr
435 440 445

Lys Glu Pro Asp Ser Val Asp Thr Gly Met Val Asp Glu Met Val Glu
450 455 460

Lys His Gly Phe Ser Lys Glu Ile Ala Lys Lys Ser Glu Met Phe Ala
465 470 475 480

Leu Asp Glu Glu Arg Phe Ala Phe Ala Arg Ala Leu Ser Arg Leu Ser
485 490 495

Glu Met Ser Ser Thr Asp Trp Val Thr Lys Pro Thr Tyr
500 505

<210> 50
 <211> 1710
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1710)

<400> 50
 atg aag gat tta aaa tta tgg aat ttc aaa ggc aaa ttt ata agc aga 48
 Met Lys Asp Leu Lys Leu Ser Asn Phe Lys Gly Lys Thr Ile Ser Arg
 1 5 10 15
 acc agt cac tgg gga ctt acg ggt aag aag ttg cgg tat ttc atc acc 96
 Thr Ser His Trp Gly Leu Thr Gly Lys Lys Leu Arg Tyr Phe Ile Thr
 20 25 30
 atc gca tct atg acg ggc ttc tcc ctg ttt gga tac gac cea ggg ttg 144
 Ile Ala Ser Met Thr Gly Phe Ser Leu Phe Gly Tyr Asp Gln Gly Leu
 35 40 45
 atg gca agt cca att act ggt aac cag ttc aac tat gaa ttt cca gca 192
 Met Ala Ser Leu Ile Thr Gly Lys Gln Phe Asn Tyr Glu Phe Pro Ala
 50 55 60
 acc aac gaa aat ggc gat cat gac aga cac gca act gta gtg cag ggc 240
 Thr Lys Glu Asn Gly Asp His Asp Arg His Ala Thr Val Val Gln Gly
 65 70 75 80
 gct aca acc tcc tgt tat gaa tta ggt tgt ttc gca ggt tct ata ttc 288
 Ala Thr Thr Ser Cys Tyr Glu Leu Gly Cys Phe Ala Gly Ser Leu Phe
 85 90 95
 gtt atg ttc tgc ggt gaa aga att ggt aga aaa cca tta atc ctg atg 336
 Val Met Phe Cys Gly Glu Arg Ile Gly Arg Lys Pro Leu Ile Leu Met
 100 105 110
 ggt tcc gta ata acc atc att ggt gcc gtt att tct aca tgc gca ttc 384

Gly Ser Val Ile Thr Ile Ile Gly Ala Val Ile Ser Thr Cys Ala Phe	
115 120 125	
cgf ggt tac tgg gca tta ggc cag ttt atc atc gga aga gtc gtc acc	432
Arg Gly Tyr Trp Ala Leu Gly Gln Phe Ile Ile Gly Arg Val Val Thr	
130 135 140	
ggf gtt gga aca ggg ttg aat aca tct act att ccc gtt tgg caa tca	480
Gly Val Gly Thr Gly Leu Asn Thr Ser Thr Ile Pro Val Trp Gln Ser	
145 150 155 160	
gaa atg tca aaa gct gaa aat aga ggg ttg ctg gtc aat tta gaa ggt	528
Glu Met Ser Lys Ala Glu Asn Arg Gly Leu Leu Val Asn Leu Glu Gly	
165 170 175	
tac aca aat gct ttt ggt act atg att gct tat tgg att gat ttt ggg	576
Ser Thr Ile Ala Phe Gly Thr Met Ile Ala Tyr Trp Ile Asp Phe Gly	
180 185 190	
ttg tct tat acc aac agt tct gtt cag tgg aga ttc ccc gtg tca atg	624
Leu Ser Tyr Thr Asn Ser Ser Val Gln Trp Arg Phe Pro Val Ser Met	
195 200 205	
caa atc ggt ttt gct ctc ttc atg ctt gct ttc atg att aca cta cct	672
Glu Ile Val Phe Ala Leu Phe Leu Leu Ala Phe Met Ile Lys Leu Pro	
210 215 220	
gaa tag cca cgt tgg ctg att tct caa agt cga aca gaa gaa gct cgt	720
Glu Ser Pro Arg Trp Leu Ile Ser Gln Ser Arg Thr Glu Glu Ala Arg	
225 230 235 240	
tac ttg gta gga aca cta gac gac ggc gat cca aat cat gag gaa gtt	768
Tyr Leu Val Gly Thr Leu Asp Asp Ala Asp Pro Asn Asp Glu Glu Val	
245 250 255	
ata aca gaa gtt gct atg ctt cac gat gct gtt aac agg acc aaa cac	816
Ile Thr Glu Val Ala Met Leu His Asp Ala Val Asn Arg Thr Lys His	
260 265 270	
gag aaa cat tca ctg tca agt ttg ttc tcc aga ggc agg tcc caa aat	864
Glu Lys His Ser Leu Ser Ser Leu Phe Ser Arg Gly Arg Ser Gln Asn	
275 280 285	

ott cag agg gct ttg att gca got tca acg caa ttt ttc cag caa ttt	912
Leu Gln Arg Ala Leu Ile Ala Ala Ser Thr Gln Phe Phe Gln Gln Phe	
290 295 300	
act ggt tgt aac gct gcc ata tac tac tct act gta tta ttc aac aaa	950
Thr Gly Cys Asn Ala Ala Ile Tyr Tyr Ser Thr Val Leu Phe Asn Lys	
305 310 315 320	
aca att aaa tta gac tat aga tta tca atg atc ata ggt ggg gtc ttc	1008
Thr Ile Lys Leu Asp Tyr Arg Leu Ser Met Ile Ile Gly Gly Val Phe	
325 330 335	
gca aac atc tac gcc tta tct act att ggt tca ttt ttt cta att gaa	1056
Ala Thr Ile Tyr Ala Leu Ser Thr Ile Gly Ser Phe Phe Leu Ile Gln	
340 345 350	
aag cta ggt aga cgt aag ctg ttt tta tta ggt gcc aca ggt caa gca	1104
Lys Leu Gly Arg Arg Lys Leu Phe Ser Leu Gly Ala Thr Gly Gln Ala	
355 360 365	
gtt tca ttc aca att aca ttt gcc tgc ttg gtc aac gaa aat aaa gaa	1152
Val Ser Phe Thr Ile Thr Phe Ala Cys Leu Val Lys Glu Asn Lys Glu	
370 375 380	
aac gcc aga ggt got gcc gtc gcc tta ttt ttg ttc att aca ttc ttt	1200
Asn Ala Arg Gly Ala Ala Val Gly Leu Phe Leu Phe Ile Thr Phe Phe	
385 390 395 400	
ggt ttg tct ttg cta tca tta cca tgg ata tac cca cca gaa att gcc	1248
Gly Leu Ser Leu Leu Ser Leu Pro Trp Ile Tyr Pro Pro Glu Ile Ala	
405 410 415	
tca atg aac gtt cgt gca tca aca aac got ttc tcc aca tgt act aat	1296
Ser Met Lys Val Arg Ala Ser Thr Asn Ala Phe Ser Thr Cys Thr Asn	
420 425 430	
tgg ttg tgt aac ttt gcg gtt gtc acg ttc aac cca ata ttt att gga	1344
Trp Leu Cys Asn Phe Ala Val Val Met Phe Thr Pro Ile Phe Ile Gly	
435 440 445	
cag tcc ggt tgg ggt tgc tac tta ttt ttt got gtt atg aat tat tta	1392

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Gln Ser Gly Trp Gly Cys Tyr Leu Phe Phe Ala Val Met Asn Tyr Leu
 450 455 460
 tac att cca gtt alc ttc ttt ttc lac ucl gaa auc gcc gga aga agt 1440
 Tyr Ile Pro Val Ile Phe Phe Phe Tyr Pro Glu Thr Ala Gly Arg Ser
 465 470 475 480
 ttg gaq gaa alc gac alc alc ttt gct aaa sca tac gag gat gcc act 1488
 Leu Glu Glu Ile Asp Ile Ile Phe Ala Lys Ala Tyr Glu Asp Gly Thr
 485 490 495
 can cca tgg aga gtt gct aac cat ttg ccc aag tta tcc cta caa gaa 1536
 Gln Pro Trp Arg Val Ala Asn His Leu Pro Lys Leu Ser Leu Glu Glu
 500 505 510
 qcc gaa gat cat gcc aat gca ttg ggc tct tat gac gac gaa atg gaa 1584
 Val Glu Asp His Ala Asn Ala Leu Gly Ser Tyr Asp Asp Glu Met Glu
 515 520 525
 aas gag gac ttt ggt gaa gat aga gta gaa gac acc tat aac caa att 1632
 Lys Glu Asp Phe Gly Glu Asp Arg Val Glu Asp Thr Tyr Asn Gln Ile
 530 535 540
 aac ggc gat aat tgg tct agt tct tca aac atc aaa aat gaa gat aca 1680
 Asn Gly Asp Asn Ser Ser Ser Ser Ser Asn Ile Lys Asn Glu Asp Thr
 545 550 555 560
 gtg aac gat aaa gca aat ttt gag ggt tga 1710
 Val Asn Asp Lys Ala Asn Phe Glu Gly
 565

<210> 51

<211> 569

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 51

Met Lys Asp Asn Lys Leu Ser Asn Phe Lys Gly Lys Phe Ile Ser Arg
 1 5 10 15

Thr Ser His Trp Gly Leu Thr Gly Lys Lys Leu Arg Tyr Phe Ile Thr
20 25 30

Ile Ala Ser Met Thr Gly Phe Ser Leu Phe Gly Tyr Asp Gln Gly Leu
35 40 45

Met Ala Ser Leu Ile Thr Gly Lys Gln Phe Asn Tyr Glu Phe Pro Ala
50 55 60

Thr Lys Glu Asn Gly Asp His Asp Arg His Ala Thr Val Val Gln Gly
65 70 75 80

Ala Thr Thr Ser Cys Tyr Glu Leu Gly Cys Phe Ala Gly Ser Leu Phe
85 90 95

Val Met Phe Cys Gly Glu Arg Ile Gly Arg Lys Pro Leu Ile Leu Met
100 105 110

Gly Ser Val Ile Thr Ile Ile Gly Ala Val Ile Ser Thr Cys Ala Phe
115 120 125

Arg Gly Tyr Trp Ala Leu Gly Gln Phe Ile Ile Gly Arg Val Val Thr
130 135 140

Gly Val Gly Thr Gly Leu Asn Thr Ser Thr Ile Pro Val Trp Gln Ser
145 150 155 160

Glu Met Ser Lys Ala Glu Asn Arg Gly Leu Leu Val Asn Leu Glu Gly
165 170 175

Ser Thr Phe Ala Phe Gly Thr Met Ile Ala Tyr Trp Ile Asp Phe Gly

	180	195	150
Leu Ser Tyr Thr Asn Ser Ser Val Gln Trp Arg Phe Pro Val Ser Met	195	200	205
Gln Ile Val Phe Ala Leu Phe Leu Leu Ala Phe Met Ile Lys Leu Pro	210	215	220
Glu Ser Pro Arg Trp Leu Ile Ser Gln Ser Arg Thr Glu Glu Ala Arg	225	230	235
			240
Tyr Leu Val Gly Thr Leu Asp Asp Ala Asp Pro Asn Asp Glu Glu Val	245	250	255
Ile Thr Glu Val Ala Met Leu His Asp Ala Val Asn Arg Thr Lys His	260	265	270
Glu Lys His Ser Leu Ser Ser Leu Phe Ser Arg Gly Arg Ser Gln Asn	275	280	285
Leu Gln Arg Ala Leu Ile Ala Ala Ser Thr Gln Phe Phe Gln Gln Phe	290	295	300
Met Gly Cys Asn Ala Ala Ile Tyr Tyr Ser Thr Val Leu Phe Asn Lys	305	310	315
			320
Thr Ile Lys Leu Asp Tyr Arg Leu Ser Met Ile Ile Gly Gly Val Phe	325	330	335
Ala Thr Ile Tyr Ala Leu Ser Thr Ile Gly Ser Phe Phe Leu Ile Glu	340	345	350

Lys Leu Gly Arg Arg Lys Leu Phe Leu Leu Gly Ala Thr Gly Gln Ala
355 360 365

Val Ser Phe Thr Ile Thr Phe Ala Cys Leu Val Lys Glu Asn Lys Glu
370 375 380

Asn Ala Arg Gly Ala Ala Val Gly Leu Phe Leu Phe Ile Thr Phe Phe
385 390 395 400

Gly Leu Ser Leu Leu Ser Leu Pro Trp Ile Tyr Pro Pro Glu Ile Ala
405 410 415

Ser Met Lys Val Arg Ala Ser Thr Asn Ala Phe Ser Thr Cys Thr Asn
420 425 430

Trp Leu Cys Asn Phe Ala Val Val Met Phe Thr Pro Ile Phe Ile Gly
435 440 445

Gln Ser Gly Trp Gly Cys Tyr Leu Phe Phe Ala Val Met Asn Tyr Leu
450 455 460

Tyr Ile Pro Val Ile Phe Phe Phe Tyr Pro Glu Thr Ala Gly Arg Ser
465 470 475 480

Leu Glu Glu Ile Asp Ile Ile Phe Ala Lys Ala Tyr Glu Asp Gly Thr
485 490 495

Gln Pro Trp Arg Val Ala Asn His Leu Pro Lys Leu Ser Leu Gln Glu
500 505 510

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Val Glu Asp His Ala Asn Ala Leu Gly Ser Tyr Asp Asp Glu Met Glu
 515 520 525

Lys Glu Asp Phe Gly Glu Asp Arg Val Glu Asp Thr Tyr Asn Gln Ile
 530 535 540

Asn Gly Asp Asn Ser Ser Ser Ser Ser Asn Ile Lys Asn Glu Asp Thr
 545 550 555 560

Val Asn Asp Lys Ala Asn Phe Glu Gly
 565

<210> 52

<211> 432

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(132)

<400> 52

atg gag acc aat ttt tcc ttc gac tgg aat tta att gtt att atc att 48
 Met Glu Thr Asn Phe Ser Phe Asp Ser Asn Leu Ile Val Ile Ile Ile
 1 5 10 15

atc acg ttg tat gcc aca aca att att gct aaa aga ttt tta tct act 96
 Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
 20 25 30

cca aaa atg gta tcc cag gaa acc gtt gct cac gta aag gat ctg att 144
 Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
 35 40 45

ggc caa aag gaa gtg ttt gtt gca gaa aag acc tac tgc cct tac tgt 192
 Gly Glu Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys
 50 55 60

aaa gct act ttg tct acc atc ttc caa gaa ttg aac gtt ccc aaa tcc 240
 Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
 65 70 75 80

aag gcc att gtg ttg gaa tta gat gaa atg agc aat ggc tca gag att 285
 Lys Ala Leu Val Leu Glu Leu Asp Glu Met Ser Asn Gly Ser Glu Ile
 85 90 95

caa gar gct tta gaa gaa atc tgc ggc caa aaa act gta cct aac gta 330
 Gln Asp Ala Leu Glu Glu Ile Ser Gly Gln Lys Thr Val Pro Asn Val
 100 105 110

aac atc aat ggc aag cac att ggt ggc aac agc gat ttg gaa act ttg 384
 Tyr Ile Asn Gly Lys His Ile Gly Gly Asn Ser Asp Leu Glu Thr Leu
 115 120 125

aag aaa aat ggc aag tta gct gaa ata ttg aag ccc gta ttt caa tag 432
 Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val Phe Gln
 130 135 140

<210> 53

<211> 143

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 53

Met Glu Thr Asn Phe Ser Phe Asp Ser Asn Leu Ile Val Ile Phe Ile
 1 5 10 15

Ile Thr Leu Phe Ala Thr Arg Ile Ile Ala Lys Arg Phe Leu Ser Thr
 20 25 30

Pro Lys Met Val Ser Gln Glu Thr Val Ala His Val Lys Asp Leu Ile
 35 40 45

Gly Gln Lys Glu Val Phe Val Ala Ala Lys Thr Tyr Cys Pro Tyr Cys

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50 55 60
 Lys Ala Thr Leu Ser Thr Leu Phe Gln Glu Leu Asn Val Pro Lys Ser
 65 70 75 80
 Lys Ala Leu Val Leu Glu Leu Asp Glu Met Ser Asn Gly Ser Glu Ile
 85 90 95
 Gln Asp Ala Leu Glu Gln Ile Ser Gly Gln Lys Thr Val Pro Asn Val
 100 105 110
 Tyr Ile Asn Gly Lys His Ile Gly Gly Asn Ser Asp Leu Glu Thr Leu
 115 120 125
 Lys Lys Asn Gly Lys Leu Ala Glu Ile Leu Lys Pro Val Phe Gln
 130 135 140

<210> 54
 <211> 426
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(426)

<400> 54
 atg aaa tgt cac gag aaa cgg acc ctt gcc ttt ttg gcg acg gca ctt 48
 Met Lys Cys His Ala Lys Arg Thr Leu Ala Phe Leu Ala Thr Ala Leu
 1 5 10 15
 ccc cta tct gga aaa agc cga gca tgc acc cgt acc cca caa agc ttc 96
 Pro Leu Ser Gly Lys Ser Arg Ala Cys Thr Arg Thr Pro Gln Ser Phe
 20 25 30

get too egg goa gca gag nag ttt ctt ttt too oge tge tte 144
Ala Ser Gly Phe Arg Ala Ala Ala Pro Phe Leu Phe Ser Arg Cys Phe
35 40 45

gac att tgt att act cat tgc gaa ctt ttt cac ttg cca tat tgg ttc .192
Ala Leu Cys Ile Thr His Cys Ala Leu Phe His Leu Pro Tyr Ser Phe
30 55 60

acc ggt ttt tct llt tat ttc ttc gtc ttt ttt cgt ctt ttt ctt cnc 240
Thr Gly Phe Ser Phe Tyr Phe Phe Val Phe Phe Arg Leu Phe Leu His
65 70 75 80

tgg ata tac gct CCC tgu all tgu aat agu aca tat gtg tat ata tat 288
Tip Ile Tyr Ala Phe Cys Ile Cys Asn Ser Thr Tyr Val Tyr Ile Tyr
 35 90 95

aag caa gtg ttg agc ttg cct gtc aaa tcc tcc atg tgt cct tct cgt 326
Lys Glu Val Leu Ser Leu Pro Val Lys Ser Ser Met Cys Pro Ser Arg
100 105 110

cta tct tgt tct gtc tgg tat aga gta ala cll aca tae ata tac gta 364
 Leu Ser Cys Ser Val Trp Tyr Arg Val Ile Leu Thr Tyr Ile Tyr Val
 115 120 125

cat tgt ttc dgc tgg cta gtt ogt aac cac ctc ctt tcc tag 126
 His Cys Phe Arg Trp Leu Val Arg Asn His Leu Leu Ser
 130 135 140

<210> 55

<211> 141

<212> PRT

<213> Saccharomyces cerevisiae

<400> 55

Met Lys Cys His Ala Lys Arg Thr Leu Ala Phe Leu Ala Thr Ala Leu
1 5 10 15

Pro Leu Ser Gly Lysa Ser Arg Ala Cys Thr Arg Thr Pro Gln Ser Phe
20 25 30

Ala Ser Gly Phe Arg Ala Ala Ala Pro Phe Leu Phe Ser Arg Cys Phe
25 40 45

Ala Leu Cys Ile Thr His Cys Ala Leu Phe His Leu Pro Tyr Ser Phe
50 55 60

Thr Gly Phe Ser Phe Tyr Phe Phe Val Phe Phe Arg Leu Phe Leu His
65 70 75 80

Trp Ile Tyr Ala Phe Cys Ile Cys Asn Ser Thr Tyr Val Tyr Ile Tyr
85 90 95

Lys Gln Val Leu Ser Leu Pro Val Lys Ser Ser Met Cys Pro Ser Arg
100 105 110

Leu Ser Cys Ser Val Trp Tyr Arg Val Ile Leu Thr Tyr Ile Tyr Val
115 120 125

His Cys Phe Arg Trp Leu Val Arg Asn His Leu Leu Ser
130 135 140

<210> 56

<211> 1488

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1488)

<400> 56

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atg aaa act gat aga tta ctg att aac gct tcc ccg gag aca tgt acc	48
Met Lys Thr Asp Arg Leu Leu Ile Asn Ala Ser Pro Glu Thr Cys Thr	
1 5 10 15	
aag gga gat gct gag atg gat act atg gat act att gac aga atg aca	96
Lys Gly Asp Ala Glu Met Asp Thr Met Asp Thr Ile Asp Arg Met Thr	
20 25 30	
tca gtt aaa gtt tta cgg gaa ggc aag gta tta agc aac ttc gaa gaa	144
Ser Val Lys Val Leu Ala Gly Gly Lys Val Leu Ser Asn Phe Glu Glu	
35 40 45	
cgg ggc tta atg agg tgc ggt tat cat gat gca aaa aac lyy gtc aga	192
Pro Gly Leu Met Arg Cys Gly Tyr His Asp Ala Lys Asn Trp Val Arg	
50 55 60	
aga tta ccg agc gaa aca att gtc ggt gag gac acg agt aat tta tac	240
Arg Leu Ser Ser Glu Thr Ile Val Gly Glu Asp Thr Ser Asn Leu Tyr	
65 70 75 80	
cca ttt tat gtt gat act gca tac gat gta agg cgt ttg aga aag gat	288
Pro Phe Tyr Val Asp Thr Ala Tyr Asp Val Arg Arg Leu Arg Lys Asp	
85 90 95	
att ata aat gct aag gtt gac ttg cag gtt gaa aac ctg ata ata atc	336
Leu Ile Asn Ala Lys Val Asp Leu Gln Val Glu Asn Leu Ile Ile Ile	
100 105 110	
tgc aat att aat gat att tcc act gta ttt ctc atg aga gaa gag gtg	384
Cys Asn Ile Asn Asp Ile Ser Thr Val Phe Leu Met Arg Gln Val Val	
115 120 125	
gaa cgg atc tta cgc aat ttc cat tca ata acc gln tat gta caa gat	432
Glu Trp Ile Leu Arg Asn Phe His Ser Ile Thr Val Tyr Val Gln Asp	
130 135 140	
att ttt aaa aag tca act cag ttt gct gtt ggt gac ctc tgc aaa gac	480
Ile Phe Lys Lys Ser Thr Gln Phe Ala Val Gly Asp Leu Cys Lys Asp	
145 150 155 160	
agu aat tgc agt aaa aac aga gta aag tat tgg tca aaa gaa ttt gtt	528
Ser Asn Cys Ser Tyr Asn Arg Val Lys Tyr Trp Ser Lys Glu Phe Val	

165	170	175	
aaa aaa cac gat tca ttc ttt gac ttg atg att acc cta ggg ggt gat			576
Lys Lys His Asp Ser Phe Phe Asp Leu Met Ile Thr Leu Gly Gly Asp			
180	185	190	
gga act gtc ctt ttt gct tca tct ata ttc acg aaa gat gtt ccg ccg			624
Gly Thr Val Leu Phe Ala Ser Ser Ile Phe Thr Lys Asp Val Pro Pro			
195	200	205	
att gtt cca ttt gcc ctt gga tca tta gga ttt cta acc aat ctt gaa			672
Ile Val Pro Phe Ala Leu Gly Ser Leu Gly Phe Leu Thr Asn Phe Glu			
210	215	220	
ttt caa aat ttc aaa gaa acg ttg aaa cat atc tta acc gat gag gtt			720
Phe Gln Asn Phe Lys Glu Thr Leu Lys His Ile Leu Thr Asp Glu Val			
225	230	235	240
cgt att aat tta cga atg agg ttg cca tgc aaa ctc tac cgt aga aat			768
Arg Ile Asn Leu Arg Met Arg Leu Gln Cys Lys Leu Tyr Arg Arg Asn			
245	250	255	
aaa cca gaa att gat gcc gca aat ggg aga aaa ata tgt tac atc gat			816
Iys Pro Glu Ile Asp Ala Ala Thr Gly Arg Lys Ile Cys Tyr Ile Asp			
260	265	270	
ttc atc tcc gaa cat cac gta ttg aac gaa gta acc ata gat aga ggt			864
Phe Ile Ser Glu His His Val Leu Asn Glu Val Thr Ile Asp Arg Gly			
275	280	285	
cca gct cct tgt tta tcc cta tta gaa ctc tat gga aac gac tca cta			912
Pro Ala Pro Cys Leu Ser Leu Leu Glu Leu Tyr Gly Asn Asp Ser Leu			
290	295	300	
atg acc aag gtt cag gga gat gga ttg att gtt gcc acg cct acg gga			960
Met Thr Lys Val Gln Gly Asp Gly Leu Ile Val Ala Thr Pro Thr Gly			
305	310	315	320
tcc acg gca tac tca ttg agt gca gga ggc tct tta ata tgg cca agc			1008
Ser Thr Ala Tyr Ser Leu Ser Ala Gly Gly Ser Leu Ile Ser Pro Ser			
325	330	335	

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gta aat gcc ata ggg gtg acg cct ata tgt cct cat act tgg agc ttt	1056
Val Asn Ala Ile Ala Val Thr Pro Ile Cys Pro His Thr Leu Ser Phe	
340 345 350	
agg ccc ata att tta cca gac agc atg gaa tta aaa gtt aga gta gat	1104
Arg Pro Ile Ile Leu Pro Asp Ser Met Glu Leu Lys Val Arg Val Asp	
355 360 365	
atg aac tca aga ggg acg tgg tgg gtg aat ttt gac gga aaa gat aga	1152
Met Asn Ser Arg Gly Thr Ser Trp Val Asn Phe Asp Gly Lys Asp Arg	
370 375 380	
gtt gac ttg aaa cag ggt gac tat gtt ggg ata act gca agc ccc tat	1200
Val Glu Leu Lys Gln Gly Asp Tyr Val Val Ile Thr Ala Ser Pro Tyr	
385 390 395 400	
tcg gta ccg act atc gag tca tct gcc agt gaa ttt ttt gaa act atc	1248
Ser Val Pro Thr Ile Glu Ser Ser Ala Ser Glu Phe Phe Glu Ser Ile	
405 410 415	
agt aaa aat ctt act tgg aat gac cgc gaa gag cag aag cca ttt gca	1296
Ser Lys Asn Leu Asn Trp Asn Asp arg Glu Glu Gln Lys Pro Phe Ala	
420 425 430	
cat att ctc tcg ccc aac aat caa gaa aca tat aga tta gcc tca tgg	1344
His Ile Leu Ser Pro Lys Asn Gln Glu Lys Tyr Arg Leu Asp Ser Ser	
435 440 445	
aaa aat gga aac gac acc ata agt aat ccc ctc gag agt tca tgc ata	1392
Lys Asn Gly Asn Asp Thr Ile Ser Asn Pro Leu Glu Ser Ser Cys Ile	
450 455 460	
agc tca gat gca caa gat gag gag agg aaa tcc gta acg gaa aca gaa	1440
Ser Ser Asp Ala Gln Asp Glu Glu Arg Lys Ser Val Thr Glu Thr Glu	
465 470 475 480	
aca gaa ala gtt gtt gaa cgg act cgt cag gcc cat ttt gca atc tta	1488
Thr Glu Ile Val Val Glu Arg Thr Arg Gln Ala His Phe Ala Ile	
485 490 495	

<211> 498

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 57

Met Lys Thr Asp Arg Leu Leu Ile Asn Ala Ser Pro Glu Thr Cys Thr
1 5 10 15

Lys Gly Asp Ala Glu Met Asp Thr Met Asp Thr Ile Asp Arg Met Thr
20 25 30

Ser Val Lys Val Leu Ala Glu Gly Lys Val Leu Ser Asn Phe Glu Glu
35 40 45

Pro Gly Leu Met Arg Cys Gly Tyr His Asp Ala Lys Asn Trp Val Arg
50 55 60

Arg Leu Ser Ser Glu Thr Ile Val Gly Glu Asp Thr Ser Asn Leu Tyr
65 70 75 80

Pro Phe Tyr Val Asp Thr Ala Tyr Asp Val Arg Arg Leu Arg Lys Asp
85 90 95

Leu Ile Asn Ala Lys Val Asp Leu Gln Val Glu Asn Leu Ile Ile Ile
100 105 110

Cys Asn Ile Asn Asp Ile Ser Thr Val Phe Leu Met Arg Glu Val Val
115 120 125

Glu Trp Ile Leu Arg Asn Phe His Ser Ile Thr Val Tyr Val Gln Asp
130 135 140

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Ile Phe Lys Lys Ser Thr Gln Phe Ala Val Gly Asp Leu Cys Lys Asp
 145 150 155 160

Ser Asn Cys Ser Lys Asn Arg Val Lys Tyr Trp Ser Lys Glu Phe Val
 165 170 175

Lys Lys His Asp Ser Phe Phe Asp Leu Met Ile Thr Leu Gly Gly Asp
 180 185 190

Gly Thr Val Leu Phe Ala Ser Ser Ile Phe Thr Lys Asp Val Pro Pro
 195 200 205

Ile Val Pro Phe Ala Leu Gly Ser Leu Gly Phe Leu Thr Asn Phe Glu
 210 215 220

Phe Gln Asn Phe Lys Glu Thr Leu Lys His Ile Leu Thr Asp Glu Val
 225 230 235 240

Arg Ile Asn Leu Arg Met Arg Leu Gln Cys Lys Leu Tyr Arg Arg Asn
 245 250 255

Lys Pro Glu Ile Asp Ala Ala Thr Gly Arg Lys Ile Cys Tyr Ile Asp
 260 265 270

Phe Ile Ser Glu His His Val Leu Asn Glu Val Thr Ile Asp Arg Gly
 275 280 285

Pro Ala Pro Cys Leu Ser Leu Leu Glu Leu Tyr Gly Asn Asp Ser Leu
 290 295 300

Met Thr Lys Val Gln Gly Asp Gly Leu Ile Val Ala Thr Pro Thr Gly
 305 310 315 320

Ser Thr Ala Tyr Ser Leu Ser Ala Gly Gly Ser Leu Ile Ser Pro Ser
325 330 335

Val Asn Ala Ile Ala Val Thr Pro Ile Cys Pro His Thr Leu Ser Phe
340 345 350

Arg Pro Ile Ile Leu Pro Asp Ser Met Glu Leu Lys Val Arg Val Asp
355 360 365

Met Asn Ser Arg Gly Thr Ser Trp Val Asn Phe Asp Gly Lys Asp Arg
370 375 380

Val Glu Leu Lys Gln Gly Asp Tyr Val Val Ile Thr Ala Ser Pro Tyr
385 390 395 400

Ser Val Pro Thr Ile Glu Ser Ser Ala Ser Glu Phe Phe Glu Ser Ile
405 410 415

Ser Lys Asn Leu Asn Trp Asn Asp Arg Glu Glu Gln Lys Pro Phe Ala
420 425 430

His Ile Leu Ser Pro Lys Asn Gln Glu Lys Tyr Arg Leu Asp Ser Ser
435 440 445

Lys Asn Gly Asn Asp Thr Ile Ser Asn Pro Leu Glu Ser Ser Cys Ile
450 455 460

Ser Ser Asp Ala Gln Asp Glu Glu Arg Lys Ser Val Thr Glu Thr Glu
465 470 475 480

Thr Glu Ile Val Val Glu Arg Thr Arg Gln Ala His Phe Ala Ile
 495 490 495

<210> 58

<211> 1125

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1125)

<400> 58

atg agg ata cag cag ctt ttt gtt tta tct aat gtt gcc atc atc gca 48
 Met Arg Ile Gln Ser Leu Phe Val Leu Phe Asn Val Ala Ile Ile Ala
 1 5 10 15

tgg tca tat cca tat gag cct tta agg gtt tta caa gta gga gag aa- 96
 Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
 20 25 30

gag gta atg gag gtt ccc gaa tca gaa aag cta aac tta cga aga aga 144
 Glu Val Met Glu Val Pro Gln Ser Glu Lys Leu Asn Leu Arg Arg Arg
 35 40 45

ggc gtc aaa ttc ttt gat gtc acc aaa cac act tct ttc tta ccc ttc 192
 Gly Val Lys Phe Phe Asp Val Thr Lys His Thr Ser Phe Leu Pro Phe
 50 55 60

ttt aac aag gag gaa gag cca aca gta cca acg tat aac tat cct cct 240
 Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro
 65 70 75 80

gag ata cag aac aca gaa gta gtc gat gat cag att aag aat ata gac 288
 Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp
 85 90 95

aag ggc tct atg cac aag aac ttg gca aag ttt aca aat tct tac acc 336
 Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr

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100	105	110	
cgt tac tac aag tcc gat cac ggc ttt gaa tct gcc gag tgg tta gct			384
Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Trp Leu Ala			
115	120	125	
gca act atc gct aat att aca aaa gat att ccc cca gat acg ttg act			432
Ala Thr Ile Ala Asn Ile Thr Lys Asp Ile Pro Gln Asp Thr Leu Thr			
130	135	140	
att gaa cat ttt gat cac aaa gaa tgg aag caa tat leu att ata gtc			480
Ile Glu His Phe Asp His Lys Glu Trp Lys Gln Tyr Ser Ile Ile Val			
145	150	155	160
cgt gtc acg gga tct act acg cca gaa gat att ata ata att ggt tct			528
Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser			
165	170	175	
cat caa gat tct atc aat ctg cta ctg cca tcc ata atg gca gct cca			576
His Gln Asp Ser Ile Asn Leu Leu Leu Pro Ser Ile Met Ala Ala Pro			
180	185	190	
ggc gcc gac cac aat ggc tca gcc acg gtg act aat atg gag gct ctg			624
Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu			
195	200	205	
aga tta tat acg gaa aat ttt ccc aag aga gga ttt aga tct aac aac			672
Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Asn Asn			
210	215	220	
act gtg gaa ttt cac ttt tac tcc gcc gaa gag ggg gga tgg ttg ggt			720
Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Leu Gly			
225	230	235	240
tct ctg gat gtt ttt aca gcc tat gcc aaa cag aaa aag cat gtg aga			768
Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Gln Lys Lys His Val Arg			
245	250	255	
gcc atg ctt cag caa gac atg acg gga tat gtt tct gat cca gaa gat			816
Ala Met Leu Gln Gln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp			
260	265	270	

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gaa cat gag ggg att gtc acc gac tac act act ccc gca tta act gat 864
 Glu His Val Gly Ile Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp
 275 280 285

ttt ata aaa cta att atc aac tct tat cta tcc att cct tac agg gat 912
 Phe Ile Lys Leu Ile Ile Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp
 290 295 300

aca caa tgt ggc tat gct tgc agc gat cat ggg agt gcc acc aga aac 960
 Thr Gln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn
 305 310 315 320

ggg ttt cca ggc tcc ttc gtg att gaa agt gag ttc aaa aag act aac 1008
 Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn
 325 330 335

aag tat att ccc agc acc atg gat act atg gac aga tta agt ctc gct 1056
 Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala
 340 345 350

cat atg gag gaa cac aca aaa act gta tta ggg gta atc att gaa ctc 1104
 His Met Ala Glu His Thr Lys Ile Val Leu Gly Val Ile Ile Glu Leu
 355 360 365

ggg tca tgg tcc gct tgg taa 1125
 Gly Ser Trp Ser Ala Trp
 370

<210> 59

<211> 374

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 59

Met Arg Ile Gln Ser Leu Phe Val Leu Phe Asn Val Ala Ile Ile Ala
 1 5 10 15

Trp Ser Tyr Pro Tyr Glu Pro Leu Arg Val Leu Gln Val Gly Glu Asn
 20 25 30

Glu Val Met Glu Val Pro Glu Ser Glc Lys Leu Asn Ien Arg Arg Arg
35 40 45

Gly Val Lys Phe Phe Asp Val Thr Lys His Thr Ser Phe Leu Pro Phe
50 55 60

Phe Asn Lys Glu Glu Glu Pro Thr Val Pro Thr Tyr Asn Tyr Pro Pro
65 70 75 80

Glu Ile Ser Asn Lys Glu Val Val Asp Asp Ser Ile Lys Asn Ile Asp
85 90 95

Lys Gly Ser Met His Lys Asn Leu Ala Lys Phe Thr Ser Phe Tyr Thr
100 105 110

Arg Tyr Tyr Lys Ser Asp His Gly Phe Glu Ser Ala Glu Trp Leu Ala
115 120 125

Ala Thr Ile Ala Asn Ile Thr Lys Asp Ile Pro Gln Asp Thr Leu Thr
130 135 140

Ile Glu His Phe Asp His Lys Glu Trp Lys Gln Tyr Ser Ile Ile Val
145 150 155 160

Arg Val Thr Gly Ser Thr Thr Pro Glu Asp Ile Ile Ile Ile Gly Ser
165 170 175

His Gln Asp Ser Ile Asn Leu Leu Leu Pro Ser Ile Met Ala Ala Pro
180 185 190

Gly Ala Asp Asp Asn Gly Ser Gly Thr Val Thr Asn Met Glu Ala Leu .
195 200 205

Arg Leu Tyr Thr Glu Asn Phe Leu Lys Arg Gly Phe Arg Pro Asn Asn
210 215 220

Thr Val Glu Phe His Phe Tyr Ser Ala Glu Glu Gly Gly Leu Leu Gly
225 230 235 240

Ser Leu Asp Val Phe Thr Ala Tyr Ala Lys Gln Lys Lys His Val Arg
245 250 255

Ala Met Leu Cln Cln Asp Met Thr Gly Tyr Val Ser Asp Pro Glu Asp
260 265 270

Glu His Val Gly Leu Val Thr Asp Tyr Thr Thr Pro Ala Leu Thr Asp
275 280 285

Phe Ile Tyr Leu Phe Ile Asn Ser Tyr Leu Ser Ile Pro Tyr Arg Asp
290 295 300

Thr Cln Cys Gly Tyr Ala Cys Ser Asp His Gly Ser Ala Thr Arg Asn
305 310 315 320

Gly Phe Pro Gly Ser Phe Val Ile Glu Ser Glu Phe Lys Lys Thr Asn
325 330 335

Lys Tyr Ile His Ser Thr Met Asp Thr Leu Asp Arg Leu Ser Leu Ala
340 345 350

His Met Ala Glu His Thr Lys Ile Val Leu Gly Val Ile Ile Glu Leu

355

360

365

Gly Ser Trp Ser Ala Trp

370

<210> 50

<211> 1470

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1470)

<400> 50

atg aca asa agt gat tta tta ttt gat aaa ttc aac gac aac cat gga 48

Met Thr Lys Ser Asp Leu Leu Phe Asp Lys Phe Asn Asp Lys His Gly

1 5 10 15

aag ttt cta gtt ttt ttt ggt acc ttt gta gat acc cct aaa tta gga 96

Lys Phe Leu Val Phe Phe Gly Thr Phe Val Asp Thr Pro Lys Leu Gly

20 25 30

gag atg aga atc aga gag aac aca tct gtt gga gtt ctc aac gga atc 144

Gln Leu Arg His Arg Glu Lys Thr Ser Val Gly Val Leu Asn Gly Ile

35 40 45

atc agg ttt gtg aac aga aat tca ctc gat cct gtc aac gat tgc tta 192

Ile Arg Phe Val Asn Arg Asn Ser Leu Asp Pro Val Lys Asp Cys Leu

50 55 60

gat cac gat agt agc tca tca cca gag gat gtc acg gtg gtt gac ata 240

Asp His Asp Ser Ser Leu Ser Pro Glu Asp Val Thr Val Val Asp His

65 70 75 80

att gga aca gac aag act cga aat aac agc ttt tat ttt cca ggt ttt 288

Ile Gly Lys Asp Lys Thr Arg Asn Asn Ser Phe Tyr Phe Pro Gly Phe

85 90 95

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gtt gac acg cat aac cat gtc tgg caa tat cca aat gtc ggc gta ttt	336
Val Asp Thr His Asn His Val Ser Gln Tyr Pro Asn Val Gly Val Phe	
100 105 110	
ggg aat tct acc ctg ctg gat tgg cta gag aag tat acc ttc ccc ata	384
Gly Asn Ser Thr Leu Leu Asp Trp Leu Glu Lys Tyr Thr Phe Pro Ile	
115 120 125	
gaa gcc gca cta gca aac gaa aat att gcc aga gaa gtt tac aat aag	432
Glu Ala Ala Leu Ala Asn Glu Asn Ile Ala Arg Gln Val Tyr Asn Lys	
130 135 140	
gta ata agt aag acg att tca cac ggt aca acg act gtg gct tac tat	480
Val Ile Ser Lys Thr Leu Ser His Gly Thr Thr Thr Val Ala Tyr Tyr	
145 150 155 160	
aat acc att gat ctc aag tcc act aag ctc ttg gct caa cta agc tcc	528
Asn Thr Ile Asp Leu Lys Ser Thr Lys Leu Leu Ala Gln Leu Ser Ser	
165 170 175	
tta ttg ggg cag cgt gtt ctt gtt gga aac gtg tgc atg gat acc aat	576
Leu Leu Gly Gln Arg Val Leu Val Gly Lys Val Cys Met Asp Thr Asn	
180 185 190	
cgt ccc gag tat tat att gaa gat act aaa act tcc ttt gaa agc act	624
Gly Pro Gln Tyr Tyr Ile Glu Asp Thr Lys Thr Ser Phe Gln Ser Thr	
195 200 205	
gtg aaa gtt gtt aag tac ata cgg gaa acc att tgt gat ccc ctc gta	672
Val Lys Val Val Lys Tyr Ile Arg Glu Thr Ile Cys Asp Pro Leu Val	
210 215 220	
aat cct ata gtg aca cca agg ttc ggg ccc tct tgt tct aga gaa cta	720
Asn Pro Ile Val Thr Pro Arg Phe Ala Pro Ser Cys Ser Arg Glu Leu	
225 230 235 240	
atg caa cag ttg tcc aag cta gtc aag gat gaa aac ata cac gtt caa	768
Met Gln Gln Leu Ser Lys Leu Val Lys Asp Glu Asn Ile His Val Gln	
245 250 255	
acc cac ttg tgg gaa aat aag gag gag ata cag tgg gtt caa gat tta	816
Thr His Leu Ser Glu Asn Lys Glu Gln Ile Gln Trp Val Gln Asp Leu	

260	265	270	
ttt ccc gaa tgt gag agc tat act gat gta tac gac aaa tat ggg ctg			964
Phe Pro Glu Cys Glu Ser Tyr Thr Asp Val Tyr Asp Lys Tyr Gly Leu			
275	280	285	
ctc aca gaa aaa aca gta ttg gaa cat tgt att cat cta aca gat gcc			912
Leu Thr Glu Lys Thr Val Leu Ala His Cys Ile His Leu Thr Asp Ala			
290	295	300	
gaa gcg cgt gtg att aaa cag cgt cgc tgt ggt ata tct cat tgt ccc			360
Glu Ala Arg Val Ile Lys Gln Arg Arg Cys Gly Ile Ser His Cys Pro			
305	310	315	320
att tcc aac tcc tcc ctg act tct gga gag tgt agg gtt cga tgg tgg			1008
Ile Ser Asn Ser Ser Leu Thr Ser Gly Gln Cys Arg Val Arg Trp Leu			
325	330	335	
ctg gac cag gcc ata aag gtt ggt cta gcc acc gac gtc tca gcc ggt			1056
Leu Asp Gln Gly Ile Lys Val Gly Leu Gly Thr Asp Val Ser Ala Gly			
340	345	350	
cat tcc tgt aac ata ctc acc acc gga agg cag gcc ttt gaa gtt tca			1104
His Ser Cys Ser Ile Leu Thr Thr Gly Arg Gln Ala Phe Ala Val Ser			
355	360	365	
agg cat ttg gca atg aga gaa act gat cat gca aaa ctt tca gtc tcc			1152
Arg His Leu Ala Met Arg Gln Thr Asp His Ala Lys Leu Ser Val Ser			
370	375	380	
gag tgc cta ttt ctt gct aca atg ggc gga gca cca gtc ttg cgt atg			1200
Glu Cys Leu Phe Leu Ala Thr Met Gly Gly Ala Gln Val Leu Arg Met			
385	390	395	400
gat gag acc ctg ggg act ttt gac gtc ggt aag cag ttt gac gct cca			1248
Asp Glu Thr Leu Gly Thr Phe Asp Val Gly Lys Gln Phe Asp Ala Gln			
405	410	415	
atg atc gat acc aat gct ccc ggc tca aac gag gat atg ttt cat tgg			1296
Met Ile Asp Thr Asn Ala Pro Gly Ser Asn Val Asp Met Phe His Trp			
420	425	430	

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cag cta aag gag aag gat caa atg caa gag caa gag cta gag caa ggg 1344
 Gln Leu Lys Glu Lys Asp Gln Met Gln Glu Gln Glu Gln Glu Gly
 435 440 445

caa gac cct tat aag aac caa cag atg ctt act aat gaa gac ata atc 1392
 Gln Asp Pro Tyr Lys Asn Pro Pro Leu Leu Thr Asn Glu Asp Ile Ile
 450 455 460

gca aaa tgg ttc ttc aac ggt gat gat cgc aac acc act aaa gtt tgg 1440
 Ala Lys Trp Phe Phe Asn Gly Asp Asp Arg Asn Thr Thr Lys Val Trp
 465 470 475 480

gta gcc ggc cag caa gtc taa cag att tag 1476
 Val Ala Gly Gln Gln Val Tyr Gln Ile
 485

<210> 51

<211> 489

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 51

Met Thr Lys Ser Asp Leu Leu Phe Asp Lys Phe Asn Asp Lys His Gly
 1 5 10 15

Lys Phe Leu Val Phe Phe Gly Thr Phe Val Asp Thr Pro Lys Leu Gly
 20 25 30

Glu Leu Arg Ile Arg Glu Lys Thr Ser Val Gly Val Leu Asn Gly Ile
 35 40 45

Ile Arg Phe Val Asn Arg Asn Ser Leu Asp Pro Val Lys Asp Cys Leu
 50 55 60

Asp His Asp Ser Ser Leu Ser Pro Glu Asp Val Thr Val Val Asp Ile
 65 70 75 80

Ile Gly Lys Asp Lys Thr Arg Asn Asn Ser Phe Tyr Phe Pro Gly Phe
85 90 95

Val Asp Thr His Asn His Val Ser Gln Tyr Pro Asn Val Gly Val Phe
100 105 110

Gly Asn Ser Thr Leu Leu Asp Trp Leu Glu Tyr Tyr Thr Phe Pro Ile
115 120 125

Glu Ala Ala Leu Ala Asn Glu Asn Ile Ala Arg Glu Val Tyr Asn Lys
130 135 140

Val Ile Ser Lys Thr Leu Ser His Gly Thr Thr Thr Val Ala Tyr Tyr
145 150 155 160

Asn Thr Ile Asp Leu Lys Ser Thr Lys Leu Leu Ala Gln Leu Ser Ser
165 170 175

Leu Leu Gly Glu Arg Val Leu Val Gly Tyr Val Cys Met Asp Thr Asn
180 185 190

Gly Pro Glu Tyr Tyr Ile Glu Asp Thr Lys Thr Ser Phe Glu Ser Thr
195 200 205

Val Lys Val Val Lys Tyr Ile Arg Glu Thr Ile Cys Asp Pro Leu Val
210 215 220

Asn Pro Ile Val Thr Pro Arg Phe Ala Pro Ser Cys Ser Arg Glu Leu
225 230 235 240

Met Gln Gln Leu Ser Lys Leu Val Lys Asp Glu Asn Ile His Val Gln
245 250 255

Thr His Leu Ser Glu Asn Lys Glu Glu Ile Gln Trp Val Gln Asp Leu
260 265 270

Phe Pro Glu Cys Glu Ser Tyr Thr Asp Val Tyr Asp Lys Tyr Gly Leu
275 280 285

Leu Thr Glu Lys Thr Val Leu Ala His Cys Phe His Leu Thr Asp Ala
290 295 300

Glu Ala Arg Val Ile Lys Gln Arg Arg Cys Gly Ile Ser His Cys Pro
305 310 315 320

Ile Ser Asn Ser Ser Leu Thr Ser Gly Glu Cys Arg Val Arg Trp Leu
325 330 335

Leu Asp Gln Gly Phe Lys Val Gly Leu Gly Thr Asp Val Ser Ala Gly
340 345 350

His Ser Cys Ser Ile Leu Thr Thr Gly Arg Gln Ala Phe Ala Val Ser
355 360 365

Arg His Leu Ala Met Arg Gln Thr Asp His Ala Lys Leu Ser Val Ser
370 375 380

Glu Cys Leu Phe Leu Ala Thr Met Gly Gly Ala Gln Val Leu Arg Met
385 390 395 400

Asp Gln Thr Leu Gly Thr Phe Asp Val Gly Lys Gln Phe Asp Ala Gln

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405

410

415

Met Ile Asp Thr Asn Ala Pro Gly Ser Asn Val Asp Met Phe His Trp
 420 425 430

Gln Asn Lys Glu Lys Asp Gln Met Gln Glu Gln Glu Gln Glu Gly
 435 440 445

Gln Asp Pro Tyr Lys Asn Pro Pro Leu Leu Thr Asn Glu Asp Ile Ile
 450 455 460

Ala Lys Trp Phe Phe Asn Gly Asp Asn Arg Asn Thr Thr Lys Val Trp
 465 470 475 480

Val Ala Gly Gln Gln Val Tyr Gln Ile
 485

<210> 62

<211> 4x1

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(441)

<400> 62

atg aaa ggc tca ccc att tet cca ttt agt aag acc tct att aat gct 40
 Met Lys Gly Ser Pro Ile Ser Cln Phe Ser Lys Thr Ser Ile Asn Ala
 1 5 10 15

ctt acc agg cct tgg aag aaa tac aga ggt gaa tta ttt tat ggg 96
 Leu Thr Arg Pro Trp Lys Lys Tyr Arg Asp Gly Glu Leu Phe Tyr Gly
 20 25 30

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tta tca aaa gtt ggg aat aag aga gtg cag ttg acc acg aag caa ggt 144
 Leu Ser Lys Val Gly Asn Lys Arg Val Pro Leu Thr Thr Lys Gln Gly
 35 40 45

aac aag acg atg tac aaa ggg aca aga ggt tca ggg att ggt aga cat 192
 Asn Lys Thr Met Tyr Lys Gly Thr Arg Ala Ser Gly Ile Gly Arg His
 50 55 60

aca aaa ttc ggt ggt tat gtg ata aac tgg aag aaa gtc aga acc tat 240
 Thr Lys Phe Gly Gly Tyr Val Ile Asn Trp Lys Lys Val Arg Thr Tyr
 65 70 75 80

gtr acc cca gat atg gtt aac ttc gaa tta aag ccc tac gtt aac gca 288
 Val Thr Pro Asp Met Val Asn Phe Glu Leu Tyr Pro Tyr Val Asn Ala
 85 90 95

cat gta cca cct cta aaa cac gaa ttt aaa gga ttt acg ggc ggc cca 336
 Asn Val Pro Pro Leu Lys His Glu Phe Lys Gly Phe Ser Gly Gly Pro
 100 105 110

tta gat cct cgt tta cag tta tta aag ata aaa gaa tac ata gta aac 384
 Leu Asp Pro Arg Leu Gln Leu Leu Lys Ile Lys Glu Tyr Ile Val Asn
 115 120 125

ggg agg gta cca agc gaa ggg gcc acc gac act tca tgt tat aag gag 432
 Gly Arg Val Gln Ser Glu Gly Ala Thr Asp Thr Ser Cys Tyr Lys Glu
 130 135 140

cgt aga taa 441
 Arg Gly
 145

<210> 63

<211> 146

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 63

Met Lys Gly Ser Pro Ile Ser Gln Phe Ser Lys Thr Ser Ile Asn Ala
 1 5 10 15

Leu Thr Arg Pro Trp Lys Lys Tyr Arg Asp Gly Glu Leu Phe Tyr Gly
 20 25 30

Leu Ser Lys Val Gly Asn Lys Arg Val Pro Leu Thr Thr Lys Gln Gly
 35 40 45

Asn Lys Thr Met Tyr Lys Gly Thr Arg Ala Ser Gly Ile Gly Arg His
 50 55 60

Thr Lys Phe Gly Gly Tyr Val Ile Asn Trp Lys Lys Val Arg Thr Tyr
 65 70 75 80

Val Thr Pro Asp Met Val Asn Phe Glu Leu Lys Pro Tyr Val Asn Ala
 85 90 95

Asn Val Pro Pro Leu Lys His Glu Phe Lys Gly Phe Ser Gly Gly Pro
 100 105 110

Leu Asp Pro Arg Leu Cln Leu Leu Lys Ile Lys Glu Tyr Ile Val Asn
 115 120 125

Gly Arg Val Gln Ser Glu Gly Ala Thr Asp Thr Ser Cys Tyr Lys Glu
 130 135 140

Arg Gly
 145

<210> 64

<211> 429

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (429)

<400> 64

atg gcg tat aat caa gaa gat agt aaa aga cta tca gac aag tat aag 48

Met Ala Tyr Asn Gln Glu Asp Ser Lys Arg Leu Ser Asp Lys Tyr Lys

1 5 10 15

aag gag gga cat ttt gac aag ttg aaa aga gaa ata ttg tct aac cca 96

Lys Glu Gly His Phe Asp Lys Ile Lys Arg Glu Ile Leu Ser Asn Pro

20 25 30

tgg aat aat aca gaa gag aat agt gaa tct ttt gaa caa gcg ctt cgg 144

Trp Asn Asn Thr Glu Glu Asn Ser Glu Ser Phe Glu Gln Ala Leu Arg

35 40 45

aaa aga gtt gcc agt acg gtt aaa gaa atg gtt aac gaa gat gaa gaa 192

Lys Arg Val Ala Ser Thr Val Lys Glu Met Val Asn Glu Asp Glu Glu

50 55 60

tta ata ttt aaa aac aga ggg cta acc agt gca ttg att gaa tca caa 240

Leu Ile Phe Lys Asn Arg Gly Leu Thr Ser Ala Leu Ile Gln Ser Gln

65 70 75 80

ttg gtc aag gac aac tac cta aag ctg ggt agt aaa atg gag ggg gat 288

Leu Val Lys Asp Asn Tyr Leu Lys Leu Gly Ser Lys Met Glu Gly Asp

85 90 95

aat ggt gat ggt gag aag aaa ttt gac ttg gat gtc tat cta cgg tct 336

Asn Gly Asp Gly Glu Lys Lys Phe Asp Leu Asp Val Tyr Val Arg Ser

100 105 110

aag tta cag gat ccc aaa cta ttg gaa atg ata aag gga aac ctt cag 384

Lys Leu Glu Asp Pro Lys Leu Leu Glu Met Ile Lys Gly Gln Leu Gln

115 120 125

gaa aca ctg aac tct tat gaa gag gaa gca aat gga agt acg taa 429

Glu Thr Leu Asn Ser Tyr Glu Glu Glu Ala Asn Gly Ser Thr

130 135 140

<210> 65

<211> 142

<212> PRT

<213> Saccharomyces cerevisiae

<400> 65

Met Ala Tyr Asn Gln Glu Asp Ser Lys Arg Leu Ser Asp Lys Tyr Lys
1 5 10 15

Lys Gln Gly His Phe Asp Lys Leu Lys Arg Glu Ile Leu Ser Asn Pro
20 25 30

Tyr Asn Asn Thr Glu Glu Asn Ser Glu Ser Phe Glu Gln Ala Leu Arg
35 40 45

Lys Arg Val Ala Ser Thr Val Lys Glu Met Val Asn Glu Asp Glu Glu
50 55 60

Leu Ile Phe Lys Asn Arg Gly Leu Thr Ser Ala Leu Ile Glu Ser Gln
65 70 75 80

Leu Val Lys Asp Asn Tyr Leu Lys Leu Gly Ser Lys Met Glu Gly Asp
85 90 95

Asn Gly Asp Gly Glu Lys Lys Phe Asp Leu Asp Val Tyr Val Arg Ser
100 105 110

Lys Leu Gln Asp Pro Lys Leu Leu Glu Met Ile Lys Gly Gln Leu Gln
115 120 125

Gln Thr Leu Asn Ser Tyr Glu Glu Glu Ala Asn Gly Ser Thr

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130
135
140

<210> 66
<211> 462
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> {1}..(462)

<400> 66
atg acc ttt tta caa ttt atc aat aat aat agn caa gaa gga caa ggt      48
Met Thr Phe Leu Gln Phe Ile Asn Asn Asn Arg Gln Glu Gly Gln Gly
1          5          10          15

tat att tca gaa aaa tta ttc aaa att aag aag aat gag atg ata aga      36
Tyr Ile Ser Glu Lys Leu Phe Lys Thr Lys Lys Asn Glu Met Ile Arg
          20          25          30

aaa aca gtt acc aat tta gta gct gta aga tta aaa aac tta tcc cag      144
Lys Thr Val Thr Asn Leu Val Ala Val Arg Leu Lys Asn Leu Ser His
          35          40          45

gaa tat gat gta ata gag aat tat ctg cgc tat ata gct agc acc agt      192
Glu Phe Asp Val Ile Glu Asn Tyr Leu Arg Tyr Ile Ala Ser Thr Ser
          50          55          60

gaa cat cta ttt act gct att aag cgc cac ttt aac aaa tgt gcc aga      240
Glu His Leu Phe Thr Ala Ile Lys Arg His Phe Asn Lys Cys Ala Arg
65          70          75          80

aaa ctt ttg aca gaa gca atc gac tcc aaa tca aac tca gaa act gct      288
Lys Leu Leu Lys Glu Ala Ile Asp Ser Lys Ser Asn Ser Glu Thr Ala
          85          90          95

acg gcg gtt ctg caa gaa gga ttt tct ggc att tgc tta ttg aaa gcg      336
Thr Val Val Leu Gln Glu Gly Phe Ser Gly Ile Cys Leu Leu Tyr Ala
          100          105          110

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tct tca att ata tta aaa uta aaa ttg aag ttt cca aaa aag aaa gat 384
 Ser Ser Ile Ile Leu Lys Leu Lys Leu Lys Phe Pro Lys Lys Lys Asp
 115 120 125

aga act gat att agc aaa ttg tgt gac aag aac gaa cgg atg aca cag 432
 Arg Thr Asp Ile Ser Lys Leu Cys Asp Gys Lys Glu Arg Met Thr Glu
 130 135 140

tgg tta gaa att tca att ttg atg aac tga 462
 Trp Leu Glu Ile Ser Ile Leu Met Asn
 145 150

<210> 67
 <211> 153
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 67

Met Thr Phe Leu Gln Phe Ile Asn Asn Asn Arg Gln Glu Gly Gln Gly
 1 5 10 15

Tyr Ile Ser Gln Lys Leu Phe Lys Thr Lys Lys Asn Glu Met Ile Arg
 20 25 30

Lys Thr Val Thr Asn Leu Val Ala Val Arg Leu Lys Asn Leu Ser His
 35 40 45

Glu Phe Asp Val Ile Glu Asn Tyr Leu Arg Tyr Ile Ala Ser Thr Ser
 50 55 60

Glu His Leu Phe Thr Ala Ile Lys Arg His Phe Asn Lys Cys Ala Arg
 65 70 75 80

Lys Leu Leu Lys Glu Ala Ile Asp Ser Lys Ser Asn Ser Glu Thr Ala

85

90

55

Thr Val Val Leu Gln Glu Gly Phe Ser Gly Ile Cys Leu Leu Lys Ala
 100 105 110

Ser Ser Ile Ile Leu Lys Leu Lys Leu Lys Phe Pro Lys Lys Lys Asp
 115 120 125

Arg Thr Asp Ile Ser Lys Leu Cys Asp Lys Lys Gln Arg Met Thr Gln
 130 135 140

Trp Leu Glu Ile Ser Ile Leu Met Asn
 145 150

<210> 58

<211> 1584

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1584)

<400> 68

atg agt ctc tgg cag gag tca cct tta ccc cat atc aag gat gtt gtt 40

Met Ser Leu Ser Gln Val Ser Pro Leu Pro His Ile Lys Asp Val Val

1 5 10 15

tta gga gat aca gta ggc caa ggc gca ttc gcc tgc gtt aaa aat gct 80

Leu Gly Asp Thr Val Gly Gln Gly Ala Phe Ala Cys Val Lys Asn Ala

20 25 30

cat ctt cna atg gat ccc tcc att att cta gct gtt aaa ttc att cat 144

His Leu Trp Met Asp Pro Ser Ile Ile Leu Ala Val Lys Phe Ile His

35 40 45

gtt ccc act tgc aaa aaa atg gga ctc agt gac aag gat atc acn aaa	192
Val Pro Thr Cys Lys Lys Met Gly Leu Ser Asp Lys Asp Ile Thr Lys	
50 55 60	
gag gtt gtt ttg caa tgc aag tgt tct aag cat cct aat gtt ttg aga	240
Glu Val Val Ileu Gln Ser Lys Cys Ser Lys His Pro Asn Val Leu Arg	
65 70 75 80	
ctt atc gat tgt aat gtc tct aaa gaa tat atg tgg ata att ctg gag	288
Leu Ile Asp Cys Asn Val Ser Lys Glu Tyr Met Trp Ile Ile Ileu Glu	
85 90 95	
atg gca gat ggt ggt gat cta ttt gat aag att gag cct gac gll gga	336
Met Ala Asp Gly Gly Asp Leu Phe Asp Lys Ile Glu Pro Asp Val Gly	
100 105 110	
gtt gat tcc gac gtg gcc caa ttt tac ttt caa cag ctc gtt agt gct	384
Val Asp Ser Asp Val Ala Gln Phe Tyr Phe Gln Gln Leu Val Ser Ala	
115 120 125	
att aat tat ctg cat gta gaa tgt gga gtt gct cac aca gac atc aag	432
Ile Asn Tyr Leu His Val Gln Cys Gly Val Ala His Arg Asp Ile Lys	
130 135 140	
cct gaa aac atc tta ctc gat aag aac gga aat ctg aag cta gct gat	480
Pro Glu Asn Ile Ileu Leu Asp Lys Asn Gly Asn Ileu Lys Leu Ala Asp	
145 150 155 160	
ttt ggg ctc gcc tct caa ttt agg agg aaa gat ggt aca tta cgt gta	528
Phe Gly Leu Ala Ser Gln Phe Arg Arg Lys Asp Gly Thr Leu Arg Val	
165 170 175	
tcc atg gat caa agg ggt tct cca ccc tac atg gct cct gaa gta tta	576
Ser Met Asp Gln Arg Gly Ser Pro Pro Tyr Met Ala Pro Glu Val Leu	
180 185 190	
tat tct gaa gag ggt tat tac gca gat cga aca gat ata tgg tct att	624
Tyr Ser Glu Glu Gly Tyr Tyr Ala Asp Arg Thr Asp Ile Trp Ser Ile	
195 200 205	
ggc atc ctc ttg ttc gta ttg ttg act ggt caa aag cct tgg gaa tta	672
Gly Ile Leu Leu Phe Val Leu Leu Thr Gly Gln Thr Pro Trp Glu Leu	

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210	215	220	
cct tca tta gag aac gaa gat ttc gtc ttt ttt att gaa aat gat gga			720
Pro Ser Leu Glu Asn Glu Asp Phe Val Phe Phe Ile Glu Asn Asp Gly			
225	230	235	240
aat tta aac tgg gga ccc tgg tca aag ata gaa ttt act cac tgg aac			768
Asn Leu Asn Trp Gly Pro Trp Ser Lys Ile Glu Phe Thr His Leu Asn			
245	250	255	
cta ctc cga aaa att tta cca cct gac cca aat aag agg gtg aca ttg			816
Leu Leu Arg Lys Ile Leu Gln Pro Asp Pro Asn Lys Arg Val Thr Leu			
260	265	270	
aag gct tta aag tta cat cct tgg gta tta cgt cga gct tca ttt tct			864
Lys Ala Leu Lys Leu His Pro Trp Val Leu Arg Arg Ala Ser Phe Ser			
275	280	285	
ggg gat gat ggt ctc tgt aat gac cct gaa ctc ttg gct aag aac ctg			912
Gly Asp Asp Gly Leu Cys Asn Asp Pro Glu Leu Leu Ala Lys Lys Leu			
290	295	300	
ttc tct cac tta aaa gtc tca ctg agt aac gaa aat tat ttg aac ttc			960
Phe Ser His Leu Lys Val Ser Leu Ser Asn Gln Asn Tyr Leu Lys Phe			
305	310	315	320
act caa gat aca aac tct aat aat aag tac att tct act cag cca att			1008
Thr Gln Asp Thr Asn Ser Asn Asn Arg Tyr Ile Ser Thr Gln Pro Ile			
325	330	335	
ggc aac gaa ttg gct gag ctt gaa cac gac tca atg cat ttc cag aca			1056
Gly Asn Gln Leu Ala Glu Leu Glu His Asp Ser Met His Phe Gln Thr			
340	345	350	
gtt tgg aat aca caa cgt gca ttt acc tgg tat gat tca aat aag aac			1104
Val Ser Asn Thr Gln Arg Ala Phe Thr Ser Tyr Asp Ser Asn Thr Asn			
355	360	365	
tat aat aac cga aca ggt atg aca caa gag gct aag tgg aag caa ttc			1152
Tyr Asn Ser Gly Thr Gly Met Thr Gln Glu Ala Lys Trp Thr Gln Phe			
370	375	380	

ata	aga	tat	gat	atc	gct	gac	tta	cag	ttt	cat	tct	gat	gaa	aat	gat	1200
Ile	Ser	Tyr	Asp	Ile	Ala	Ala	Leu	Gln	Phe	His	Ser	Asp	Glu	Asn	Asp	
385					390				395					400		

tgt	aat	gaa	tta	gta	aaa	aga	cat	tta	caa	ttt	aat	ccg	aat	aaa	ctt	1248
Cys	Asn	Glu	Leu	Val	Lys	Arg	His	Leu	Gln	Phe	Asn	Pro	Asn	Lys	Leu	
				405					410					415		

acc	aag	ttc	tac	acg	ttg	aaa	cat	atg	gat	gtt	ttg	tta	ccg	att	ctg	1296
Thr	Lys	Phe	Tyr	Thr	Leu	Gln	Pro	Met	Asp	Val	Leu	Leu	Pro	Ile	Leu	
				420					425					430		

gag	aaa	gac	ttg	aat	tta	tca	caa	att	aga	gta	aaa	ccc	gac	ctt	ttt	1344
Glu	Lys	Ala	Leu	Asn	Leu	Ser	Gln	Ile	Arg	Val	Lys	Pro	Asp	Leu	Phe	
		435					440							445		

gag	aat	ttt	gaa	aga	ttg	tgc	gaa	tta	ttg	ggg	tat	gat	aac	gtt	ttc	1392
Ala	Asn	Phe	Glu	Arg	Leu	Cys	Glu	Leu	Leu	Gly	Tyr	Asp	Asn	Val	Phe	
		450					455							460		

cca	ctt	att	ata	aat	att	aaa	ccc	aaa	agt	aat	ggg	ggg	tat	caa	tta	1440
Pro	Leu	Ile	Ile	Asn	Ile	Lys	Thr	Lys	Ser	Asn	Gly	Gly	Tyr	Gln	Leu	
465						470								475		480

tgc	ggg	agc	att	ccc	atc	att	agg	att	gaa	gaa	gag	ttg	aaa	agt	gtc	1488
Cys	Gly	Ser	Ile	Ser	Ile	Ile	Lys	Ile	Glu	Glu	Glu	Leu	Lys	Ser	Val	
						485								490		

aga	ttt	gaa	aga	aaa	act	ggg	gat	ccc	tta	gaa	tgg	aga	aga	ctg	ttc	1536
Gly	Phe	Glu	Arg	Lys	Thr	Gly	Asp	Pro	Leu	Glu	Trp	Arg	Arg	Leu	Phe	
						500								505		510

aag	aaa	att	tca	act	atc	tgt	agg	gat	att	atc	cta	att	ccc	aac	tga	1584
Lys	Lys	Ile	Ser	Thr	Ile	Cys	Arg	Asp	Ile	Ile	Leu	Ile	Pro	Asn		
						515								520		525

<210> 69

<211> 527

<212> PPT

<213> Saccharomyces cerevisiae

<400> 59

Met Ser Leu Ser Gln Val Ser Pro Leu Pro His Ile Lys Asp Val Val

1 5 10 15

Leu Gly Asp Thr Val Gly Gln Gly Ala Phe Ala Cys Val Lys Asn Ala

20 25 30

His Leu Gln Met Asp Pro Ser Ile Ile Leu Ala Val Lys Phe Ile His

35 40 45

Val Pro Thr Cys Lys Lys Met Gly Leu Ser Asp Lys Asp Ile Thr Lys

50 55 60

Glu Val Val Leu Gln Ser Lys Cys Ser Lys His Pro Asn Val Leu Arg

65 70 75 80

Leu Ile Asp Cys Asn Val Ser Lys Glu Tyr Met Trp Ile Ile Leu Glu

85 90 95

Met Ala Asp Gly Gly Asp Leu Phe Asp Tyr Phe Glu Pro Asp Val Gly

100 105 110

Val Asp Ser Asp Val Ala Gln Phe Tyr Phe Gln Gln Leu Val Ser Ala

115 120 125

Ile Asn Tyr Leu His Val Glu Cys Gly Val Ala His Arg Asp Ile Lys

130 135 140

Pro Glu Asn Ile Leu Leu Asp Lys Asn Gly Asn Leu Lys Leu Ala Asp

145 150 155 160

Phe Gly Leu Ala Ser Gln Phe Arg Arg Lys Asp Gly Thr Leu Arg Val
165 170 175

Ser Met Asp Gln Arg Gly Ser Pro Pro Tyr Met Ala Pro Glu Val Leu
180 185 190

Tyr Ser Glu Glu Gly Tyr Tyr Ala Asp Arg Thr Asp Ile Trp Ser Ile
195 200 205

Gly Ile Leu Leu Phe Val Leu Leu Thr Gly Gln Thr Pro Trp Glu Leu
210 215 220

Pro Ser Leu Glu Asn Glu Asp Phe Val Phe Phe Ile Glu Asn Asp Gly
225 230 235 240

Asn Leu Asn Trp Gly Pro Trp Ser Lys Ile Glu Phe Thr His Leu Asn
245 250 255

Leu Leu Arg Lys Ile Leu Gln Pro Asp Pro Asn Lys Arg Val Thr Leu
260 265 270

Lys Ala Leu Lys Leu His Pro Trp Val Leu Arg Arg Ala Ser Phe Ser
275 280 285

Gly Asp Asp Gly Leu Cys Asn Asp Pro Glu Leu Leu Ala Lys Lys Leu
290 295 300

Phe Ser His Leu Lys Val Ser Leu Ser Asn Glu Asn Tyr Leu Lys Phe
305 310 315 320

Thr Gln Asp Thr Asn Ser Asn Asn Arg Tyr Ile Ser Thr Gln Pro Ile

325	330	335	
Gly Asn Glu Leu Ala Glu Leu Glu His Asp Ser Met His Phe Gln Thr			
340	345	350	
Val Ser Asn Thr Gln Arg Ala Phe Thr Ser Tyr Asp Ser Asn Thr Asn			
355	360	365	
Tyr Asn Ser Gly Thr Gly Met Thr Gln Glu Ala Lys Trp Thr Gln Phe			
370	375	380	
Ile Ser Tyr Asp Ile Ala Ala Leu Gln Phe His Ser Asp Glu Asn Asp			
385	390	395	400
Cys Asn Glu Leu Val Lys Arg His Leu Gln Phe Asn Pro Asn Lys Leu			
405	410	415	
Thr Lys Phe Tyr Thr Leu Gln Pro Met Asp Val Leu Leu Pro Ile Leu			
420	425	430	
Glu Lys Ala Leu Asn Leu Ser Gln Ile Arg Val Lys Pro Asp Leu Phe			
435	440	445	
Ala Asn Phe Glu Arg Leu Cys Glu Leu Leu Gly Tyr Asp Asn Val Phe			
450	455	460	
Pro Leu Ile Ile Asn Ile Lys Thr Lys Ser Asn Gly Gly Tyr Gln Leu			
465	470	475	480
Cys Gly Ser Ile Ser Ile Ile Lys Ile Glu Glu Glu Leu Lys Ser Val			
485	490	495	

Gly Phe Gln Arg Lys Thr Gly Asp Pro Leu Glu Trp Arg Arg Leu Phe
 500 505 510

Lys Lys Ile Ser Thr Ile Cys Arg Asp Ile Ile Leu Ile Pro Asn
 515 520 525

<210> 70
 <211> 849
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(849)

<400> 70
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 Met Asp Pro Ser Leu Val Leu Glu Gln Thr Ile Gln Asp Val Ser Asn
 1 5 10 15
 atc cca tca gaa ttt cgt tac ctc tta gag gag atc ggt tca aat gat 96
 Leu Pro Ser Gln Phe Arg Tyr Leu Leu Glu Glu Ile Gly Ser Asn Asp
 20 25 30
 ttg aag ctg atc gaa gaa aaa aag aaa tac gag caa aaa gaa tca caa 144
 Leu Lys Leu Ile Glu Glu Lys Lys Lys Tyr Glu Gln Lys Gln Ser Gln
 35 40 45
 ata cac aaa ttt ata aga cag caa ggc tca ata cag aaa cat cca cag 192
 Ile His Lys Phe Ile Arg Gln Gln Gly Ser Ile Pro Lys His Pro Gln
 50 55 60
 gaa gat ggg ctt gac aaa gaa ata aaa gaa tca ctt ttg aaa tgt cag 240
 Glu Asp Gly Leu Asp Lys Glu Ile Lys Glu Ser Leu Leu Lys Cys Gln
 65 70 75 80
 tct ttg caa aga gaa aaa tgc gtt ctg gag aac aat gcc ttg ttt ata 288
 Ser Leu Gln Arg Glu Lys Cys Val Leu Ala Asn Thr Ala Leu Phe Leu

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	85	90	95	
	att gct aga cac ttg aat aag ttg gaa aaa aac atc gct tta ttg gag			336
	Ile Ala Arg His Leu Asn Lys Leu Glu Lys Asn Ile Ala Leu Leu Glu			
	100	105	110	
	gaa gat ggt gtc cta gcc ccc gtg gaa gaa gat gga gac atg gat agc			384
	Glu Asp Gly Val Leu Ala Pro Val Glu Glu Asp Gly Asp Met Asp Ser			
	115	120	125	
	gct gct gaa gcc tct aga gaa agt tca gtt gtg agt aac agt agc gtg			432
	Ala Ala Glu Ala Ser Arg Glu Ser Ser Val Val Ser Asn Ser Ser Val			
	130	135	140	
	aaa aag aga aga gct gca tca agc tca gga tcc gtt cca ccc act ttg			480
	Lys Lys Arg Arg Ala Ala Ser Ser Ser Gly Ser Val Pro Pro Thr Leu			
	145	150	155	160
	aaa aag aaa aaa act agt cga acc tct aac ctg cca aat gaa att gac			528
	Lys Lys Lys Lys Thr Ser Arg Thr Ser Lys Leu Gln Asn Glu Ile Asp			
	165	170	175	
	gtt tct tca aga gaa aag tct gtt act cca gtg agc cca agc att gaa			576
	Val Ser Ser Arg Glu Lys Ser Val Thr Pro Val Ser Pro Ser Ile Glu			
	180	185	190	
	aag aag att gca aga acc aaa gaa ttc aaa aac agt aga aat ggt aca			624
	Lys Lys Ile Ala Arg Thr Lys Glu Phe Lys Asn Ser Arg Asn Gly Lys			
	195	200	205	
	ggc caa aac ggt tcc cct gaa aac gag gaa gag gac aaa act tta tac			672
	Gly Gln Asn Gly Ser Pro Glu Asn Glu Glu Glu Asp Lys Thr Leu Tyr			
	210	215	220	
	tgc ttc tgt caa aga gtt tgc ttt gga gaa atg gtt gca tgt gat gga			720
	Cys Phe Cys Gln Arg Val Ser Phe Gly Glu Met Val Ala Cys Asp Gly			
	225	230	235	240
	ccc aac tgt aaa taa gaa tgg ttt cat tat gat tgt gta aat tta aaa			768
	Pro Asn Cys Lys Tyr Glu Trp Phe His Tyr Asp Cys Val Asn Leu Lys			
	245	250	255	

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gaa cct ccg aaa gga aca tgg lac tgt ccc gaa tgt aaa att gag atg 816
 Glu Pro Pro Lys Gly Thr Trp Tyr Cys Pro Glu Cys Lys Ile Glu Met
 260 265 270

gaa aaa aac aaa ctg aaa aga aaa cgt aac tga 849
 Glu Lys Asn Lys Leu Lys Arg Lys Arg Asn
 275 280

<210> 71
 <211> 282
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 71

Met Asp Pro Ser Leu Val Leu Glu Gln Thr Ile Gln Asp Val Ser Asn
 1 5 10 15

Leu Pro Ser Glu Phe Arg Tyr Leu Leu Glu Glu Ile Gly Ser Asn Asp
 20 25 30

Leu Lys Leu Ile Glu Glu Lys Lys Lys Tyr Glu Gln Lys Glu Ser Gln
 35 40 45

Ile His Lys Phe Ile Arg Gln Gln Gly Ser Ile Pro Lys His Pro Gln
 50 55 60

Glu Asp Gly Leu Asp Lys Glu Ile Lys Glu Ser Leu Leu Lys Cys Gln
 65 70 75 80

Ser Leu Gln Arg Glu Lys Cys Val Leu Ala Asn Thr Ala Leu Phe Leu
 85 90 95

Ile Ala Arg His Leu Asn Lys Leu Glu Lys Asn Ile Ala Leu Leu Glu
 100 105 110

Glu Asp Gly Val Leu Ala Pro Val Glu Glu Asp Gly Asp Met Asp Ser
115 120 125

Ala Ala Glu Ala Ser Arg Glu Ser Ser Val Val Ser Asn Ser Ser Val
130 135 140

Lys Lys Arg Arg Ala Ala Ser Ser Ser Gly Ser Val Pro Pro Thr Leu
145 150 155 160

Lys Lys Lys Lys Thr Ser Arg Thr Ser Lys Leu Gln Asn Glu Ile Asp
165 170 175

Val Ser Ser Arg Glu Lys Ser Val Thr Pro Val Ser Pro Ser Ile Glu
180 185 190

Lys Lys Ile Ala Arg Thr Lys Glu Thr Lys Asn Ser Arg Asn Gly Lys
195 200 205

Gly Gln Asn Gly Ser Pro Glu Asn Glu Glu Glu Asp Lys Thr Leu Tyr
210 215 220

Cys Phe Cys Gln Arg Val Ser Phe Gly Glu Met Val Ala Cys Asp Gly
225 230 235 240

Pro Asn Cys Lys Tyr Glu Trp Phe His Tyr Asp Cys Val Asn Leu Lys
245 250 255

Glu Pro Pro Lys Gly Thr Trp Tyr Cys Pro Glu Cys Lys Ile Glu Met
260 265 270

280

<212> Saccharomyces cerevisiae

<222> {1}...{1479}

atg gag agt cga act aca ggg cct tta acg act gaa acc tac gat ggc 40
Met Glu Ser Arg Thr Thr Gly Pro Leu Thr Thr Glu Thr Tyr Asp Gly
1 5 10 15

ddc act gtg gcc ttc atg ata tta ggt gcc gcc cta gta ttt ttt atg 96
 Pro Thr Val Ala Phe Met Ile Leu Gly Ala Ala Leu Val Phe Phe Met
 20 25 30

gtg ccc gga ttg gga ttc ttg tac tac gga ttg gca aga agg aag tct 144
Val Pro Gly Leu Gly Phe Leu Tyr Ser Gly Leu Ala Arg Arg Lys Ser
35 40 45

gca cta gca cta atc tgg gtt gta tta atg gcg acf elg gtc ggt aca 192
Ala Leu Ala Leu Ile Trp Val Val Leu Met Ala Thr Leu Val Gly Ile
50 55 60

ctg caa tgg tat ttc tgg ggt tac tct cta gct ttt tca aag tcc gct 240
Leu Gln Trp Tyr Phe Trp Gly Tyr Ser Leu Ala Phe Ser Gys Ser Ala
65 70 75 80

cag aat aat aaa taa att ggg aac cta gat tgg ttt ggc ttt aga aac 288
 Pro Asn Asn Lys phe Ile Gly Asn Leu Asp Ser Phe Gly Phe Arg Asn
 85 90 95

gag tac gga aaa aaa ttc gat gaa gat gcc tac cct gag ccc gag tat 336
Val Tyr Gly Lys Lys Phe Asp Glu Asp Ala Tyr Pro Glu Leu Ala Tyr

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	100	105	110	
gca acc ttc caa atg atg ttt tgg tgc gtc aac tta agt att atc gct				384
Ala Thr Phe Gln Met Met Phe Ser Cys Val Asn Leu Ser Ile Ile Ala				
115	120	125		
ggc gcc act gcc gaa aga ggc agg ctg cta ccg cac atg gtt ttt ctg				432
Gly Ala Thr Ala Glu Arg Gly Arg Leu Leu Pro His Met Val Phe Leu				
130	135	140		
lll all cta gct acc att gga tat tgt cca gtg acg tat tgg att tgg				480
Phe Ile Leu Ala Thr Ile Gly Tyr Cys Pro Val Thr Tyr Trp Ile Trp				
145	150	155	160	
tca cca ggt ggt tgg gca tac caa tgg gga gcc ctg gat tgg gca ggc				528
Ser Pro Gly Gly Trp Ala Tyr Gln Trp Gly Val Leu Asp Trp Ala Gly				
165	170	175		
ggc ggc aac att gaa ata tta agc gct gtt tcc ggg ttt gtt tac tct				576
Gly Gly Asn Ile Glu Ile Leu Ser Ala Val Ser Gly Phe Val Tyr Ser				
180	185	190		
tgg ttt ttg ggc aaa aga aat gaa aag tta ctg ata aat ttc agg cct				624
Trp Phe Leu Gly Lys Arg Asn Glu Lys Ile Ile Ile Asn Phe Arg Pro				
195	200	205		
cat aat gtt tca ttg gtc act cta ggc aca tcc ata ctg tgg ttt ggc				672
His Asn Val Ser Leu Val Thr Leu Gly Thr Ser Ile Leu Trp Phe Gly				
210	215	220		
tgg ctg cta ttt aat cct gca tcc tca tta tcc cca aat ttg agg tca				720
Trp Leu Leu Phe Asn Ser Ala Ser Ser Leu Ser Pro Asn Leu Arg Ser				
225	230	235	240	
gtt tat gca ttc atg aat aca tgc ctg agt gcc att act ggt ggg atg				768
Val Tyr Ala Phe Met Asn Thr Cys Leu Ser Ala Ile Thr Gly Gly Met				
245	250	255		
acg tgg tgt att ctg gat tac aga tgg gag aag aaa tgg tgg aca gtt				816
Thr Trp Cys Leu Leu Asp Tyr Arg Ser Glu Lys Lys Trp Ser Thr Val				
260	265	270		

ggt ctg tgc tcc ggt atc att tct ggg ctg gtg gct gca acg cca agc	864
Gly Leu Cys Ser Gly Ile Ile Ser Gly Leu Val Ala Ala Thr Pro Ser	
275 380 284	
tca ggc tgt ata acc ctt tac ggt tca ctt att caa ggc att gtg gcg	912
Ser Gly Cys Ile Thr Leu Tyr Gly Ser Leu Ile Gln Gly Ile Val Ala	
290 295 300	
ggg gta gtg tgt aac ttt ggc acg aag ttg aaa tac tac gct aaa gta	960
Gly Val Val Cys Asn Phe Ala Thr Lys Leu Lys Tyr Tyr Ala Lys Val	
305 310 315 320	
gat gat gcc atg gac att cta gct gag cac ggg gtt gca ggc gta ata	1008
Asp Asp Ala Met Asp Ile Leu Ala Glu His Gly Val Ala Gly Val Ile	
325 330 335	
gga cta att ttc act gcc ctt ttt gga gca gac tgg gtc att ggt atg	1056
Gly Leu Ile Phe Asn Ala Leu Phe Gly Ala Asp Trp Val Ile Gly Met	
340 345 350	
gat ggc act acc gag cac gag ggc ggc tgg gta act cac aat cag aag	1104
Asp Gly Thr Thr Glu His Glu Gly Gly Trp Val Thr His Asn Tyr Lys	
355 360 365	
caa atg lyl aag cag atc gct tac att gcc gca tcc att ggg tac act	1152
Gln Met Tyr Lys Gln Ile Ala Tyr Ile Ala Ala Ser Ile Gly Tyr Thr	
370 375 380	
gct gct gta acc gca ata atc tgc ttt gtg ctg ggc tuc ata ccc ggt	1200
Ala Ala Val Thr Ala Ile Ile Cys Phe Val Leu Gly Tyr Ile Pro Gly	
385 390 395 400	
atg agg cta aga ata tca gaa gag gca gag gag ggc ggt atg gac gaa	1248
Met Arg Leu Arg Ile Ser Glu Glu Ala Glu Glu Ala Gly Met Asp Glu	
405 410 415	
gat caa att ggc gaa ttt gcg tac gat tat gtg gaa gtg aga aga gat	1296
Asp Gln Ile Gly Glu Phe Ala Tyr Asp Tyr Val Glu Val Arg Arg Asp	
420 425 430	
tac tat cta lyy ggt gta gac gaa gat tca caa cgc tct gat gta aat	1344
Tyr Tyr Leu Trp Gly Val Asp Glu Asp Ser Gln Arg Ser Asp Val Asn	

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435	440	445	
cac cgg gtc aac aac gct cat ttg gcc gct gaa cgt agc agt agc ggt	1392		
His Arg Val Asn Asn Ala His Leu Ala Ala Glu Arg Ser Ser Ser Gly			
450	455	460	
act aat agt tcc tgg gat ggg aat gga gaa atg att caa tcc gaa aag	1440		
Thr Asn Ser Ser Ser Asp Gly Asn Gly Glu Met Ile Gln Ser Gln Tyr			
465	470	475	480
atc cta cca atc cat caa gaa gat cct gcc aat agg taa	1479		
Ile Leu Pro Ile His Gln Glu Asp Pro Ala Asn Arg			
485	490		
<p><210> 73</p> <p><211> 492</p> <p><212> PRT</p> <p><213> <i>Saccharomyces cerevisiae</i></p> <p><400> 73</p>			
Met Gln Ser Arg Thr Thr Gly Pro Leu Thr Thr Glu Thr Tyr Asp Gly			
1	5	10	15
Pro Thr Val Ala Phe Met Ile Leu Gly Ala Ala Leu Val Phe Phe Met			
20	25	30	
Val Pro Gly Leu Gly Phe Leu Tyr Ser Gly Leu Ala Arg Arg Tyr Ser			
35	40	45	
Ala Leu Ala Leu Ile Trp Val Val Leu Met Ala Thr Leu Val Gly Ile			
50	55	60	
Leu Gln Trp Tyr Phe Trp Gly Tyr Ser Leu Ala Phe Ser Lys Ser Ala			
65	70	75	80

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Pro Asn Asn Lys Phe Ile Gly Asn Leu Asp Ser Phe Gly Phe Arg Asn
85 50 95

Val Tyr Gly Lys Lys Phe Asp Glu Asp Ala Tyr Pro Glu Leu Ala Tyr
100 105 110

Ala Thr Phe Gln Met Met Phe Ser Cys Val Asn Leu Ser Ile Ile Ala
115 120 125

Gly Ala Thr Ala Glu Arg Gly Arg Leu Leu Pro His Met Val Phe Leu
130 135 140

Phe Ile Leu Ala Thr Ile Gly Tyr Cys Pro Val Thr Tyr Trp Ile Trp
145 150 155 160

Ser Pro Gly Gly Trp Ala Tyr Gln Trp Gly Val Leu Asp Trp Ala Gly
165 170 175

Gly Gly Asn Ile Glu Ile Leu Ser Ala Val Ser Gly Phe Val Tyr Ser
180 185 190

Trp Phe Leu Gly Lys Arg Asn Glu Lys Leu Leu Ile Asn Phe Arg Pro
195 200 205

His Asn Val Ser Leu Val Thr Leu Gly Thr Ser Ile Leu Trp Thr Gly
210 215 220

Trp Leu Leu Phe Asn Ser Ala Ser Ser Leu Ser Pro Asn Leu Arg Ser
225 230 235 240

Val Tyr Ala Phe Met Asn Thr Cys Leu Ser Ala Ile Thr Gly Gly Met
245 250 255

Thr Trp Cys Leu Leu Asp Tyr Arg Ser Glu Lys Lys Trp Ser Thr Val
260 265 270

Gly Leu Cys Ser Gly Ile Ile Ser Gly Leu Val Ala Ala Thr Pro Ser
275 280 285

Ser Gly Cys Ile Thr Leu Tyr Gly Ser Leu Ile Gln Gly Ile Val Ala
290 295 300

Gly Val Val Cys Asn Phe Ala Thr Lys Leu Lys Tyr Tyr Ala Lys Val
305 310 315 320

Asp Asp Ala Met Asp Ile Leu Ala Glu His Gly Val Ala Gly Val Ile
325 330 335

Gly Leu Ile Phe Asn Ala Leu Phe Gly Ala Asp Trp Val Ile Gly Met
340 345 350

Asp Gly Thr Thr Glu His Glu Gly Gly Trp Val Thr His Asn Tyr Lys
355 360 365

Gln Met Tyr Lys Gln Ile Ala Tyr Ile Ala Ala Ser Ile Gly Tyr Thr
370 375 380

Ala Ala Val Thr Ala Ile Ile Cys Phe Val Leu Gly Tyr Ile Pro Gly
385 390 395 400

Met Arg Leu Arg Ile Ser Glu Glu Ala Glu Glu Ala Gly Met Asp Glu
405 410 415

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Asp Gln Ile Gly Glu Phe Ala Tyr Asp Tyr Val Glu Val Arg Arg Asp
 420 425 430

Tyr Tyr Leu Trp Gly Val Asp Glu Asp Ser Gln Arg Ser Asp Val Asn
 435 440 445

His Arg Val Asn Asn Ala His Leu Ala Ala Glu Arg Ser Ser Ser Gly
 450 455 460

Thr Asn Ser Ser Ser Asp Gly Asn Gly Glu Met Ile Gln Ser Glu Lys
 465 470 475 480

Ile Leu Pro Ile His Gln Glu Asp Pro Ala Asn Arg
 485 490

<210> 74

<211> 939

<212> DNA

<313> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> [1]..(939)

<400> 74

atg tgc att tta atg gcc aca agg gca cat cct gac tat gaa ctg atc 48
 Met Cys Ile Leu Met Ala Thr Arg Ala His Pro Asp Tyr Glu Leu Ile
 1 5 10 15

tta ata tot aac aga gac gaa ttc ttg gcc aga aac aca cat gct aca 96
 Leu Ile Ser Asn Arg Asp Glu Phe Leu Ala Arg Lys Thr His Ala Thr
 20 25 30

lgc lgg cat aac aal gat ttt atc ctt tca ccc taa gat ctg gcc aaa 144
 Cys Trp His Asn Asn Asp Phe Ile Asn Ser Pro Tyr Asp Leu Ala Lys

35	40	45	
acc tca gca gaa aaa caa ata ttt ggc act tgg tct ggc ata aat aaa			192
Thr Ser Ala Glu Lys Gln Ile Phe Gly Thr Trp Ser Gly Ile Asn Lys			
50	55	60	
gaa gga aaa tta gcc act att ctt aat tta aaa ctt gac aat gag caa			240
Glu Gly Lys Leu Ala Thr Ile Leu Asn Leu Lys Leu Asp Asn Glu Gln			
65	70	75	80
aat aat acg aaa tca aga tcc cgt ggt ctg tta cca ttt ata ttt ttg			288
Asn Asn Thr Lys Ser Arg Ser Arg Gly Leu Leu Pro Phe Ile Phe Leu			
85	90	95	
tgg atc cat aaa gca gat ttc gaa gat tgg gac aat tcc aaa aag ttt			336
Ser Ile His Lys Ala Asp Phe Gln Asp Trp Asp Asn Tyr Lys Lys Phe			
100	105	110	
gaa ggt cac tat gat ggg ttg aag tcc acc ggt gat tct aat ttt ttt			384
Glu Gly His Tyr Asp Gly Leu Lys Ser Thr Gly Asp Phe Asn Phe Phe			
115	120	125	
tac qgc gac gtt atc aaa aag caa tat aaa gtt act gat tct cta gga			432
Tyr Gly Asp Val Ile Lys Lys Gln Tyr Lys Val Ile Asp Ser Leu Gly			
130	135	140	
aga act ttc gac gty ttg agt tct acc tgt agg aaa gat ctt gat tct			480
Arg Thr Phe Asp Val Leu Ser Ser Thr Cys Arg Lys Asp Leu Asp Ser			
145	150	155	160
tac aly gtt gtt tct aat ggt caa ttc tat gac agc tcc agt ata cca			528
Tyr Met Val Val Ser Asn Gly Lys Phe Tyr Asp Ser Ser Ser Ile Pro			
165	170	175	
ggg cag gct tgg gaa aaa gta aag gta gca cgt gat agt tta gaa aat			576
Gly Gln Ala Trp Glu Lys Val Lys Val Ala Arg Asp Ser Leu Glu Asn			
180	185	190	
cta gtt tta gaa aat att gaa tca gat gag gag aaa ata ata tca agt			624
Leu Val Leu Glu Asn Ile Glu Ser Asp Glu Glu Lys Ile Ile Ser Ser			
195	200	205	

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tgc ttt caa ctc gcc tgg aag tct tcc ctt cca agc act att tca aac 672
 Cys Phe Gln Leu Ala Ser Lys Ser Ser Leu Pro Ser Thr Ile Ser Asn
 210 215 220

cca gat gtc ttg cag atg gta gat cca aat gta acc atg aat acc ata 720
 Pro Asp Val Leu Gln Met Val Asp Pro Asn Val Thr Met Asn Thr Ile
 225 230 235 240

tac gta cca cct tta cgg agg cct ccc agg gat gac tta ggt gcc tca 768
 Tyr Val Pro Pro Leu Arg Arg Pro Pro Arg Asp Asp Asn Gly Ala Ser
 245 250 255

att cct gat ggt gat tac tac gga acg cgc tct caa ata ggt tta ctc 816
 Ile Pro Asp Gly Asp Tyr Tyr Gly Thr Arg Ser Gln Ile Val Leu Leu
 260 265 270

gtg agc aag gat tca acg aga gtt acc ttt ata gaa agg gtc ctt tat 864
 Val Ser Lys Asp Ser Thr Arg Val Thr Phe Ile Glu Arg Val Leu Tyr
 275 280 285

agc tca gat gaa gac gtg cgc aag tat tgg gta acc tca cct aag gag 912
 Ser Ser Asp Glu Asp Val Arg Lys Tyr Ser Val Thr Ser Pro Lys Glu
 290 295 300

gaa aaa agg ttt aaa ctc aaa atg taa 939
 Glu Lys Arg Phe Lys Phe Lys Leu
 305 310

<210> 75

<211> 312

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 75

Met Cys Ile Leu Met Ala Thr Arg Ala His Pro Asp Tyr Glu Leu Ile
 1 5 10 15

Leu Ile Ser Asn Arg Asp Glu Phe Leu Ala Arg Lys Thr His Ala Thr
 20 25 30

Cys Trp His Asn Asn Asp Phe Ile Leu Ser Pro Tyr Asp Leu Ala Lys
15 40 45

Thr Ser Ala Glu Lys Gln Ile Phe Gly Thr Trp Ser Gly Ile Asn Lys
50 55 60

Glu Gly Lys Leu Ala Thr Ile Leu Asn Leu Lys Leu Asp Asn Glu Gln
65 70 75 80

Asn Asn Thr Lys Ser Arg Ser Arg Gly Leu Leu Pro Phe Ile Phe Leu
85 90 95

Ser Ile His Lys Ala Asp Phe Glu Asp Trp Asp Asn Tyr Lys Lys Phe
100 105 110

Glu Gly His Tyr Asp Gly Leu Lys Ser Thr Gly Asp Phe Asn Phe Phe
115 120 125

Tyr Gly Asp Val Ile Lys Lys Gln Tyr Lys Val Ile Asp Ser Leu Gly
130 135 140

Arg Thr Phe Asp Val Leu Ser Ser Thr Cys Arg Lys Asp Leu Asp Ser
145 150 155 160

Tyr Met Val Val Ser Asn Gly Lys Phe Tyr Asp Ser Ser Ser Ile Pro
165 170 175

Gly Gln Ala Trp Glu Lys Val Lys Val Ala Arg Asp Ser Leu Glu Asn
180 185 190

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Leu Val Leu Glu Asn Ile Gln Ser Asp Glu Glu Lys Ile Ile Ser Ser
195 200 205

Cys Phe Gln Leu Ala Ser Lys Ser Ser Leu Pro Ser Thr Ile Ser Asn
210 215 220

Pro Asp Val Leu Gln Met Val Asp Pro Asn Val Thr Met Asn Thr Ile
225 230 235 240

Tyr Val Pro Pro Leu Arg Arg Pro Pro Arg Asp Asp Leu Gly Ala Ser
245 250 255

Ile Pro Asp Gly Asp Tyr Tyr Gly Thr Arg Ser Gln Ile Val Leu Leu
260 265 270

Val Ser Lys Asp Ser Thr Arg Val Thr Phe Ile Glu Arg Val Leu Tyr
275 280 285

Ser Ser Asp Glu Asp Val Arg Lys Tyr Ser Val Thr Ser Pro Lys Glu
290 295 300

Glu Lys Arg Phe Lys Phe Lys Leu
305 310

<210> 76

<211> 2595

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (2595)

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<400> 76

atg tac atg gcc agc tgt ggc ccc aag aat aat gtg ctg tgt ttc cca 40

Met Tyr Met Ala Arg Cys Gly Pro Lys Asn Asn Val Leu Cys Phe Pro

1

5

10

15

ttt caa ctt tcc ttt cta ttt tca aaa cga cta ata aat aag cgt ttc 96

Phe Gln Leu Ser Phe Leu Phe Ser Lys Arg Leu Ile Asn Lys Arg Phe

20

25

30

aag tat acc cta caa act gan gat gaa aag aat atg atg ggg agt tta 144

Lys Tyr Thr Leu Gln Thr Glu Asp Glu Lys Asn Met Met Gly Ser Leu

35

40

45

agt aaa aat aaa ata ata aca cct gaa gac gtt gag ttc aca tta gca 192

Ser Lys Asn Lys Ile Ile Thr Pro Glu Asp Val Glu Phe Lys Leu Ala

50

55

60

caa tta cga gaa ttt tct aat act tta aaa gaa cgc att cac aac act 240

Gln Leu Arg Glu Phe Ser Asn Thr Leu Lys Glu Arg Ile His Asn Thr

65

70

75

80

aaa tgg gtg aat tca gat ggc cac caa agc aat agt atc gca cca atc 288

Lys Ser Val Asn Ser Asp Gly His Gln Ser Asn Ser Ile Ala Pro Ile

85

90

95

tca gaa gag tca agg aat gtt aat gtc acc aaa aca tca tct gtt cct 336

Ser Glu Asp Ser Arg Asn Val Asn Val Thr Lys Thr Ser Ser Val Pro

100

105

110

aat gaa gaa aaa tcc aaa aat cta tca gat ttg att cat tct tgg ttc 384

Asn Glu Glu Lys Ser Lys Asn Leu Ser Asp Leu Ile His Ser Ser Phe

115

120

125

tta gaa aaa atg gat cac ctg gta cca aaa gtt ata aga gaa aga gta 432

Leu Glu Lys Met Asp His Leu Val Pro Lys Val Ile Arg Glu Arg Val

130

135

140

gca gac gac gac ata ctt gca aaa aac ctt ttt gat aga tca cac agt 480

Ala Asp Asp Asp Ile Leu Ala Lys Asn Leu Phe Asp Arg Ser His Ser

145

150

155

160

aat tgg gca cct gtc ata gat agg ctt tat gtc agt gag aaa cgg ttc 528

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Ser	Trp	Ala	Pro	Val	Ile	Asp	Arg	Leu	Tyr	Val	Ser	Glu	Lys	Arg	Phe		
				165					170					175			
atg	gat	att	gat	ccc	aga	gaa	ttt	tct	gtt	tgg	tta	aat	ggc	aca	gtc	573	
Met	Asp	Ile	Asp	Ser	Arg	Glu	Phe	Ser	Val	Trp	Leu	Asn	Gly	Thr	Val		
				180				185					190				
aaa	tat	tig	cca	ttt	cat	agt	ata	cta	cac	tig	gat	gaa	atg	cta	cca	624	
Lys	Tyr	Leu	Pro	Phe	His	Ser	Ile	Leu	His	Leu	Asp	Glu	Met	Leu	Leu		
			195				200					205					
gaa	caa	atc	aat	gga	gat	gtt	cta	aaa	ttt	aat	acc	cac	atg	tac	gaa	672	
Glu	Gln	Ile	Asn	Gly	Asp	Val	Val	Lys	Phe	Asn	Thr	His	Met	Tyr	Glu		
	210					215					220						
tgt	atc	ttt	aac	aac	tta	gga	aat	tta	aaa	cca	act	aat	ttt	aat	cag	720	
Cys	Ile	Phe	Asn	Asn	Leu	Gly	Asn	Leu	Lys	Pro	Thr	Asn	Phe	Asn	Gln		
225					230					235				240			
gat	ggc	act	aac	gat	aaa	gtt	atc	ccc	aaa	atg	aaa	gag	tig	tta	gag	768	
Asp	Gly	Thr	Asn	Asp	Lys	Val	Ile	Leu	Lys	Met	Lys	Glu	Leu	Leu	Glu		
				245					250				255				
agg	tat	gat	aag	gca	tta	aaa	ata	act	gaa	gaa	aga	att	aac	aaa	aaa	816	
Arg	Tyr	Asp	Lys	Ala	Leu	Lys	Ile	Thr	Glu	Gln	Arg	Ile	Asn	Lys	Lys		
			260					265				270					
gaa	gga	ttc	cct	ccc	aaa	gta	cca	aag	atg	acg	caa	gca	ata	ctt	aat	864	
Glu	Gly	Phe	Pro	Ser	Lys	Val	Pro	Lys	Met	Thr	Gln	Ala	Ile	Leu	Asn		
		275					280				285						
aat	tgt	tta	aaa	tac	tgg	acc	aag	tgt	tca	agg	ttt	cac	gac	atg	gat	912	
Asn	Cys	Leu	Lys	Tyr	Ser	Thr	Lys	Cys	Ser	Ser	Phe	His	Asp	Met	Asp		
	290					295					300						
tat	thr	att	aca	aaa	ttc	aga	gat	gat	tat	ggc	ata	act	cct	aat	aag	960	
Tyr	Phe	Ile	Thr	Lys	Phe	Arg	Asp	Asp	Tyr	Gly	Ile	Thr	Pro	Asn	Lys		
305					310				315				320				
caa	aac	cta	act	act	gta	ata	caa	ttc	tac	tct	agg	aag	gaa	atg	act	1008	
Gln	Asn	Leu	Thr	Thr	Val	Ile	Gln	Phe	Tyr	Ser	Arg	Lys	Glu	Met	Thr		
				325					330				335				

aag caa gcc tgg aat act ttt gaa acc atg aaa ttt tta tct aca aaq	1056
Lys Gln Ala Trp Asn Thr Phe Asp Thr Met Lys Phe Leu Ser Thr Lys	
340 345 350	
cat ttc cct gat atc tgc aca tat aac aca atg ctg cga ata tgc gag	1104
His Phe Pro Asp Ile Cys Thr Tyr Asn Thr Met Leu Arg Ile Cys Gln	
355 360 365	
aag gaa cgg aat ttt cct aag gcc ttg gat tta ttt caa gaa att caa	1152
Lys Gln Arg Asn Phe Pro Lys Ala Leu Asp Leu Phe Gln Glu Ile Gln	
370 375 380	
gac cac aat ata aag cct aca aca aac act cac ata atg atg gca aga	1200
Asp His Asn Ile Lys Pro Thr Thr Asn Thr Tyr Ile Met Met Ala Arg	
385 390 395 400	
gag ttg gct tct tgg agc agt aat gcc gtt gtc agt gag ggt aaa tca	1248
Val Leu Ala Ser Ser Ser Ser Asn Ala Val Val Ser Glu Gly Lys Ser	
405 410 415	
gac tct cta aga tta ctg gga tgg aaa tac ctt cat gag ttg gag gac	1296
Asn Ser Leu Arg Leu Leu Gly Trp Lys Tyr Leu His Glu Leu Glu Asp	
420 425 430	
aag aat ctt tac aga cat aaa aaa gat gac tta aat tta ttt ttg gct	1344
Lys Asn Leu Tyr Arg His Lys Lys Asp Asp Leu Asn Leu Phe Leu Ala	
435 440 445	
atg atg gca tta gcc gcg ttt gat ggt gat att gaa tta agt aga gct	1392
Met Met Ala Leu Ala Ala Phe Asp Gly Asp Ile Glu Leu Ser Arg Ala	
450 455 460	
cta tat tac ttg ttc atc gcg aaa aag cac aaa act ttg tgc gca aat	1440
Leu Tyr Tyr Leu Phe Ile Ala Lys Lys Tyr Lys Thr Leu Cys Ala Asn	
465 470 475 480	
tgg aac gga aac aat ctg gta gat caa gat aca att tgg aag leu aat	1488
Trp Lys Gly Asn Ile Leu Val Asp Gln Asp Thr Ile Trp Lys Ser Thr	
485 490 495	
tta atg cca gaa atg ctg aat tat ttg atg ctt gct tat gca aga ttt	1536

Leu Met Pro Glu Met Leu Asn Tyr Leu Met Ileu Ala Tyr Ala Arg Phe	
500 505 510	
gat ccc aga aat ttg cca gtc tta tcc ggt tat gaa aaa ggc att gaa	1584
Asp Pro Arg Asn Leu Pro Val Leu Ser Gly Tyr Glu Lys Gly Ile Glu	
515 520 525	
ttg aga aga aaa ttt ctt cgc gaa ttt gat tcc tcc atg agg tta gat	1632
Leu Arg Arg Lys Phe Leu Arg Glu Phe Asp Ser Ser Met Arg Leu Asp	
530 535 540	
gat aca gac aaa ttg gtc aaa ttt aaa tta cca ttt ctt cca att agt	1680
Asp Thr Asp Lys Leu Val Lys Phe Lys Leu Pro Phe Leu Pro Ile Ser	
545 550 555 560	
gac cta aat tcg gag cca caa gta ttg gcg gaa tct aac gca atc tgg	1728
Asp Leu Asn Ser Glu Ala Gln Val Leu Ala Glu Ser Asn Ala Ile Trp	
565 570 575	
agt ttc aat atg gaa aat gga gga acg cgc aat aca ttg aca tct tca	1776
Ser Phe Asn Met Glu Asn Gly Gly Thr Arg Asn Thr Leu Thr Ser Ser	
580 585 590	
cat gaa gcg gcg ttg gag gat atc aaa aaa tat agg caa tta ctt gat	1824
Asn Glu Ala Ala Leu Glu Asp Ile Lys Lys Tyr Arg Gln Leu Leu Asp	
595 600 605	
tcg ttt gcg caa gaa gca gag gat ttc aac gag ttt aag ttt aaa gtt	1872
Ser Phe Ala Gln Glu Ala Glu Asp Phe Asn Glu Phe Lys Phe Lys Val	
610 615 620	
atg tac gaa gtg acg aaa atg caa aga gaa agt att aat gtg aac gtc	1920
Met Tyr Glu Val Thr Lys Met Gln Arg Glu Ser Ile Asn Val Asn Val	
625 630 635 640	
ttc aat aaa att tca cta cac aca tat ttg tca att ccc att aac tta	1968
Phe Asn Lys Ile Ser Leu His Thr Tyr Leu Ser Ile Pro Ile Asn Leu	
645 650 655	
aaa caa cag aag gaa ttc ttg cga agg ttg acg ttc ttc act ttc caa	2016
Lys Gln Gln Lys Glu Phe Leu Arg Arg Leu Thr Phe Phe Thr Phe Gln	
660 665 670	

caa cac gaa ttt gaa gct gtc ata aag cgt tgg tat gaa gga tac cgt Gln His Glu Phe Glu Ala Val Ile Lys Arg Leu Tyr Glu Gly Tyr Arg 675 680 685	2064
aat att cct tgg tcc cat aag cgt gac caa aat tca ata tca acc gaa Asn Ile Pro Ser Ser His Thr Arg Asp Gln Asn Ser Ile Ser Thr Glu 690 695 700	2112
gac atc tca gta tcc aaa cct gag acc aag gaa gac ctc aac tta ata Ala Ile Ser Val Ser Lys Pro Glu Thr Thr Glu Asp Leu Asn Leu Ile 705 710 715 720	2160
atg cat gat ata tgg tat att aca tgt ttg agg cac aaa atc atg atg Met His Asp Ile Trp Tyr Ile Thr Cys Leu Arg His Lys Ile Met Met 725 730 735	2208
gac acc aag tta tat gag ctg gtg atg aaa gcc gct ata gaa ttt cca Asp Thr Thr Leu Tyr Glu Leu Val Met Lys Ala Ala Ile Glu Phe Gln 740 745 750	2256
aat gag gac tta gca aag aaa gta tga cat gat agg ggt aaa ttt agg Asn Gln Asp Leu Ala Lys Lys Val Trp Asn Asp Arg Gly Lys Phe Arg 755 760 765	2304
acc aat gta cag ttt ctg aca atg gac caa aga ata aga ata gca aag Thr Thr Val Pro Phe Leu Lys Met Asp Gln Arg Ile Arg Ile Ala Lys 770 775 780	2352
gat caa aaa ttt gcc cat cta atg gtc gaa ttc ttc aca aag caa gga Asp Gln Lys Phe Ala His Leu Met Val Glu Phe Phe Thr Lys Gln Gly 785 790 795 800	2400
aag tat tgg gac gcc ata gct atc ala tlg tat tca aaa aat cgc ttc Lys Tyr Ser Asp Ala Ile Ala Ile Ile Leu Ser Ser Lys Asn Arg Phe 805 810 815	2448
aat tgg act tat tcc atg gtt agg aat ttg cat aaa gca tta gaa gaa Asn Trp Thr Tyr Ser Met Val Arg Asn Leu His Lys Ala Leu Glu Gln 820 825 830	2496
atc gag gal aga aat agc gtt gaa atc tta ctg gat gta gta aac aaa	2544

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Ile Glu Asp Arg Asn Ser Val Glu Ile Leu Leu Asp Val Val Asn Lys
 835 840 845

aag tca cac gca aag gcc ctg aag tgg gag gaa caa gaa ctt aac atg 2592
 Lys Ser His Ala Lys Ala Leu Lys Trp Glu Glu Gln Glu Leu Asn Met
 850 855 860

tag 2595

<210> 77
 <211> 864
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 77

Met Tyr Met Ala Arg Cys Gly Pro Lys Asn Asn Val Leu Cys Phe Pro
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Phe Gln Leu Ser Phe Leu Phe Ser Lys Arg Leu Ile Asn Lys Arg Phe
 20 25 30

Lys Tyr Thr Leu Gln Thr Glu Asp Glu Lys Asn Met Met Gly Ser Leu
 35 40 45

Ser Lys Asn Lys Ile Ile Thr Pro Glu Asp Val Glu Phe Lys Leu Ala
 50 55 60

Glu Leu Arg Glu Phe Ser Asn Thr Leu Lys Glu Arg Ile His Asn Thr
 65 70 75 80

Lys Ser Val Asn Ser Asp Gly His Gln Ser Asn Ser Ile Ala Pro Ile
 85 90 95

Ser Glu Asp Ser Arg Asn Val Asn Val Thr Lys Thr Ser Ser Val Pro

101	105	110
Asn Glu Glu Lys Ser Lys Asn Icu Ser Asp Leu Ile His Ser Ser Phe		
115	120	125
Leu Glu Lys Met Asp His Leu Val Pro Lys Val Ile Arg Glu Arg Val		
130	135	140
Ala Asp Asp Asp Ile Leu Ala Lys Asn Leu Phe Asp Arg Ser Phe Ser		
145	150	155
Asn Trp Ala Pro Val Ile Asp Arg Leu Tyr Val Ser Glu Lys Arg Phe		
165	170	175
Met Asp Ile Asp Ser Arg Glu Phe Ser Val Trp Leu Asn Gly Thr Val		
180	185	190
Lys Tyr Leu Pro Phe His Ser Ile Leu His Leu Asp Glu Met Leu Leu		
195	200	205
Glu Gln Ile Asn Gly Asp Val Val Lys Phe Asn Thr His Met Tyr Glu		
210	215	220
Cys Ile Phe Asn Asn Leu Gly Asn Leu Lys Pro Thr Asn Phe Asn Gln		
225	230	235
Asp Gly Thr Asn Asp Lys Val Ile Leu Lys Met Lys Glu Leu Leu Glu		
245	250	255
Arg Tyr Asp Lys Ala Leu Lys Ile Thr Glu Glu Arg Ile Asn Lys Lys		
260	265	270

Gln Gly Phe Pro Ser Lys Val Pro Lys Met Thr Gln Ala Ile Leu Asn
275 280 285

Asn Cys Leu Lys Tyr Ser Thr Lys Cys Ser Ser Phe His Asp Met Asp
290 295 300

Tyr Phe Ile Thr Lys Phe Arg Asp Asp Tyr Gly Ile Thr Pro Asn Lys
305 310 315 320

Gln Asn Leu Thr Thr Val Ile Gln Phe Tyr Ser Arg Tyr Gln Met Thr
325 330 335

Lys Gln Ala Trp Asn Thr Phe Asp Thr Met Lys Phe Leu Ser Thr Tyr
340 345 350

His Phe Pro Asp Ile Cys Thr Tyr Asn Thr Met Leu Arg Ile Cys Gln
355 360 365

Lys Glu Arg Asn Phe Pro Lys Ala Leu Asp Leu Phe Gln Gln Ile Gln
370 375 380

Asp His Asn Ile Lys Pro Thr Thr Asn Thr Tyr Ile Met Met Ala Arg
385 390 395 400

Val Leu Ala Ser Ser Ser Ser Asn Ala Val Val Ser Glu Gly Lys Ser
405 410 415

Asp Ser Leu Arg Leu Leu Gly Trp Lys Tyr Leu His Gln Leu Gln Asp
420 425 430

Lys Asn Leu Tyr Arg His Lys Lys Asp Asp Leu Asn Leu Phe Leu Ala
435 440 445

Met Met Ala Leu Ala Ala Phe Asp Gly Asp Ile Glu Leu Ser Arg Ala
450 455 460

Leu Tyr Tyr Leu Phe Ile Ala Lys Lys Tyr Lys Thr Leu Cys Ala Asn
465 470 475 480

Trp Lys Gly Asn Ile Leu Val Asp Gln Asp Thr Ile Trp Lys Ser Thr
485 490 495

Leu Met Pro Glu Met Leu Asn Tyr Leu Met Leu Ala Tyr Ala Arg Phe
500 505 510

Asp Pro Arg Asn Leu Pro Val Leu Ser Gly Tyr Glu Lys Gly Ile Gln
515 520 525

Leu Arg Arg Lys Phe Leu Arg Glu Phe Asp Ser Ser Met Arg Leu Asp
530 535 540

Asp Thr Asp Lys Leu Val Lys Phe Lys Leu Pro Phe Leu Pro Ile Ser
545 550 555 560

Asp Leu Asn Ser Glu Ala Gln Val Leu Ala Glu Ser Asn Ala Ile Trp
565 570 575

Ser Phe Asn Met Glu Asn Gly Gly Thr Arg Asn Thr Leu Thr Ser Ser
580 585 590

Asn Glu Ala Ala Leu Glu Asp Ile Lys Lys Tyr Arg Gln Leu Leu Asp
595 600 605

Ser Phe Ala Gln Glu Ala Gln Asp Phe Asn Glu Phe Lys Phe Lys Val
610 615 620

Met Tyr Glu Val Thr Lys Met Gln Arg Glu Ser Ile Asn Val Asn Val
625 630 635 640

Phe Asn Lys Ile Ser Leu His Thr Tyr Leu Ser Ile Pro Ile Asn Leu
645 650 655

Lys Gln Gln Lys Glu Phe Leu Arg Arg Leu Tar Phe Phe Thr Phe Gln
660 665 670

Gln His Glu Phe Glu Ala Val Ile Lys Arg Leu Tyr Glu Gly Tyr Arg
675 680 685

Asn Ile Pro Ser Ser His Thr Arg Asp Glu Asn Ser Ile Ser Thr Gln
690 695 700

Ala Ile Ser Val Ser Lys Pro Glu Thr Thr Glu Asp Leu Asn Leu Ile
705 710 715 720

Met His Asp Ile Trp Tyr Ile Thr Cys Leu Arg His Lys Ile Met Met
725 730 735

Asp Thr Thr Leu Tyr Glu Leu Val Met Lys Ala Ala Ile Glu Phe Gln
740 745 750

Asn Glu Asp Leu Ala Lys Lys Val Trp Asn Asp Arg Gly Lys Phe Arg
755 760 765

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Thr Thr Val Pro Phe Leu Lys Met Asp Gln Arg Ile Arg Ile Ala Lys
 770 775 780

Asp Gln Lys Phe Ala His Leu Met Val Gln Phe Phe Thr Lys Gln Gly
 785 790 795 800

Lys Tyr Ser Asp Ala Ile Ala Ile Ile Leu Ser Ser Lys Asn Arg Phe
 805 810 815

Asn Trp Thr Tyr Ser Met Val Arg Asn Leu His Lys Ala Leu Gln Gln
 820 825 830

Ile Glu Asp Arg Asn Ser Val Glu Ile Leu Leu Asp Val Val Asn Lys
 835 840 845

Lys Ser His Ala Lys Ala Leu Lys Trp Gln Glu Gln Glu Leu Asn Met
 850 855 860

<210> 78

<211> 357

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(357)

<400> 78

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 Met Gln Thr Met Gly Gly Gly His Leu Leu Leu Ser Gln Leu Lys Gly
 1 5 10 15

tct ttc ttt ctc cta ctt ttg gca tac ttt ttc agg ggc aga agt cct 96
 Ser Phe Phe Leu Leu Leu Leu Ala Tyr Phe Phe Arg Gly Arg Ser Pro
 20 25 30

tat tac gca cgt tgs tac cgc cgg att gct gtt aca cct ggt gcc atc 144
 Tyr Tyr Ala Arg Cys Tyr Arg Arg Leu Ala Val Thr Pro Gly Ala Ile
 35 40 45

act att gcc att gcc att gct acc gat tca att ccg gcg att gca aag 192
 Thr Ile Ala Ile Ala Ile Ala Thr Asp Ser Ile Pro Ala Leu Ala Lys
 50 55 60

tcc aaa gtt ctg gcy tgc gtt tgt tct cac acc gat ccc tgt acc gcg 240
 Ser Lys Val Leu Val Ser Val Cys Ser His Thr Asp Pro Cys Thr Ala
 65 70 75 80

tct tgt aac ctg atc ccc ttc acc acc cgc acc ttc tgc aac agc ctg acg 288
 Ser Cys Asn Leu Ile Pro Phe Pro Arg Pro Phe Ser Asn Ser Leu Thr
 85 90 95

cgc ttc ctc ttt tct ttg ggc tgc gcc cgt ttt tgc att tcc ttt ccc 336
 Arg Phe Leu Phe Cys Leu Gly Ser Ala Arg Phe Cys Ile Ser Phe Pro
 100 105 110

tgt ttc gga ttg agt ata cac 357
 Cys Phe Gly Leu Ser Ile
 115

<210> 79

<211> 118

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 79

Met Gln Thr Met Gly Gly Glu His Leu Leu Leu Ser Gln Leu Lys Gly
 1 5 10 15

Ser Phe Phe Leu Leu Leu Leu Ala Tyr Phe Phe Arg Gly Arg Ser Pro
 20 25 30

Tyr Tyr Ala Arg Cys Tyr Arg Arg Leu Ala Val Thr Pro Gly Ala Ile

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35

40

45

Thr Ile Ala Ile Ala Ile Ala Thr Asp Ser Ile Pro Ala Leu Ala Lys
 50 55 60

Ser Lys Val Leu Val Ser Val Cys Ser His Thr Asp Pro Cys Thr Ala
 65 70 75 80

Ser Cys Asn Leu Ile Pro Phe Pro Arg Pro Phe Ser Asn Ser Leu Thr
 85 90 95

Arg Phe Leu Phe Cys Leu Gly Ser Ala Arg Phe Cys Ile Ser Phe Pro
 100 105 110

Cys Phe Gly Leu Ser Ile
 115

<210> 80

<211> 1062

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1062)

<400> 80

atg att caa ttt aaa agt cca ggt aac tgg ctg ttc ata gta ccc tgg 48
 Met Ile Gln Phe Lys Ser Pro Gly Asn Trp Leu Phe Ile Val Pro Trp
 1 5 10 15

att gcc ttc att cca tgg tat ggt atg ctg ata gcc atg ctt att tgg 26
 Ile Ala Phe Ile Pro Trp Tyr Gly Met Leu Ile Ala Met Leu Ile Cys
 20 25 30

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tgg gcc agt caa ggc cat ccc ata tat tgg ttc atg cac tgg gag caa	144
Trp Ala Ser Gln Gly His Pro Ile Tyr Trp Phe Met His Ser Glu Gln	
35 40 45	
ttc cct gtc taa att tca gat ala ggt gcc act aat tta agg cca ctg	192
Phe Pro Val Tyr Ile Ser Asp Ile Gly Ala Thr Asn Leu Arg Pro Leu	
50 55 60	
ttt ata tgg tgc gcc ggc tgg cag ggt cta ggc tat gta atc act gtt	240
Phe Ile Ser Cys Ala Gly Trp Gln Gly Leu Gly Tyr Val Ile Thr Val	
65 70 75 80	
gcc ctt gag ttt ttt caa aga tcc ggc tat ctg cct ttc caa ctg aaa	288
Ala Leu Glu Phe Phe Gln Arg Ser Gly Tyr Leu Pro Phe Gln Ile Lys	
85 90 95	
aaa aaa gac cct cct atc cct gat tcc acc tct tat gct gag aaa tgg	336
Lys Lys Asp Pro Ser Ile Ser Asp Ser Thr Ser Tyr Ala Glu Lys Leu	
100 105 110	
cac agc ggt aaa tcc tta atg cct cca tat tcc acc aag gat gaa cgg	384
His Ser Gly Lys Tyr Leu Met Pro Pro Tyr Tyr Thr Lys Asp Glu Arg	
115 120 125	
acc ctg att ttc gca gat ttt gtt ctc ggc agc att ggt gaa cta gcc	432
Asn Leu Ile Phe Phe Ala Ala Phe Val Leu Gly Ser Ile Gly Glu Leu Ala	
130 135 140	
ctt tta ttc agt tcc atc ttc tcc acc gcc ctg tcc cat cgc gtt cac	480
Leu Leu Phe Ser Ser Ile Phe Ser Thr Ala Leu Tyr His Arg Val His	
145 150 155 160	
att gct atg gtc tct gtt ttc gcc gtc ttc atg ttc cta tcc act tgc	528
Ile Ala Met Val Ser Val Phe Val Val Phe Met Phe Leu Ser Thr Cys	
165 170 175	
tgc ttg att gca gag tat ttc ctc atg gga agg cac tat gcc tca gtc	576
Cys Leu Ile Ala Glu Tyr Phe Leu Met Gly Arg His Tyr Ala Ser Val	
180 185 190	
cac ccc cta gcc agc cct cat ttc aat cct caa tca tct gaa aaa agc	624
His Pro Leu Ala Ser Pro His Phe Asn Pro Gln Ser Ser Glu Lys Ser	

195	200	205	
ttt aac caa gat tat aac acc gtg gat gag ctg cct tgg tat aac tgg			672
Phe Asn Gln Asp Tyr Asn Thr Val Asp Glu Leu Pro Trp Tyr Tyr Trp			
210	215	220	
aaa ggc cat gta tgg aat aaa tct acc atc agt gca act cta aga gtt			720
Lys Gly His Val Trp Asn Lys Phe Thr Ile Ser Ala Thr Leu Lys Val			
225	230	235	240
ata tgg tta act ctg gca gtc gta tgg gcc att tgt ttt ggt gct atc			768
Ile Trp Leu Thr Leu Ala Val Val Trp Ala Ile Cys Phe Gly Ala Ile			
245	250	255	
aat gat aga tct aag agt gct tgt ttc gaa tgg ttg cta gca tct tgg			816
Asn Asp Arg Ser Lys Ser Ala Cys Phe Glu Trp Leu Leu Ala Phe Trp			
260	265	270	
ttt ggt atc ata ttt atg att ctt tcc gcc gac ttt tat tta ggt cga			864
Phe Gly Ile Ile Phe Met Ile Leu Ser Ala Asp Phe Tyr Leu Gly Gly			
275	280	285	
aga tac aga caa tcc cgc tat ttc aac cac gtg gaa tca ttt tgg ggt			912
Arg Tyr Arg Gln Ser Arg Tyr Phe Asn His Val Glu Ser Phe Ser Gly			
290	295	300	
tat tac aag tat gac aag gag cta ggc ctg tac cac agt gaa gac gtt			960
Tyr Tyr Lys Tyr Asp Lys Ala Leu Gly Leu Tyr His Ser Glu Asp Val			
305	310	315	320
ttg cct tgg gac gat aac gcc ggc gtc att gcc aca gaa aca gca cct			1008
Leu Pro Ser Asp Asp Asn Ala Gly Val Ile Ala Thr Glu Thr Ala Ser			
325	330	335	
tca aat att tac aat aat tcc tct tcc aac gaa tct att caa gta gtc			1056
Ser Asn Ile Tyr Asn Asn Ser Ser Ser Asn Glu Ser Ile Gln Val Val			
340	345	350	
gta tga			1062
Val			

<210> 81

<211> 353

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 81

Met Ile Gln Phe Lys Ser Pro Gly Asn Trp Leu Phe Ile Val Pro Trp
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Ile Ala Phe Ile Pro Trp Tyr Gly Met Leu Ile Ala Met Leu Ile Cys
20 25 30

Trp Ala Ser Gln Gly His Pro Ile Tyr Trp Phe Met His Ser Glu Gln
35 40 45

Phe Pro Val Tyr Ile Ser Asp Ile Gly Ala Thr Asn Leu Arg Pro Leu
50 55 60

Phe Ile Ser Cys Ala Gly Trp Gln Gly Leu Gly Tyr Val Ile Thr Val
65 70 75 80

Ala Leu Glu Phe Phe Gln Arg Ser Gly Tyr Leu Pro Phe Gln Leu Lys
85 90 95

Lys Lys Asp Pro Ser Ile Ser Asp Ser Thr Ser Tyr Ala Glu Lys Leu
100 105 110

His Ser Gly Lys Tyr Leu Met Pro Pro Tyr Tyr Thr Lys Asp Glu Arg
115 120 125

Asn Leu Ile Phe Ala Ala Phe Val Val Gly Ser Ile Gly Glu Leu Ala
130 135 140

Leu Leu Phe Ser Ser Ile Phe Ser Thr Ala Leu Tyr His Arg Val His
145 150 155 160

Ile Ala Met Val Ser Val Phe Val Val Phe Met Phe Leu Ser Thr Cys
165 170 175

Cys Leu Ile Ala Glu Tyr Phe Leu Met Gly Arg His Tyr Ala Ser Val
180 185 190

His Pro Leu Ala Ser Pro His Phe Asn Pro Gln Ser Ser Glu Lys Ser
195 200 205

Phe Asn Gln Asp Tyr Asn Thr Val Asp Glu Leu Pro Trp Tyr Lys Trp
210 215 220

Lys Gly His Val Trp Asn Lys Phe Thr Ile Ser Ala Thr Leu Lys Val
225 230 235 240

Ile Trp Leu Thr Leu Ala Val Val Trp Ala Ile Cys Phe Gly Ala Ile
245 250 255

Asn Asp Arg Ser Lys Ser Ala Cys Phe Glu Trp Leu Leu Ala Phe Trp
260 265 270

Phe Gly Ile Ile Phe Met Ile Leu Ser Ala Asp Phe Tyr Leu Gly Gly
275 280 285

Arg Tyr Arg Gln Ser Arg Tyr Phe Asn His Val Glu Ser Phe Ser Gly
290 295 300

Tyr Tyr Lys Tyr Asp Lys Ala Leu Gly Leu Tyr His Ser Glu Asp Val
 305 310 315 320

Leu Pro Ser Asp Asp Asn Ala Gly Val Ile Ala Thr Glu Thr Ala Ser
 325 330 335

Ser Asn Ile Tyr Asn Asn Ser Ser Ser Asn Glu Ser Ile Gln Val Val
 340 345 350

Val

<210> 82
 <211> 975
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(975)

<400> 82
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 gcc cag aag ata tgg aag ttt ggt tgg ttt gtg gct ggt ggg cta gca 96
 Ala Gln Lys Ile Ser Lys Phe Gly Ser Phe Val Ala Gly Gly Leu Ala
 20 25 30
 gca tgt ata gct gtt aca gtt act aat cag atc gaa ttg att aaa atc 144
 Ala Cys Ile Ala Val Thr Val Thr Asn Pro Ile Glu Leu Ile Lys Ile
 35 40 45
 aga atg cag ctt caa ggt gaa atg tca gca tca gct gca aaa gtt tat 192

Arg Met Gln Leu Gln Gly Glu Met Ser Ala Ser Ala Ala Lys Val Tyr	
50 55 60	
aaa aat cca atc caa ggt atg gcg gta att ttc caa aac gaa ggt ata	240
Lys Asn Pro Ile Gln Gly Met Ala Val Ile Phe Lys Asn Glu Gly Ile	
65 70 75 80	
aaa ggt ctg caa aaa ggg tta aat gct gct tat atc tat caa all ggg	288
Lys Gly Leu Gln Lys Gly Leu Asn Ala Ala Tyr Ile Tyr Gln Ile Gly	
85 90 95	
ulu aat ggt tcc aga tta ggg ttt tat gag cca atc aga tca tca tta	336
Leu Asn Gly Ser Arg Leu Gly Phe Tyr Glu Pro Ile Arg Ser Ser Leu	
100 105 110	
aat cag ctt ttc ttc cca gat caa gag cca cat aag gta cag agc gtc	384
Asn Gln Leu Phe Phe Pro Asp Gln Glu Pro His Lys Val Gln Ser Val	
115 120 125	
gga gtt aac gtc ttt tct ggt ggc gca tct ggt ata att ggt gca gtc	432
Gly Val Asn Val Phe Ser Gly Ala Ala Ser Gly Ile Ile Gly Ala Val	
130 135 140	
att ggc tct cca tta ttc ttg gtg aaa aca aga ctt caa tca tat tcc	480
Ile Gly Ser Pro Leu Phe Leu Val Lys Thr Arg Leu Gln Ser Tyr Ser	
145 150 155 160	
gag ttt ata aaa att ggt gaa caa acg cac cac acc ggt gtt tgg aac	528
Glu Phe Ile Lys Ile Gly Glu Gln Thr His Tyr Thr Gly Val Trp Asn	
165 170 175	
ggg tta gta acc att tta aaa acc gaa ggt gtt aag ggt cta ttc aga	576
Gly Leu Val Thr Ile Phe Lys Thr Gln Gly Val Lys Gly Leu Phe Arg	
180 185 190	
ggt att gat gcg gca att tta agg aca ggt gct ggt acc tct gtt caa	624
Gly Ile Asp Ala Ala Ile Leu Arg Thr Gly Ala Gly Ser Ser Val Gln	
195 200 205	
tta cct atc tac aac aca gca aag aac att tgg gtc aaa aat gat ctg	672
Leu Pro Ile Tyr Asn Thr Ala Lys Asn Ile Leu Val Lys Asn Asp Leu	
210 215 220	

atg aac gat ggc cca gca tta cat tta act gct agt act atc tcc ggg 720
 Met. Lys Asp Gly Pro Ala Leu His Leu Thr Ala Ser Thr Ile Ser Gly
 225 230 235 240

tta ggc gtt gcc gtc gtt atg aac cca tgg gat gtc att ttg aca aga 768
 Leu Gly Val Ala Val Val Met Asn Pro Trp Asp Val Ile Leu Thr Arg
 245 250 255

atc tac aat caa aaa ggt gac ttg tac aag gga cct ata gat tgt ttg 816
 Ile Tyr Asn Gln Lys Gly Asp Leu Tyr Lys Gly Pro Ile Asp Cys Leu
 260 265 270

gtc aaa act gtt aga atc gaa ggt gta acc gct ttg tat aag ggt ttc 864
 Val Lys Thr Val Arg Ile Gln Gly Val Thr Ala Leu Tyr Lys Gly Phe
 275 280 285

gcc gct caa gtg ttc aga atc gca cct cat aca atc atg tgt ttg acc 912
 Ala Ala Gln Val Thr Arg Ile Ala Pro His Thr Ile Met Cys Leu Thr
 290 295 300

ttc atg gaa cag aca atg aaa cta gtt tat tgg ata gag tgg agc gtt 960
 Phe Met Glu Gln Thr Met Lys Leu Val Tyr Ser Ile Gln Ser Arg Val
 305 310 315 320

tta ggc cat aat taa 975
 Leu Gly His Asn

<210> 83

<211> 324

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 83

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 1 5 10 15

Ala Gln Lys Ile Ser Lys Phe Gly Ser Phe Val Ala Gly Gly Leu Ala

	20		25		30
Ala Cys Ile Ala Val Thr Val Thr Asn Pro Ile Glu Leu Ile Lys Ile					
	35		40		45
Arg Met Gln Leu Gln Gly Glu Met Ser Ala Ser Ala Ala Lys Val Tyr					
	50		55		60
Lys Asn Pro Ile Gln Gly Met Ala Val Ile Phe Lys Asn Glu Gly Ile					
	65		70		75
					80
Lys Gly Leu Gln Lys Gly Leu Asn Ala Ala Tyr Ile Tyr Gln Ile Gly					
		85		90	
					95
Leu Asn Gly Ser Arg Leu Gly Phe Tyr Glu Pro Ile Arg Ser Ser Leu					
	100		105		110
Asn Gln Leu Phe Phe Pro Asp Gln Glu Pro His Lys Val Gln Ser Val					
	115		120		125
Gly Val Asn Val Phe Ser Gly Ala Ala Ser Gly Ile Ile Gly Ala Val					
	130		135		140
Ile Gly Ser Pro Leu Phe Leu Val Lys Thr Arg Leu Gln Ser Tyr Ser					
	145		150		155
					160
Glu Phe Ile Lys Ile Gly Glu Gln Thr His Tyr Thr Gly Val Asp Asn					
	165		170		175
Gly Leu Val Thr Ile Phe Lys Thr Glu Gly Val Lys Gly Leu Phe Arg					
	180		185		190

Gly Ile Asp Ala Ala Ile Leu Arg Thr Gly Ala Gly Ser Ser Val Cln
195 200 205

Leu Pro Ile Tyr Asn Thr Ala Lys Asn Ile Ile Val Lys Asn Asp Leu
210 215 220

Met Lys Asp Gly Pro Ala Leu His Leu Thr Ala Ser Thr Ile Ser Gly
225 230 235 240

Leu Gly Val Ala Val Val Met Asn Pro Trp Asp Val Ile Leu Thr Arg
245 250 255

Ile Tyr Asn Gln Lys Gly Asp Leu Tyr Lys Gly Pro Ile Asp Cys Leu
260 265 270

Val Lys Thr Val Arg Ile Glu Gly Val Thr Ala Leu Tyr Lys Gly Phe
275 280 285

Ala Ala Gln Val Phe Arg Ile Ala Pro His Thr Ile Met Cys Leu Thr
290 295 300

Phe Met Glu Gln Thr Met Lys Leu Val Tyr Ser Ile Glu Ser Arg Val
305 310 315 320

Leu Gly His Asn

<210> 04

<211> 1062

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1)..(1062)

<400> 84

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Met	Ser	Thr	Ala	Gln	Lys	Ala	Lys	Ile	Leu	Gln	Leu	Ile	Asp	Ser	Cys	
1			5					10					15			

tgc	caa	aat	gca	aaa	agg	aca	caa	ctg	aaa	tct	tta	tca	ttt	gtt	att	96
Cys	Gln	Asn	Ala	Lys	Ser	Thr	Gln	Leu	Lys	Ser	Leu	Ser	Phe	Val	Ile	
			20					25					30			

gga	gca	gta	aat	ggc	acg	acg	aaa	gaa	gct	aaa	aga	acc	tac	att	caa	144
Gly	Ala	Val	Asn	Gly	Thr	Thr	Lys	Glu	Ala	Lys	Arg	Thr	Tyr	Ile	Gln	
			35					40					45			

gaa	cag	tgt	gaa	ttt	ttg	gag	aag	tta	cga	caa	caa	aag	ata	aga	gag	192
Glu	Gln	Cys	Glu	Phe	Leu	Glu	Lys	Leu	Arg	Gln	Gln	Lys	Ile	Arg	Glu	
			50					55					60			

gga	aga	att	aac	ata	ttg	tct	atg	gat	gct	ggc	gtt	tct	aac	ttt	gct	240
Gly	Arg	Ile	Asn	Ile	Leu	Ser	Met	Asp	Ala	Gly	Val	Ser	Asn	Phe	Ala	
65					70					75				80		

ttc	tct	cag	atg	caa	ttg	ctc	aat	aat	gat	cag	ctc	cct	aaa	gta	cta	288
Phe	Ser	Lys	Met	Gln	Leu	Leu	Asn	Asn	Asp	Pro	Leu	Pro	Lys	Val	Leu	
					85					90				95		

gac	tgg	caa	aag	aca	aat	cta	gag	gag	aaa	ttt	ttt	caa	aac	ctc	aaa	336
Asp	Trp	Gln	Lys	Ile	Asn	Leu	Glu	Glu	Lys	Phe	Phe	Gln	Asn	Leu	Lys	
						100				105				110		

aag	tta	agc	ttg	aat	cct	gct	gaa	act	tct	gag	cct	gta	ttc	aac	ctc	384
Lys	Leu	Ser	Leu	Asn	Pro	Ala	Glu	Thr	Ser	Glu	Leu	Val	Phe	Asn	Leu	
						115				120				125		

acg	gag	tat	tta	ttt	gaa	tct	atg	cag	ata	cca	gat	atg	ttt	aca	att	432
Thr	Glu	Tyr	Leu	Phe	Glu	Ser	Met	Pro	Ile	Pro	Asp	Met	Phe	Thr	Ile	
						130				135				140		

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gaa agg cca cgt acc aga act atg tat tog agg cat att tta gac cca 480
Glu Arg Gln Arg Thr Arg Thr Met Ser Ser Arg His Ile Leu Asp Pro
145 150 155 160

att tta aaa gtg aat att ctc gaa cag att ctt ttc tct aac ttg gaa 528
ile leu lys val asn ile leu glu gln ile leu phe ser asn leu glu
165 170 175

aat aat atg aag tat acg aat aaa ata cgg aat acg tcc aag ttg agg 576
Aan Lys Met Lys Tyr Thr Asn Lys Ile Pro Asn Thr Ser Lys Iou Arg
180 185 190

tat atg gta tgt tgg tcc gat cca cat cgg atg act tca Lal Lys Lys 624
Tyr Met Val Cys Ser Ser Asp Pro His Arg Met Thr Ser Tyr Trp Cys
195 300 305

att Cca aga gaa gag aca ccg acc agt tca aaa aag tta aaa tct aac 072
ile Pro Arg Glu Glu Thr Pro Thr Ser Ser Lys Lys Leu Lys Ser Asn
217 215 220

aaa cat agc aaa gat tct cga ata aag cta gtc aaa aaa ata ctt tca 720
lye uia ser lys asp ser arg ile lys leu val lys lys ile leu ser
225 230 235 240

act tca ata cta gaa ggt act tca act agt tct aca aaa ctg gtc gag 768
Thr Ser Ile Leu Glu Gly Asn Ser Thr Ser Ser Thr Lys Leu Val Glu
245 350 355

CUC Ala Gga gtt tgg aat aat agg ata aga aat gcc ccl ucc aua aua 816
 Phe Ile Gly Val Tip Asn Asn Arg Ile Arg Asn Ala Leu Thr Iya Iya
 250 265 272

55a agt ttc aag cta tgt gat ata cta gag atc cua gat aat tcg ggg 264
 Lys Ser Phe Lys Leu Cys Asp Ile Leu Glu Ile Gln Asp Asn Ser Gly
 275 280 285

gtg aga cca gnt gat gat ttg gca gat tca ttc ctc cat tgt ttg taa 912
Val Arg Lys Asp Asp Asp Leu Ala Asp Ser Phe Leu His Cys Leu Ser
290 295 300

tgg atg gag tgg tta aaa ant tat gaa agt att act qaa ctc ttg aat 960
 Trp Met Glu Trp Leu Lys Asn Tyr Glu Ser Ile Thr Glu Leu Leu Asn

305	320	315	320	
taa aaa aca ctg gtt aaa aca cag ttc gga cag gtg ttt gaa ttt tgt				1009
Ser Lys Thr Leu Val Lys Thr Gln Phe Gly Gln Val Phe Glu Phe Cys				
	325	330	335	
gaa aat aag gta caa aag ctg aaa ttt ttg cag aac act tac aac aat				1056
Glu Asn Lys Val Gln Lys Leu Lys Phe Leu Gln Asn Thr Tyr Asn Asn				
	340	345	350	
gac taa				1062
Asp				

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<210> 48
<211> 353
<212> PRP
<213> Saccharomyces cerevisiae
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2400: 85

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Cys Gln Asn Ala Lys Ser Thr Gln Leu Lys Ser Leu Ser Phe Val Ile
20 25 30

Gly Ala Val Asn Gly Thr Thr Lys Glu Ala Lys Arg Thr Tyr Ile Glu
35 40 45

Glu Gln Cys Glu Phe Leu Gln Lys Leu Arg Gln Gln Lys Ile Arg Glu
50 35 60

Gly Arg Ile Asn Ile Leu Ser Met Asp Ala Gly Val Ser Asn Phe Ala
65 70 75 80

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Phe Ser Lys Met Gln Leu Leu Asn Asn Asp Pro Leu Pro Lys Val Leu
85 90 95

Asp Trp Gln Lys Ile Asn Leu Glu Gln Lys Phe Phe Gln Asn Leu Lys
100 105 110

Lys Leu Ser Leu Asn Pro Ala Glu Thr Ser Glu Leu Val Phe Asn Leu
115 120 125

Thr Glu Tyr Leu Phe Glu Ser Met Pro Ile Pro Asp Met Phe Thr Ile
130 135 140

Glu Arg Gln Arg Thr Arg Thr Met Ser Ser Arg His Ile Leu Asp Pro
145 150 155 160

Ile Leu Lys Val Asn Ile Leu Glu Gln Ile Leu Phe Ser Asn Leu Glu
165 170 175

Asn Lys Met Lys Tyr Thr Asn Lys Ile Pro Asn Thr Ser Lys Leu Arg
180 185 190

Tyr Met Val Cys Ser Ser Asp Pro His Arg Met Thr Ser Tyr Trp Cys
195 200 205

Ile Pro Arg Glu Glu Thr Pro Thr Ser Ser Lys Lys Leu Lys Ser Asn
210 215 220

Lys His Ser Lys Asp Ser Arg Ile Lys Leu Val Lys Lys Ile Leu Ser
225 230 235 240

Thr Ser Ile Leu Glu Gly Asn Ser Thr Ser Ser Thr Lys Leu Val Glu

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245

250

255

Phe Ile Gly Val Trp Asn Asn Arg Ile Arg Asn Ala Leu Thr Lys Lys
 260 265 270

Lys Ser Phe Lys Leu Cys Asp Ile Leu Glu Ile Gln Asp Asn Ser Gly
 275 280 285

Val Arg Lys Asp Asp Asp Leu Ala Asp Ser Phe Leu His Cys Leu Ser
 290 295 300

Trp Met Glu Trp Leu Lys Asn Tyr Glu Ser Ile Thr Glu Leu Leu Asn
 305 310 315 320

Ser Lys Thr Leu Val Lys Thr Gln Phe Gly Glu Val Phe Glu Phe Cys
 325 330 335

Glu Asn Lys Val Gln Lys Leu Lys Phe Leu Gln Asn Thr Tyr Asn Asn
 340 345 350

Asp

<210> 86

<211> 2052

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (1052)

<400> 86

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cct gaa caa cac att caa aca act tct agg cta tta aca aag cta tct	96
Arg Glu Gln Asp Ile Gln Thr Thr Ser Arg Leu Leu Thr Thr Leu Ser	
20 25 30	
atc caa caa ttg gtg caa aat ggc ttg gca ata aac aac ata cat cta	144
Ile Gln Gln Leu Val Gln Asn Gly Leu Ala Ile Asn Asn Ile His Leu	
35 40 45	
gaa aac ata aga tcc ggt ctc att ggc aaa tta tal atg gaa ctg gga	192
Glu Asn Ile Arg Ser Gly Leu Ile Gly Lys Leu Tyr Met Glu Leu Gly	
50 55 60	
cct aac ttg gcg gtt aac gac aac att caa agg ggt gat att aag gct	240
Pro Asn Leu Ala Val Asn Asp Lys Ile Gln Arg Gly Asp Ile Lys Val	
65 70 75 80	
ggt gat att gtt ttg gta cgc cct gca aaa acc aaa gta aat acc aag	288
Gly Asp Ile Val Leu Val Arg Pro Ala Lys Thr Lys Val Asn Thr Lys	
85 90 95	
act aag ccc acc gtc aca aag gtg tct gaa gac tcc aat ggc gag caa	336
Thr Lys Pro Lys Val Lys Lys Val Ser Glu Asp Ser Asn Gly Glu Gln	
100 105 110	
gag gaa tgc tca ggc gtt gtc taa aac atg agt gat acc caa atc acc	384
Ala Glu Cys Ser Gly Val Val Tyr Lys Met Ser Asp Thr Gln Ile Thr	
115 120 125	
ata gct cta gaa gaa tct caa gat gtt att gct acc aca ttt tat tct	432
Ile Ala Leu Glu Glu Ser Gln Asp Val Ile Ala Thr Thr Phe Tyr Ser	
130 135 140	
tat agc aca ctt tac att tta aag act acc aat gtc gtc aag tat aat	480
Tyr Ser Lys Leu Tyr Ile Leu Lys Thr Thr Asn Val Val Thr Tyr Asn	
145 150 155 160	
aga atg gaa tcc aca atg aga aac ctg tct gaa att agt tca ccc ata	528
Arg Met Glu Ser Thr Met Arg Lys Leu Ser Glu Ile Ser Ser Pro Ile	

	165	170	175	
caa gac asa att ata caa tac ttg gta aac gaa cgc ccc ttc atc ccc				576
Gln Asp Lys Ile Ile Gln Tyr Leu Val Asn Glu Arg Pro Phe Ile Pro				
180	185	190		
aat aca aac agt ttt caa aac att aaa tct tct tta aac ccg aat ctg				624
Asn Thr Asn Ser Phe Gln Asn Ile Lys Ser Phe Leu Asn Pro Asn Leu				
195	200	205		
aat gac tcc caa aaa aat gcc att aat ttt gcc att aac aat gac ttg				572
Asn Asp Ser Gln Lys Thr Ala Ile Asn Phe Ala Ile Asn Asn Asp Leu				
210	215	220		
acc atc ata cat ggt cct cct ggt acg ggt aaa aca ttc aca tta att				720
Thr Ile Ile His Gly Pro Pro Gly Thr Gly Lys Thr Phe Thr Leu Ile				
225	230	235	240	
gaa ttg atc cag caa ttg cta att aaa aat cct gag gag aga atc tta				768
Glu Leu Ile Gln Gln Leu Leu Ile Lys Asn Pro Glu Glu Arg Ile Leu				
245	250	255		
att tgt ggg cct tcc aat att tct gtg gat acg att ctg gag agg cta				816
Ile Cys Gly Pro Ser Asn Ile Ser Val Asp Thr Ile Leu Glu Arg Leu				
260	265	270		
acg cct ctt gtg ccg aat aat tta tta tta aga atc cgt cat cct gct				864
Thr Pro Leu Val Pro Asn Asn Leu Leu Leu Arg Ile Gly His Pro Ala				
275	280	285		
agg cta tta gac tct aat aaa aga cac tct ctt gat ata ctt agt aaa				912
Arg Leu Leu Asp Ser Asn Lys Arg His Ser Leu Asp Ile Leu Ser Lys				
290	295	300		
aag aat act att gtg aag gac att tcc cag gag att gac aaa tta att				960
Lys Asn Thr Ile Val Lys Asp Ile Ser Gln Glu Ile Asp Lys Leu Ile				
305	310	315	320	
cag gag aat asa aaa cta aaa aac tat aag caa cgt aca gaa aac tgg				1008
Gln Glu Asn Lys Lys Leu Lys Asn Tyr Lys Gln Arg Lys Glu Asn Trp				
325	330	335		

aac gaa att aaa atg atg cgc aac gat tca aag aaa aga gag ttc aac Asn Glu Ile Lys Leu Leu Arg Lys Asp Leu Lys Lys Arg Glu Phe Lys 340 345 350	1056
acc att aag gac tta ata ata caa tcc aga ata gtc gtc acc aat ata Thr Ile Lys Asp Leu Ile Ile Gln Ser Arg Ile Val Val Thr Thr Leu 355 360 365	1104
cac ggt tca tca tcc aga gaa cta tgc tcc ctt tat aga gat gat cca His Gly Ser Ser Ser Arg Glu Leu Cys Ser Leu Tyr Arg Asp Asp Pro 370 375 380	1152
aat ttc cag ctt ttc gat acc ttg atc atc gat gaa gtc tca cag gcc Asn Phe Glu Leu Phe Asp Thr Leu Ile Ile Asp Glu Val Ser Gln Ala 385 390 395 400	1200
atg gaa cca caa tgc tgg atc cca cta att gca cat caa aat cag ttc Met Glu Pro Gln Cys Trp Ile Pro Leu Ile Ala His Gln Asn Gln Phe 405 410 415	1248
cac aaa cta gtc ctt gct cgt gcc aat aaa caa ttg cca ccc aca atc His Lys Leu Val Leu Ala Gly Asp Asn Lys Gln Leu Pro Pro Thr Ile 420 425 430	1296
aaa aca gaa gcc gac aaa aat glu att taa aat atg gac acc aca cta Lys Thr Glu Asp Asp Lys Asn Val Ile His Asn Leu Glu Thr Thr Leu 435 440 445	1344
ttt gac aga ata atc aaa ata ttc ccc aaa agg gat atg gta aaa ttt Phe Asp Arg Ile Ile Lys Ile Phe Pro Lys Arg Asp Met Val Lys Phe 450 455 460	1392
ctt aac gtt caa tac agg atg aat caa aaa att atg gaa ttt cca tcc Leu Asn Val Gln Tyr Arg Met Asn Gln Lys Ile Met Glu Phe Pro Ser 465 470 475 480	1440
cac taa atg tat aat ggg aaa cta ttg gcc gat gca acc gtc gcc aac His Ser Met Tyr Asn Gly Lys Leu Leu Ala Asp Ala Thr Val Ala Asn 485 490 495	1488
aga ctt ttg ata gac cta ccc acc gtc gat gct acc cca tct gag gat Arg Leu Leu Ile Asp Leu Pro Thr Val Asp Ala Thr Pro Ser Glu Asp 1536	

500	505	510	
gat gac gat aca aac att cct tta atc tgg tat gat aag caa ggt gat			1584
Asp Asp Asp Thr Lys Ile Pro Leu Ile Trp Tyr Asp Thr Gln Gly Asp			
515	520	525	
gaa ttt caa gag act gaa gag gaa gct act atc ctt gga tct aag tat			1632
Glu Phe Gln Gln Thr Ala Asp Glu Ala Thr Ile Leu Gly Ser Lys Tyr			
530	535	540	
aat gag ggc gaa aat gaa att gta aaa gaa caa att gag aat tta agg			1680
Asn Glu Gly Glu Ile Ala Ile Val Lys Glu His Ile Glu Asn Leu Arg			
545	550	555	560
tca ttc aac gtc cag gag aac tct ata ggt gtt att tct caa taa aat			1728
Ser Phe Asn Val Pro Glu Asn Ser Ile Gly Val Ile Ser Pro Tyr Asn			
565	570	575	
gca caa gtt tct cat ctg aaa aaa ttg atc cat gat gaa tta aaa tta			1776
Ala Gln Val Ser His Leu Lys Lys Leu Ile His Asp Glu Leu Lys Leu			
580	585	590	
act gat att gaa ata tca act gta gat ggg ttc cag gcc cgt gaa aaa			1824
Thr Asp Ile Glu Ile Ser Thr Val Asp Gly Phe Gln Gly Arg Glu Lys			
595	600	605	
gat gtt atc ata ttg agt tta gtt cgt agc aat gaa aaa ttt gaa gtt			1872
Asp Val Ile Ile Leu Ser Leu Val Arg Ser Asn Glu Lys Phe Glu Val			
610	615	620	
ggt ttc ctt aag gac gaa cga aga ctg aac gtc gcc atg aca aga ccc			1920
Gly Phe Leu Lys Glu Glu Arg Arg Leu Asn Val Ala Met Thr Arg Pro			
625	630	635	640
aga agg caa cta gtt gtt gtt ggc aat ata gaa gtt ctg caa agg tgc			1968
Arg Arg Gln Leu Val Val Val Gly Asn Ile Gln Val Asn Gln Arg Cys			
645	650	655	
ggt aac aag tac cta aaa agt tgg tca gaa tgg tgl gaa gag aac gct			2016
Gly Asn Lys Tyr Leu Lys Ser Trp Ser Glu Trp Cys Glu Glu Asn Ala			
660	665	670	

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gac gta agg tac ccc aac att gac gat tat ttg taa 2052
Asp Val Arg Tyr Pro Asn Ile Asp Asp Tyr Leu
675 680

<210> 87

<211> 683

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 87

Met Asn Lys Glu Leu Ala Ser Lys Phe Leu Ser Ser Ile Lys His Glu
1 5 10 15

Arg Glu Glu Asp Ile Gln Thr Thr Ser Arg Leu Leu Thr Thr Leu Ser
20 25 30

Ile Gln Gln Leu Val Gln Asn Gly Leu Ala Thr Asn Asn Ile His Leu
35 40 45

Glu Asn Ile Arg Ser Gly Leu Ile Gly Lys Leu Tyr Met Glu Ser Gly
50 55 60

Pro Asn Leu Ala Val Asn Asp Lys Ile Gln Arg Gly Asp Ile Lys Val
65 70 75 80

Gly Asp Ile Val Leu Val Arg Pro Ala Lys Thr Lys Val Asn Thr Lys
85 90 95

Thr Lys Pro Lys Val Lys Lys Val Ser Glu Asp Ser Asn Gly Glu Gln
100 105 110

Ala Glu Cys Ser Gly Val Val Tyr Lys Met Ser Asp Thr Gln Ile Thr

115	120	125
Phe Ala Leu Gln Gln Ser Gln Asp Val Ile Ala Thr Thr Phe Tyr Ser		
130	135	140
Tyr Ser Lys Leu Tyr Ile Leu Lys Thr Thr Asn Val Val Thr Tyr Asn		
145	150	155 160
Arg Met Glu Ser Thr Met Arg Lys Leu Ser Glu Ile Ser Ser Pro Phe		
165	170	175
Gln Asp Lys Ile Ile Gln Tyr Leu Val Asn Glu Arg Pro Phe Ile Pro		
180	185	190
Asn Thr Asn Ser Phe Gln Asn Ile Lys Ser Phe Leu Asn Pro Asn Leu		
195	200	205
Asn Asp Ser Gln Lys Thr Ala Ile Asn Phe Ala Ile Asn Asn Asp Leu		
210	215	220
Thr Ile Ile His Gly Pro Pro Gly Thr Gly Lys Thr Phe Thr Leu Ile		
225	230	235 240
Glu Leu Ile Gln Gln Leu Leu Ile Lys Asn Pro Glu Glu Arg Ile Leu		
245	250	255
Ile Cys Gly Pro Ser Asn Ile Ser Val Asp Thr Ile Leu Glu Arg Leu		
260	265	270
Thr Pro Leu Val Pro Asn Asn Leu Leu Leu Arg Ile Gly His Pro Ala		
275	280	285

Arg Leu Leu Asp Ser Asn Lys Arg His Ser Leu Asp Ile Leu Ser Lys
290 295 300

Lys Asn Thr Ile Val Lys Asp Ile Ser Gln Glu Ile Asp Lys Leu Ile
305 310 315 320

Gln Glu Asn Lys Lys Leu Lys Asn Tyr Lys Gln Arg Lys Glu Asn Trp
325 330 335

Asn Glu Ile Lys Leu Leu Arg Lys Asp Leu Lys Lys Arg Glu Phe Lys
340 345 350

Thr Ile Lys Asp Asn Ile Ile Gln Ser Arg Ile Val Val Thr Thr Leu
355 360 365

His Gly Ser Ser Ser Arg Glu Leu Cys Ser Leu Tyr Arg Asp Asp Pro
370 375 380

Asn Phe Gln Leu Phe Asp Thr Leu Ile Ile Asp Glu Val Ser Gln Ala
385 390 395 400

Met Glu Pro Gln Cys Trp Ile Pro Leu Ile Ala His Gln Asn Gln Phe
405 410 415

His Lys Leu Val Leu Ala Gly Asp Asn Lys Gln Leu Pro Pro Thr Ile
420 425 430

Lys Thr Glu Asp Asp Lys Asp Val Ile His Asn Leu Glu Thr Thr Leu
435 440 445

Phe Asp Arg Ile Ile Lys Ile Phe Pro Lys Arg Asp Met Val Lys Phe
450 455 460

Leu Asn Val Gln Tyr Arg Met Asn Gln Lys Ile Met Glu Phe Pro Ser
465 470 475 480

His Ser Met Tyr Asn Gly Lys Leu Leu Ala Asp Ala Thr Val Ala Asn
485 490 495

Arg Leu Leu Ile Asp Leu Pro Thr Val Asp Ala Thr Pro Ser Glu Asp
500 505 510

Asp Asp Asp Thr Lys Ile Pro Leu Ile Trp Tyr Asp Thr Gln Gly Asp
515 520 525

Glu Phe Gln Glu Thr Ala Asp Glu Ala Thr Ile Leu Gly Ser Lys Tyr
530 535 540

Asn Glu Gly Glu Ile Ala Ile Val Lys Glu His Ile Glu Asn Leu Arg
545 550 555 560

Ser Phe Asn Val Pro Glu Asn Ser Ile Gly Val Ile Ser Pro Tyr Asn
565 570 575

Ala Gln Val Ser His Leu Lys Lys Leu Ile His Asp Glu Leu Lys Leu
580 585 590

Thr Asp Ile Glu Ile Ser Thr Val Asp Gly Phe Gln Gly Arg Glu Lys
595 600 605

Asp Val Ile Ile Leu Ser Leu Val Arg Ser Asn Glu Lys Phe Glu Val
610 615 620

Gly Phe Leu Lys Glu Glu Arg Arg Leu Asn Val Ala Met Thr Arg Pro
 625 630 635 640

Arg Arg Gln Leu Val Val Val Gly Asn Ile Glu Val Leu Gln Arg Cys
 645 650 655

Gly Asn Lys Tyr Leu Lys Ser Trp Ser Glu Trp Cys Glu Glu Asn Ala
 660 665 670

Asp Val Arg Tyr Pro Asn Ile Asp Asp Tyr Leu
 675 680

<210> 88

<211> 434

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(414)

<400> 88

atg gaa act gaa gta cct gca cca gtc cga act cat tca tat gcc tta 48

Met Glu Thr Glu Val Pro Ala Pro Val Arg Thr His Ser Tyr Ala Leu

1 5 10 15

gac aga tat gtt aga cag aag agg agg gaa aag cca aga aag cag agc 96

Asp Arg Tyr Val Arg Gln Lys Arg Arg Glu Lys Glu Arg Lys Gln Ser

20 25 30

tta aag cgc gtc gaa aag aag tat act cct agt gaa tta gct ctg tac 144

Leu Lys Arg Val Glu Lys Lys Tyr Thr Pro Ser Glu Leu Ala Leu Tyr

35 40 45

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gaa att cga aac tac cna cgt tcc acg gal tta tta abc tcc aaa att 192
 Glu Ile Arg Lys Tyr Gln Arg Ser Thr Asp Leu Leu Ile Ser Lys Ile
 50 55 60

cca ttt gca agg cta gtg aaa gaa gtt aca gac gag ttt aca act aaa 240
 Pro Phe Ala Arg Leu Val Lys Glu Val Thr Asp Glu Phe Thr Thr Lys
 65 70 75 80

gat cag gat tta cgt tgg cag tca atg gag att atg gag tta cag gaa 288
 Asp Gln Asp Leu Arg Trp Gln Ser Met Ala Ile Met Ala Leu Gln Glu
 85 90 95

gca agc gaa gag tat atg gta gga tta ttg gaa cat aca aac ctc ttg 336
 Ala Ser Glu Ala Tyr Leu Val Gly Leu Leu Glu His Thr Asn Leu Leu
 100 105 110

gcg cag cat gca aac aga att act ata atg aag aac gac atg caa cta 384
 Ala Leu His Ala Lys Arg Ile Thr Ile Met Lys Lys Asp Met Gln Leu
 115 120 125

gca aga aga atc agg gga cag ttt att tgg 414
 Ala Arg Arg Ile Arg Gly Gln Phe Ile
 130 135

<210> 89
 <211> 137
 <212> FRT
 <213> *Saccharomyces cerevisiae*

<400> 89

Met Glu Thr Glu Val Pro Ala Pro Val Arg Thr His Ser Tyr Ala Leu
 1 5 10 15

Asp Arg Tyr Val Arg Gln Lys Arg Arg Glu Lys Gln Arg Lys Gln Ser
 20 25 30

Leu Lys Arg Val Glu Lys Lys Tyr Thr Pro Ser Glu Leu Ala Leu Tyr
 35 40 45

Glu Ile Arg Lys Tyr Gln Arg Ser Thr Asp Leu Leu Ile Ser Lys Ile
 50 55 60

Pro Phe Ala Arg Leu Val Lys Glu Val Thr Asp Glu Phe Thr Thr Lys
 65 70 75 80

Asp Gln Asp Leu Arg Trp Gln Ser Met Ala Ile Met Ala Leu Gln Gln
 85 90 95

Ala Ser Glu Ala Tyr Leu Val Gly Leu Leu Glu His Thr Asn Leu Leu
 100 105 110

Ala Leu His Ala Lys Arg Ile Thr Ile Met Lys Lys Asp Met Gln Leu
 115 120 125

Ala Arg Arg Ile Arg Gly Gln Phe Ile
 130 135

<210> 30

<211> 1293

<212> JNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1293)

<400> 90

atg gat gat ata agc gga agg caa act tta oct cga ata aac cgt ttg 48
 Met Asp Asp Ile Ser Gly Arg Gln Thr Leu Pro Arg Ile Asn Arg Leu
 1 5 10 15

tgg gag cac ctg gga aat ccc caa gat agt ttg tca atc cta cat ata 96

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Leu Glu His Val Gly Asn Pro Gln Asp Ser Leu Ser Ile Leu His Ile	
20 25 30	
gag gga aca aat ggt aag gag aca gta act aac ttt ttg aca tcc ata	142
Ala Gly Thr Asn Gly Lys Gln Thr Val Ser Lys Phe Leu Thr Ser Ile	
35 40 45	
ttg cag cat cag ggg aca cag cgg aac agg gtc ttg att ggt agg tat	192
Leu Gln His Pro Gly Gln Gln Arg Gln Arg Val Leu Ile Gly Arg Tyr	
50 55 60	
act aca tct tcc ttg cta aac gcc aac gaa gag gat att agc att aat	240
Thr Thr Ser Ser Leu Leu Asn Ala Lys Glu Glu Asp Ile Ser Ile Asn	
65 70 75 80	
aat gaa gcc all tcc ttg ata gag tat tct agg atc gac aag gaa ctt	288
Asn Glu Ala Ile Ser Asn Ile Glu Tyr Ser Arg Ile Glu Lys Glu Leu	
85 90 95	
ata gaa gca gat agt tct ttg aac tta cag tgc aac aac ctc gac cgc	336
Ile Glu Ala Asp Ser Ser Leu Lys Ser Gln Cys Asn Asn Leu Glu Leu	
100 105 110	
cta aca agc gta gct ctc gta tac ttc gct aag aac aat tgc aac tgg	384
Leu Thr Ser Val Ala Leu Val Tyr Phe Ala Lys Lys Asn Cys Glu Thr	
115 120 125	
tgc ata ata gaa act ggt taa gct gga aac cag gac cct gga agt ata	432
Cys Ile Ile Glu Thr Gly Leu Ala Gly Lys Gln Asp Pro Gly Ser Ile	
130 135 140	
att gct ggt aac agt aga gtc tgt tgc gcc att act aac ctg ggc att	480
Ile Ala Gly Gln Ser Arg Val Cys Cys Ala Ile Thr Asn Val Gly Ile	
145 150 155 160	
agc gat gaa gct ttt tta tgc aag ttt ttg tct aac att act gaa agc	528
Ser Asp Glu Ala Phe Leu Cys Lys Phe Leu Ser Gln Ile Thr Glu Ser	
165 170 175	
tcc aca aat aac gca att ttt cta tta gac ggt tct aat gac gaa ttt	576
Ser Thr Asn Lys Ala Ile Phe Leu Leu Asp Gly Ser Asn Asp Glu Phe	
180 185 190	

gta cga aat acg ata acg aca cgg tgc cat gat gtt gga tgt cca tta	624
Val Arg Asn Thr Ile Thr Lys Arg Cys His Asp Val Gly Cys Pro Leu	
195 200 205	
gaa atc acc gac cct tct ctt agg gat tac aat gta cac aca gac aca	672
Glu Ile Thr Asp Pro Ser Leu Arg Asp Tyr Asn Val His Thr Asp Thr	
210 215 220	
tgg ggc act ctt gaa gtt cgc ctg cca tac agt gaa gaa gaa tat caa	720
Trp Gly Thr Leu Glu Val Arg Leu Pro Tyr Ser Glu Glu Glu Tyr Gln	
225 230 235 240	
ata tct aat ctg aga gtt ggc ata ggc gtt tta gac ttt ttg agc aag	768
Ile Phe Asn Leu Arg Val Ala Ile Ala Val Leu Asp Phe Leu Ser Lys	
245 250 255	
gaa aaa aag gtt tgt att tca aag gat caa cta tcc caa ggt tta ata	816
Glu Lys Lys Val Cys Ile Ser Lys Asp Gln Leu Ser Gln Gly Leu Ile	
260 265 270	
tct gtc gat tgg cca aga cgt tta cat cgc ttc gat tcc tgt tat gaa	864
Ser Val Asp Trp Pro Arg Ser Leu His Arg Leu Asp Tyr Cys Tyr Glu	
275 280 285	
tct act agt gga aag aaa atc gca tta cta tta gac aac gca aat aat	912
Ser Thr Ser Gly Lys Lys Ile Ala Leu Leu Leu Asp Asn Ala Asn Asn	
290 295 300	
ggc aag gca gct cga aat tta gcc tgc cat tta agg acc acg tac ggt	960
Ala Lys Ala Ala Arg Asn Leu Ala Cys His Leu Arg Thr Thr Tyr Gly	
305 310 315 320	
gat aag cca tta aca ttt gtc att gct ats aca act cgg aaa aag gtg	1008
Asp Thr Pro Leu Thr Phe Val Ile Ala Ile Thr Thr Gly Lys Lys Val	
325 330 335	
tct ccc tta ctt gat cgg cta ata cgt cca caa gal tat gtt att gtc	1056
Ser Pro Leu Leu Asp Pro Leu Ile Arg Pro Gln Asp Tyr Val Ile Val	
340 345 350	
act aga ttt ggg tca gtg gtt gga atg cgg tgg atc caa tcc cta gaa	1104

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Thr Arg Phe Gly Ser Val Val Gly Met Pro Trp Ile Gln Ser Leu Glu
 355 360 365

ccc gtc aat ctt ctc gca tct atc aaa aac cgg tat acg aga aat gtt 1151
 Pro Val Asn Leu Leu Ala Phe Ile Lys Asn Arg Tyr Thr Arg Asn Val
 370 375 380

aac atg cag ccc gat ctt caa agt gtc tgg acc ttc ctt gaa aca agt 1200
 Asn Met Gln Pro Asp Leu Gln Ser Val Trp Thr Phe Leu Glu Thr Ser
 385 390 395 400

ggg tta aag acc att gtt cct gtt atc gta tgt gga tca ctg tat atc 1248
 Gly Leu Lys Thr Ile Val Pro Val Ile Val Cys Gly Ser Leu Tyr Ile
 405 410 415

tgc aaa gag cta ttg cgc tta cac aac tgt cac ttg cca gta tag 1293
 Cys Lys Glu Leu Leu Arg Ile His Asn Cys His Leu Pro Val
 420 425 430

<210> 91
 <211> 430
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 91

Met Asp Asp Ile Ser Gly Arg Gln Thr Leu Pro Arg Ile Asn Arg Leu
 1 5 10 15

Leu Glu His Val Gly Asn Pro Gln Asp Ser Leu Ser Ile Leu His Ile
 20 25 30

Ala Gly Thr Asn Gly Lys Glu Thr Val Ser Lys Phe Leu Thr Ser Ile
 35 40 45

Leu Gln His Pro Gly Gln Gln Arg Gln Arg Val Leu Ile Gly Arg Tyr
 50 55 60

Glu Ile Thr Asp Pro Ser Leu Arg Asp Tyr Asn Val His Thr Asp Thr
 210 225 230

Trp Gly Thr Leu Glu Val Arg Leu Pro Tyr Ser Glu Glu Glu Tyr Gln
225 230 235 240

Ile Phe Asn Leu Arg Val Ala Ile Ala Val Leu Asp Phe Leu Ser Lys
245 250 255

Glu Lys Lys Val Cys Ile Ser Lys Asp Gln Leu Ser Gln Gly Leu Ile
260 265 270

Ser Val Asp Trp Pro Arg Ser Leu His Arg Leu Asp Tyr Cys Tyr Glu
275 280 285

Ser Thr Ser Gly Lys Lys Ile Ala Leu Leu Leu Asp Asn Ala Asn Asn
290 295 300

Ala Lys Ala Ala Arg Asn Leu Ala Cys His Leu Arg Thr Thr Tyr Gly
305 310 315 320

Asp Thr Pro Leu Thr Phe Val Ile Ala Ile Thr Thr Gly Lys Lys Val
325 330 335

Ser Pro Leu Leu Asp Pro Leu Ile Arg Pro Gln Asp Tyr Val Ile Val
340 345 350

Thr Arg Phe Gly Ser Val Val Gly Met Pro Trp Ile Gln Ser Leu Glu
355 360 365

Pro Val Asn Leu Leu Ala Phe Ile Lys Asn Arg Tyr Thr Arg Asn Val
370 375 380

Asn Met Gln Pro Asp Leu Gln Ser Val Trp Thr Phe Leu Glu Thr Ser
385 390 395 400

Gly Leu Lys Thr Ile Val Pro Val Ile val Cys Gly Ser Leu Tyr Ile
 405 410 415

Cys Lys Glu Leu Leu Arg Leu His Asn Cys His Leu Pro Val
 420 425 430

<210> 92
 <211> 593
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (593)

<400> 92
 atg cct gtc cca tct gtt act gtc act acc gat act gaa tat gaa gaa 48
 Met Pro Val Pro Ser Val Thr Val Thr Thr Asp Asn Glu Tyr Gln Asp
 1 5 10 15
 ata tag tac ttt tct tct att gac tct tac aaa cag gag acc ttt act 96
 Ile Ser Ser Phe Ser Ser Ile Asp Ser Tyr Lys Pro Glu Pro Phe Thr
 20 25 30
 ggg ttc aaa gat tct gaa gct cca gaa cag cct att tta aaa aac gat 144
 Gly Phe Lys Asp Ser Glu Ala Pro Glu Gln Pro Leu Leu Lys Asn Asp
 35 40 45
 acc att gtt gga aag ggg caa atg gaa gat gat agt aat gta gat gat 192
 Thr Ile Val Gly Lys Gly Gln Leu Gln Asp Asp Ser Asn Val Asp Asp
 50 55 60
 caa cac cgt cat tca gat gtg cat tct cat cac agt tct agt act tta 240
 Gln His Arg His Ser Asp Val His Ser His His Ser Ser Ser Thr Leu
 65 70 75 80
 aaa agg cca act tca aat tgg ata gaa aag atg gtt acc cac aat gct 288

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[illegible]

<210> 93

<211> 230

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 93

Met Pro Val Pro Ser Val Thr Val Thr Thr Asp Asn Glu Tyr Glu Asp
1 5 10 15

Ile Ser Ser Phe Ser Ser Ile Asp Ser Tyr Lys Pro Glu Pro Phe Thr
20 25 30

Gly Phe Lys Asp Ser Glu Ala Pro Glu Gln Pro Leu Leu Lys Asn Asp
35 40 45

Thr Ile Val Gly Lys Gly Gln Leu Glu Asp Asp Ser Asn Val Asp Asp
50 55 60

Gln His Arg His Ser Asp Val His Ser His His Ser Ser Ser Thr Leu
65 70 75 80

Lys Arg Pro Thr Ser Asn Ser Ile Glu Lys Met Val Thr His Asn Ala
85 90 95

Leu Glu Gly Asn Ser Glu Thr Val Asp Ser Leu Lys Glu Asp Gly Leu
100 105 110

Asn Leu Asn Lys Lys Ala Leu Pro Asp Ile Thr Ala Pro Val Thr Asn
115 120 125

Ser Ala His Asp Ala Ala Phe Pro Glu Glu Tyr Arg Leu Glu Thr Glu
130 135 140

Thr Gly Leu Val Lys Leu Lys Thr Leu Glu Ser Leu Lys Arg Glu Asp

145 150 155 160

Ser Arg Val Ser Ser Thr Lys Lys Glu His Ile Asn Arg His Thr Asp
165 170 175

Met His Ser Thr Arg Ser Lys Val Thr Thr Asn Ser Gln Gly Ser Ser
180 185 190

Met Glu Pro Asn Lys Leu Asn Met Ala Val Glu Lys Asn Lys Lys Arg
195 200 205

Ile Glu Lys Tyr Gln Lys His Lys Ser Glu Lys Gly Ile Lys Gly Phe
210 215 220

Phe His Arg Ile Phe Asp
225 230

<210> 94
<211> 510
<212> DNA
<213> Saccharomyces cerevisiae

<220>
<221> CDS
<222> (1)..(510)

<400> 94
atg tac att cct aaa cat ttt gag tcc atg gaa ctc tca agg tac aaa 40
Met Tyr Ile Pro Lys His Phe Glu Ser Met Glu Leu Ser Arg Tyr Lys
1 5 10 15

tta tca aaa aaa ccc ccc cta gga aca cta ctc tcc tct aag gct acc 96
Leu Ser Lys Lys Pro Pro Leu Gly Thr Leu Phe Ser Ser Lys Ala Ser
20 25 30

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agg caa ggt ltu ltc gga lgg aya act tot too aat aaa gat gac ccc      144
Arg Gln Gly Phe Phe Gly Trp Arg Thr Ser Ser Asn Lys Asp Asp Pro
      35              40              45

gat ttt ggt atg tgc gca tca cat att cca ttt gta ttc gtg gag ttc      192
Asp Phe Gly Met Cys Ala Ser His Ile Pro Phe Val Phe val Glu Phe
      50              55              60

gat aat gga gag cal aaa ctg att gca cat tta gna cgg aag aat aaa      240
Asp Asn Gly Glu His Lys Leu Ile Ala His Leu Ala Arg Lys Asn Lys
      65              70              75              80

cat gtg gaa atg ctg gaa aga gtt caa aaa tgc tta gtg gta ttt cag      288
His Val Glu Met Leu Glu Arg Val Glu Lys Cys Leu Val Val Phe Gln
      85              90              95

agc gtc gal lea lac att tct ccg gcg tgg ttc cca atg aag aaa aag      336
Ser Val Asp Ser Tyr Ile Ser Pro Ala Trp Phe Pro Met Lys Lys Lys
      100              105              110

acc cat aag ttc gta cca aca cgg gat lli gac gac gtg cac gtt tac      384
Thr His Lys Phe Val Pro Thr Trp Asp Phe Ala Ala Val His Val Tyr
      115              120              125

ggt aca cca agg att atc cgc gac gat aaa gac tgg ctg att act atg      432
Gly Thr Pro Arg Ile Ile Arg Asp Asp Lys Asp Trp Leu Ile Asn Met
      130              135              140

tta tca act ttg act ggc caa gaa gaa gag aaa aga cct gag ggg gaa      480
Leu Ser Thr Leu Thr Asp Gln Glu Glu Glu Lys Arg Pro Gln Gly Glu
      145              150              155              160

aat gta cga agt aaa gtc gag cgt ttc tga                                510
Asn Val Arg Ser Lys Val Glu Arg Phe
      165

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<210> 95

<211> 169

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 95

Met Tyr Ile Pro Lys His Phe Glu Ser Met Glu Leu Ser Arg Tyr Lys
1 5 10 15

Leu Ser Lys Lys Pro Pro Leu Gly Thr Leu Phe Ser Ser Lys Ala Ser
20 25 30

Arg Gln Gly Phe Phe Cys Trp Arg Thr Ser Ser Asn Lys Asp Asp Pro
35 40 45

Asp Phe Gly Met Cys Ala Ser His Val Pro Phe Val Phe Val Glu Phe
50 55 60

Asp Asn Gly Glu His Lys Leu Ile Ala His Leu Ala Arg Lys Asn Lys
65 70 75 80

His Val Glu Met Leu Glu Arg Val Gln Lys Cys Leu Val Val Phe Glu
85 90 95

Ser Val Asp Ser Tyr Ile Ser Pro Ala Trp Phe Pro Met Lys Lys Lys
100 105 110

Thr His Lys Phe Val Pro Thr Trp Asp Phe Ala Ala Val His Val Tyr
115 120 125

Gly Thr Pro Arg Ile Ile Arg Asp Asp Lys Asp Trp Leu Ile Asn Met
130 135 140

Leu Ser Thr Leu Thr Asp Gln Glu Glu Glu Lys Arg Pro Glu Gly Glu
145 150 155 160

Asn Val Arg Ser Lys Val Glu Arg Phe
165

<210> 96

<211> 369

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(368)

<400> 96

atg gca gta ccc ggg tat tac gaa tta tat cgt aga agt acg ata ggg 48
Met Ala Val Pro Gly Tyr Tyr Glu Leu Tyr Arg Arg Ser Thr Ile Gly
1 5 10 15

aat agt ttg gtg gat gct att gat act tta att agt gat ggg aga ata 96
Asn Ser Leu Val Asp Ala Leu Asp Thr Leu Ile Ser Asp Gly Arg Ile
20 25 30

gaa gag tgg tta gct atg cgt gtt tta gag aca ttt gac aaa gtg gtg 144
Glu Ala Ser Leu Ala Met Arg Val Leu Glu Thr Phe Asp Lys Val Val
35 40 45

gct gag act tta aaa gac aat acc caa tct aaa ttg act gtg aaa gga 192
Ala Glu Thr Leu Lys Asp Asn Thr Gln Ser Lys Leu Thr Val Lys Gly
50 55 60

aac ctg gac aca tat gga tct tgc gat gat gtt tgg act ttt atc gta 240
Asn Leu Asp Thr Tyr Gly Phe Cys Asp Asp Val Trp Thr Phe Ile Val
65 70 75 80

aaa aat tgt cag gtt act gtt gag gac agc cac ggc gac gcc tcc cag 288
Lys Asn Cys Gln Val Thr Val Glu Asp Ser His Arg Asp Ala Ser Gln
85 90 95

aac ggg tct gga gat agc caa agt gta att tgg gtg gat aag ttg agg 336
Asn Gly Ser Gly Asp Ser Gln Ser Val Ile Ser Val Asp Lys Leu Arg

Seq. ID No. 1

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Asn Ser Leu Val Asp Ala Leu Asp Thr Leu Ile Ser Asp Gly Arg Ile				
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Glu Ala Ser Leu Ala Met Arg Val Leu Glu Thr Phe Asp Lys Val Val				
35	40	45		
Ala Glu Thr Leu Lys Asp Asn Thr Gln Ser Lys Leu Thr Val Lys Gly				
50	55	60		
Asn Leu Asp Thr Tyr Gly Phe Cys Asp Asp Val Trp Thr Phe Ile Val				
65	70	75	80	
Lys Asn Cys Gln Val Thr Val Glu Asp Ser His Arg Asp Ala Ser Gln				
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Asp Gly Ser Gly Asp Ser Gln Ser Val Ile Ser Val Asp Lys Leu Arg				
100	105	110		

Ile Val **Ala** Cys Asn Ser Lys Lys Ser Glu
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<211> 336

<212> DNA

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gag ttt ttc tat ttc ttt ttt att tca ttc tat aca att tgg ttc gtc 96
 Glu Phe Phe Tyr Phe Phe Phe Ile Ser Phe Tyr Thr Leu Trp Ile Val
 20 25 30

ttt ttt ctt ttg cac ttg agt ttc ttt tca aca tta tca ttc ggt ata 144
 Phe Phe Leu Leu His Leu Ser Phe Phe Ser Thr Leu Ser Phe Gly Ile
 35 40 45

ttt cac gat ttt gac acc gat gtc tac ata aaa gtg ggt aat tat atc 192
 Phe His Asp Phe Asp Thr Asp Val Tyr Ile Lys Val Gly Asn Tyr Ile
 50 55 60

ttg cat ttt ctc gaa ttg agt aaa aat agt aac ctt tta aag aat tct 240
 Leu His Phe Leu Glu Leu Ser Lys Asn Ser Asn Leu Leu Lys Asn Ser
 65 70 75 80

tca gaa atg tta aag cat ttc cga ttg gca tca ttg atg tat atg tac 288
 Ser Glu Met Leu Lys His Phe Arg Leu Ala Ser Leu Met Tyr Met Tyr
 85 90 95

gta tat aat cag atg att tgc ccc tgc tta ctt ggc atc agg aat tag 336
 Val Tyr Thr Gln Met Ile Cys Pro Ser Leu Leu Gly Ile Arg Asn
 100 105 110

<210> 99
<211> 111
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 99

Met Thr Lys Ser Ile Tyr Ile Ile Ile Gly Tyr Met Leu His Asp Glu
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Phe Phe Leu Leu His Leu Ser Phe Phe Ser Thr Leu Ser Phe Gly Ile
35 40 45

Phe His Asp Phe Asp Thr Asp Val Tyr Glu Lys Val Gly Asn Tyr Ile
50 55 60

Leu His Phe Leu Glu Leu Ser Lys Asn Ser Asn Leu Leu Lys Asn Ser
65 70 75 80

Ser Glu Met Leu Lys His Phe Arg Leu Phe Ser Leu Met Tyr Met Tyr
85 90 95

Val Tyr Thr Gln Met Ile Cys Pro Ser Leu Leu Gly Ile Arg Asn
100 105 110

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<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (301)

<400> 100

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1				5					10					15		

aag	ccc	aag	cca	goc	gta	gta	aaa	tca	tog	tgg	aga	ggt	ttt	act	ggt	96
Thr	Pro	Lys	Pro	Ala	Val	Val	Lys	Ser	Ser	Trp	Arg	Val	Phe	Thr	Val	
			20					25					30			

gct	aac	tct	aag	aga	tgt	ttc	aca	ccc	gct	gca	atc	atg	agg	acc	caa	144
Ala	Asn	Ser	Lys	Arg	Cys	Phe	Thr	Pro	Ala	Ala	Ile	Met	Arg	Asn	Gln	
			35				40						45			

gag	acc	caa	aga	gta	ggt	gat	att	ttg	caa	tct	gaa	ttg	aaa	att	gag	192
Glu	Thr	Gln	Arg	Val	Gly	Asp	Ile	Leu	Gln	Ser	Glu	Ileu	Tyr	Ile	Gln	
			50				55					60				

aag	gaa	acg	tta	cca	gag	tca	acg	tog	tta	gac	tca	ttt	aat	gac	ttc	240
Lys	Glu	Thr	Leu	Pro	Glu	Ser	Thr	Ser	Leu	Asp	Ser	Phe	Asn	Asp	Phe	
65					70					75					80	

ttg	aac	aaa	tac	aag	ttc	tca	tta	gta	gag	aca	ccc	ggt	aag	aat	gaa	288
Leu	Asn	Lys	Tyr	Lys	Phe	Ser	Leu	Val	Glu	Thr	Pro	Gly	Lys	Asn	Glu	
			85						90					95		

gct	gaa	ata	gtt	aga	aga	acc	gaa	leu	ggc	gaa	aca	gtt	cat	gtt	ttc	336
Ala	Glu	Ile	Val	Arg	Arg	Thr	Glu	Ser	Gly	Glu	Thr	Val	His	Val	Phe	
			100					105					110			

ttt	gac	gta	gct	cag	att	gct	aat	ctg	ccr	tac	aac	aac	gca	atg	gat	384
Phe	Asp	Val	Ala	Gln	Ile	Ala	Asn	Leu	Pro	Tyr	Asn	Asn	Ala	Met	Asp	
			115					120					125			

gaa	aat	acc	gag	caa	aac	gaa	gac	ggc	att	aat	gag	gat	gac	ttt	gat	432
Glu	Asn	Thr	Glu	Gln	Asn	Glu	Asp	Gly	Ile	Asn	Glu	Ala	Asp	Phe	Asp	
			130				135						140			

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gct cta tca gac aac ttt gcc aac gtt aat gtt gtt att tct aac gaa 480
 Ala Leu Ser Asp Asn Phe Ala Asn Val Asn Val Val Ile Ser Lys Glu
 145 150 155 160

agc gca agc gaa cct gca gtc tca ttt gaa tta cta atg aat tta cag 528
 Ser Ala Ser Glu Pro Ala Val Ser Phe Glu Leu Leu Met Asn Leu Gln
 165 170 175

gaa ggt tca ttt tat gtt gat agt ggt act cca tac ccc tca gtt gat 576
 Glu Gly Ser Phe Tyr Val Asp Ser Ala Thr Pro Tyr Pro Ser Val Asp
 180 185 190

gct gct ttg aat cag tct gct gag gcc gaa ala aca aga gaa ttg gta 624
 Ala Ala Leu Asn Gln Ser Ala Gln Ala Gln Phe Thr Arg Glu Leu Val
 195 200 205

tac cat ggc cca cct ttt tca aac ttg gac gaa gaa cta cca gaa tat 672
 Tyr His Gly Pro Pro Phe Ser Asn Leu Asp Glu Glu Leu Gln Glu Ser
 210 215 220

ctg gaa gct tat ttg gaa agt aga ggt gtc aat gaa gag cta gcc tct 720
 Leu Glu Ala Tyr Leu Glu Ser Arg Gly Val Asn Glu Glu Leu His Ser
 225 230 235 240

ctc att agt gca tat tcc gag ttc aaa gag aat aac gag tat att tct 768
 Phe Ile Ser Ala Tyr Ser Glu Phe Lys Glu Asn Asn Glu Tyr Ile Ser
 245 250 255

tgg ttg gaa aag atg aag aag ttt ttc cac taa 801
 Trp Leu Glu Lys Met Lys Lys Phe Phe His
 260 265

<210> 101
 <211> 266
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 101

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 20 25 30

Ala Asn Ser Lys Arg Cys Phe Thr Pro Ala Ala Ile Met Arg Asn Gln
 35 40 45

Glu Thr Gln Arg Val Gly Asp Ile Leu Gln Ser Glu Leu Lys Ile Glu
 50 55 60

Lys Glu Thr Leu Pro Glu Ser Thr Ser Leu Asp Ser Phe Asn Asp Phe
 65 70 75 80

Leu Asn Lys Tyr Lys Phe Ser Leu Val Glu Thr Pro Gly Lys Asn Glu
 85 90 95

Ala Glu Thr Val Arg Arg Thr Glu Ser Gly Glu Thr Val His Val Phe
 100 105 110

Phe Asp Val Ala Glu Ile Ala Asn Leu Pro Tyr Asn Asn Ala Met Asp
 115 120 125

Glu Asn Thr Glu Gln Asn Glu Asp Gly Ile Asn Glu Asp Asp Phe Asp
 130 135 140

Ala Leu Ser Asp Asn Phe Ala Asn Val Asn Val Val Ile Ser Lys Glu
 145 150 155 160

Ser Ala Ser Glu Pro Ala Val Ser Phe Glu Leu Leu Met Asn Leu Gln
 165 170 175

Glu Gly Ser Phe Tyr Val Asp Ser Ala Thr Pro Tyr Pro Ser Val Asp
 180 185 190

Ala Ala Leu Asn Gln Ser Ala Glu Ala Glu Ile Thr Arg Glu Leu Val
 195 200 205

Tyr His Gly Pro Pro Phe Ser Asn Leu Asp Glu Glu Leu Gln Glu Ser
 210 215 220

Leu Glu Ala Tyr Leu Glu Ser Arg Gly Val Asn Glu Glu Leu Ala Ser
 225 230 235 240

Phe Ile Ser Ala Tyr Ser Glu Phe Lys Glu Asn Asn Glu Tyr Ile Ser
 245 250 255

Trp Leu Glu Lys Met Lys Lys Phe Phe His
 260 265

<210> 102
 <211> 366
 <212> DNA
 <213> *Saccharomyces cerevisiae*

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 <221> CDS
 <222> (1) .. (966)

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 1 5 10 15

gta gcc gtt ttg aaa ggt gtt gaa aaa acc gtt cgt aag cat ttg gaa 96
 Val Ala Val Leu Lys Gly Val Glu Lys Thr Val Arg Lys His Leu Glu

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20	25	30	
aga cag gga tgg ata gag ccc cag aaa gtg gac tac gag tta att ttc			144
Arg Gln Gly Trp Ile Glu Pro Gln Lys Val Asp Tyr Glu Leu Ile Phe			
35	40	45	
act ata gat agg ttg aaa aac ttg gta gat aat aag cgt gag gct tta			192
Thr Ile Asp Arg Leu Lys Asn Leu Val Asp Asn Lys Arg Glu Ala Leu			
50	55	60	
act gcg gaa caa ccc gcc gct ggt gaa ctg agc tgg cgt aaa gta ttt			240
Thr Ala Glu Gln Pro Asp Ala Gly Glu Leu Ser Trp Arg Lys Val Phe			
65	70	75	80
aat ttc att tcc aga caa tcc agc gaa ttg gac aca cga aca tac gtt			288
Asn Phe Ile Ser Arg Gln Ser Ser Glu Leu Asp Thr Arg Ile Tyr Val			
85	90	95	
ctt ata cta ctc cta tcc ttt cta cta cct atc gag tgg act gta ctg			336
Leu Ile Leu Leu Leu Ser Phe Leu Leu Pro Ile Ala Trp Thr Val Leu			
100	105	110	
gac ggt gat cgc gag acc acg cta gaa cat aag gat aac gat tgt aat			384
Asp Gly Asp Arg Glu Thr Thr Leu Glu Asp Lys Asp Asn Asp Cys Asn			
115	120	125	
gta gat ctt att gaa aac gaa agg agg ctg aag cat tac aac gat ggt			432
Val Asp Leu Ile Glu Asn Glu Arg Arg Leu Lys His Tyr Asn Asp Gly			
130	135	140	
gaa aga gaa gta ttg caa ttt ggt aaa aat aga tcc gaa cct att ata			480
Glu Arg Ala Val Leu Glu Phe Gly Lys Asn Arg Ser Glu Pro Ile Ile			
145	150	155	160
tta agc tat aag gac atg aac gtt ttg gaa ggg gaa cat gag ttc acc			528
Leu Ser Tyr Lys Asp Met Asn Val Leu Glu Gly Glu His Glu Phe Thr			
165	170	175	
tcc aaa gag gaa cac agc aac agc cat ttg aca agc aag agc gaa aat			576
Ser Lys Glu Glu His Ser Asn Ser His Leu Thr Ser Lys Ser Glu Asn			
180	185	190	

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gca cta aac caa gta ggg agt gaa gat ttg tta ggt tgt cac ctg gaa	624
Ala Leu Asn Gln Val Gly Ser Glu Asp Asn Leu Gly Cys His Leu Glu	
195 200 205	
aag cca ttg gaa gaa gac aaa aat gaa ccg aat gga gaa gca gac ggt	672
Lys Gln Leu Glu Glu Asp Lys Asn Glu Pro Asn Gly Glu Ala Asp Gly	
210 215 220	
gag gat gat aat aac cgg gaa aag gat tgc agc tcc agt tca gaa gtt	720
Glu Asp Asp Asn Asn Arg Glu Lys Asp Cys Ser Ser Ser Ser Glu Val	
225 230 235 240	
gag tgg cag agt aaa tgc cga aag gaa agt act gca gag cct gac tct	768
Glu Ser Gln Ser Lys Cys Arg Lys Glu Ser Thr Ala Glu Pro Asp Ser	
245 250 255	
ctc tca cgg gat acc aga aca acc tct tcc ctt aaa tca agt acc tca	816
Leu Ser Arg Asp Thr Arg Thr Thr Ser Ser Leu Lys Ser Ser Thr Ser	
260 265 270	
ttc ccc ata tca ttc aag gcc tgg ata gac ctt aag tgg tta aac cag	864
Phe Pro Ile Ser Phe Lys Gly Ser Ile Asp Leu Lys Ser Asn Asn Gln	
275 280 285	
act tca tca ttg ttg cat ata caa gta tct ccc acc aaa tct agt aat	912
Pro Ser Ser Leu Leu His Ile Gln Val Ser Pro Thr Lys Ser Ser Asn	
290 295 300	
cta gat gca caa gtg aac act gaa caa gca tac tct cca cca ttt aga	960
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305 310 315 320	
tac taa	966
Tyr	

<210> 103

<211> 321

<212> FRT

<213> Saccharomyces cerevisiae

<400> 103

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Arg Glu Gly Trp Ile Glu Pro Gln Lys Val Asp Tyr Glu Leu Ile Phe
35 40 45

Thr Ile Asp Arg Leu Lys Asn Leu Val Asp Asn Lys Arg Glu Ala Leu
50 55 60

Thr Ala Glu Gln Pro Asp Ala Gly Glu Leu Ser Trp Arg Lys Val Phe
65 70 75 80

Asn Phe Ile Ser Arg Glu Ser Ser Glu Leu Asp Thr Arg Ile Tyr Val
85 90 95

Leu Ile Leu Leu Leu Ser Phe Leu Leu Pro Ile Ala Trp Thr Val Leu
100 105 110

Asp Gly Asp Arg Glu Thr Thr Leu Glu Asp Lys Asp Asn Asp Cys Asn
115 120 125

Val Asp Leu Ile Glu Asn Glu Arg Arg Leu Lys His Tyr Asn Asp Gly
130 135 140

Glu Arg Ala Val Leu Gln Phe Gly Lys Asn Arg Ser Glu Pro Ile Ile
145 150 155 160

Leu Ser Tyr Lys Asp Met Asn Val Leu Glu Gly Glu His Glu Phe Thr
165 170 175

Ser Lys Glu Glu His Ser Asn Ser His Leu Thr Ser Lys Ser Glu Asn
180 185 190

Ala Leu Asn Gln Val Gly Ser Glu Asp Leu Leu Gly Cys His Leu Glu
195 200 205

Lys Gln Leu Glu Glu Asp Lys Asn Glu Pro Asn Gly Glu Ala Asp Gly
210 215 220

Glu Asp Asp Asn Asn Arg Glu Lys Asp Cys Ser Ser Ser Ser Glu Val
225 230 235 240

Glu Ser Gln Ser Lys Cys Arg Lys Glu Ser Thr Ala Gln Pro Asp Ser
245 250 255

Leu Ser Arg Asp Thr Arg Thr Thr Ser Ser Leu Lys Ser Ser Thr Ser
260 265 270

Phe Pro Ile Ser Phe Lys Gly Ser Ile Asp Leu Lys Ser Leu Asn Gln
275 280 285

Pro Ser Ser Leu Leu His Ile Gln Val Ser Pro Thr Lys Ser Ser Asn
290 295 300

Leu Asp Ala Gln Val Asn Thr Glu Gln Ala Tyr Ser Gln Pro Phe Arg
305 310 315 320

Tyr

<210> 104
 <211> 504
 <212> DNA
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 1 5 10 15
 ttt gca tct gct tac atg ttc tgg caa ggc tta gcc att gct act aat 56
 Phe Ala Ser Ala Tyr Met Phe Trp Gln Gly Leu Ala Ile Ala Thr Asn
 20 25 30
 age gct tct cag att gtg gtg gty ctt taa ggc taa atg gaa cca gct 144
 Ser Ala Ser Pro Ile Val Val Val Ile Ser Gly Ser Met Glu Pro Ala
 35 40 45
 ttc caa agc ggt gac gtc ctt ttc cta tgg aat aga aat act ttc aac 192
 Phe Gln Arg Gly Asp Ile Leu Phe Leu Trp Asn Arg Asn Thr Phe Asn
 50 55 60
 caa gta ggt gat gtc gtg gtg tat gag gtc gaa ggc aaa caa atc ccc 240
 Gln Val Gly Asp Val Val Val Tyr Glu Val Glu Gly Lys Gln Ile Pro
 65 70 75 80
 att gtg cat aga gtt ttg agg caa cat aac aat cac gcg gac aag caa 288
 Ile Val His Arg Val Leu Arg Gln His Asn Asn His Ala Asp Lys Gln
 85 90 95
 ttc ctc ctg acc aac ggt gac aat aac gcc ggc aat gat atc tca cta 336
 Phe Leu Leu Thr Lys Gly Asp Asn Asn Ala Gly Asn Asp Ile Ser Leu
 100 105 110
 cat gct aat aag aaa att tac ttg aac aag tca aag gag att gta ggg 384

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Tyr Ala Asn Lys Lys Ile Tyr Leu Asn Lys Ser Lys Gln Ile Val Gly
115 120 125

acc gtc aag ggc tac ttt cca caa cta ggg tac att acg att cgg att 132
Thr Val Lys Gly Tyr Phe Pro Gln Leu Gly Tyr Ile Thr Ile Trp Ile
130 135 140

agc gag aac aaa tat gcc aag att gca ttg tta ggt atg ttg ggg ttg 480
Ser Glu Asn Lys Tyr Ala Lys Phe Ala Leu Leu Gly Met Leu Gly Leu
145 150 155 160

agt gct ctg ctg ggg ggc gag tag 504
Ser Ala Leu Leu Gly Gly Glu
165

<210> 105
<211> 167
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 105

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20 25 30

Ser Ala Ser Pro Ile Val Val Val Leu Ser Gly Ser Met Glu Pro Ala
35 40 45

Phe Gln Arg Gly Asp Ile Leu Phe Leu Trp Asn Arg Asn Thr Phe Asn
50 55 60

Gln val Gly Asp Val Val Val Tyr Glu Val Glu Gly Lys Gln Ile Pro
65 70 75 80

Ile Val His Arg Val Leu Arg Gln His Asn Asn His Ala Asp Lys Glu
85 90 95

Phe Leu Leu Thr Lys Gly Asp Asn Asn Ala Gly Asn Asp Ile Ser Leu
100 105 110

Tyr Ala Asn Lys Lys Ile Tyr Leu Asn Lys Ser Lys Glu Ile Val Gly
115 120 125

Thr Val Lys Gly Tyr Phe Pro Gln Leu Gly Tyr Ile Thr Ile Trp Ile
130 135 140

Ser Glu Asn Lys Tyr Ala Lys Phe Ala Leu Leu Gly Met Leu Gly Leu
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Ser Ala Leu Leu Gly Gly Gln
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<210> 106
<211> 2490
<212> DNA
<213> *Saccharomyces cerevisiae*

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<222> (1)..(2490)

<400> 106
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1 5 10 15
tcc tgg agc aat aaa gtc ctg ata gta cca acc ggt caa agc tcc tct 96

Fig. 1. Amino acid sequence of the protein.

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Ser Cys Ser Asn Iys Val Leu Ile Val Pro Thr Gly Gln Ser Ser Ser	
20 25 30	
zac gca atc act gat ttc tct gtc aga aag gag cat gct tgc gat aga	144
Asn Ala Ile Thr Asp Phe Ser Val Arg Iys Ala His Ala Cys Asp Arg	
35 40 45	
tgc aga ctg aac aac ttc aag tgt gac ggt tta aaa ccg aac tgt tca	192
Cys Arg Leu Lys Lys Ile Lys Cys Asp Gly Leu Lys Pro Asn Cys Ser	
50 55 60	
aac tgt gag aaa att gac ttc cct tgc aaa acc tgc gat aaa ctg tgc	240
Asn Cys Ala Lys Ile Asp Phe Pro Cys Lys Thr Ser Asp Lys Leu Ser	
65 70 75 80	
agg aga ggt ctt cca aag ggg tat aca gaa cta cta gaa aac gag gtc	288
Arg Arg Gly Leu Pro Lys Gly Tyr Thr Glu Leu Leu Glu Lys Glu Val	
85 90 95	
ghc cgt ttg aca aat atg aat gag agt tcc agc gcc aat gca aat tcc	336
Val Arg Leu Thr Asn Met Asn Ala Ser Ser Ser Ala Asn Ala Asn Ser	
100 105 110	
aat ttg cag ttc act aat gat aca ttt tat tgt ctt gat aat tac aac	384
Asn Leu Pro Phe Ile Asn Asp Thr Phe Tyr Cys Phe Asp Asn Tyr Asn	
115 120 125	
act cag tct gaa aat caa agg ttt ttg gga cat ttg aca tgg act att	432
Thr Glu Ser Glu Asn Gln Arg Phe Leu Gly His Leu Thr Trp Asn Ile	
130 135 140	
cta act aat act ttt cct act caa aaa gca gta gtt ttt aca gac gat	480
Leu Thr Asn Thr Phe Pro Thr Gln Lys Ala Val Val Phe Thr Asp Asp	
145 150 155 160	
cga aat aat att gat cta caa ctg caa ctg tta aca aat ttt ttg aac	528
Arg Asn Asn Ile Asp Leu Glu Leu Gln Leu Leu Thr Asn Phe Leu Asn	
165 170 175	
ctg aat ggt gac ttt aat cat ctc cca aat ttt ctt tta ctt aaa tat	576
Leu Asn Gly Asp Phe Asn His Leu Pro Asn Phe Leu Leu Leu Lys Tyr	
180 185 190	

gat tat aac ctt cag ttt ttg aaa aat ttg ttg tot gtc att att aaa	624
Asp Tyr Asn Leu Gln Phe Leu Lys Asn Leu Leu Ser Val Ile Ile Lys	
195 200 205	
gat ttt ttt aaa agg caa aat tot tlg cta ctt cta tta tac cct aca	672
Asp Phe Phe Lys Arg Gln Asn Ser Leu Leu Leu Leu Leu Tyr Pro Thr	
210 215 220	
aat tta tgg aaa aat ttg cta tta gac aag att aat tca acc gca atg	720
Asn Leu Trp Lys Asn Leu Leu Leu Asp Lys Ile Asn Ser Thr Ala Met	
225 230 235 240	
aaa ggt gaa cnc ata aat cta ctg gcg tta ctt tat att att caa ttt	768
Thr Gly Glu Pro Ile Thr Leu Leu Ala Leu Leu Tyr Ile Ile Gln Phe	
245 250 255	
aat tgg tot tgt ttt gat gat ttc aag ctt ttt aaa gtc aag aag ctt	816
Thr Trp Ser Cys Phe Asp Asp Phe Lys Leu Phe Lys Val Thr Lys Leu	
260 265 270	
tat gll tat ctg aca acc aac agc aaa tta gac ttg aaa gtt ttg caa	864
Ile Val Ser Leu Thr Thr Asn Ser Lys Leu Asp Leu Lys Val Leu Gln	
275 280 285	
ttg gtt aac tta tcc atc ttt tat ttt atg gag gcc tat gtt gac tat	912
Leu Val Asn Leu Ser Ile Phe Tyr Phe Met Gly Ala Ser Val Asp Ser	
290 295 300	
tgt aaa agt aaa agc tgg tta aca gaa cat tca aat gta aat tca gta	960
Cys Lys Ser Lys Ser Ser Leu Thr Glu His Ser Asn Val Asn Ser Val	
305 310 315 320	
ata tgg acc aat gat ttg cta aac cta aac ttt aca aat att ttg aat	1008
Ile Trp Thr Asn Asp Leu Leu Asn Leu Asn Phe Thr Asn Ile Leu Asn	
325 330 335	
atg gga ttg tac ata aat ccc aca aat ctu ull cct ctu leu ggc aac	1056
Met Gly Leu Tyr Ile Asn Pro Lys Asn Leu Ile Pro Ile Ser Gly Asn	
340 345 350	
aat aat aat aat aaa tot aat gaa gag gat gat aga ata gtg aca ttt	1104

Asn Asn Asn Asn Tyr Ser Asn Glu Glu Asp Asp Arg Ile Val Thr Phe		
355	360	365
tgg tgc ttt caa ttc tta agc tca tgg tgg tcc tta att caa gg- tta		1152
Trp Cys Phe Gln Phe Leu Ser Ser Trp Trp Ser Leu Ile Gln Gly Leu		
370	375	380
cca aag tcc aac ttt tta act gaa gaa ttt caa ccg aaa tca atc tgg		1200
Pro Lys Ser Asn Phe Leu Thr Glu Glu Phe Gln Pro Lys Ser Ile Ser		
385	390	395 400
gtt cta gaa atc ccc agg ctg aag ccc ttt gaa att tgg tta aac ttc		1248
Val Leu Glu Ile Pro Arg Leu Lys Pro Phe Glu Ile Leu Leu Asn Phe		
405	410	415
atc ata tat tct ttg gat gga tgt aat ttg ttg aat atc tca tca tta		1296
Ile Ile Tyr Ser Leu Asp Gly Cys Asn Leu Leu Asn Ile Ser Ser Leu		
420	425	430
aat gtc tgg gac cca aat ttc caa ttt ttc cag aat gaa ctg gaa agc		1344
Asn Val Ser Asp Pro Asn Phe Gln Phe Phe Gln Asn Glu Leu Glu Ser		
435	440	445
ttt aaa aaa aat tta tta ctg tgg aac ctt tat cac aat ttg agt gat		1392
Phe Lys Lys Asn Leu Leu Leu Trp Asn Leu Tyr His Asn Leu Ser Asp		
450	455	460
cac gat aac ttc cga ttc tta aca tcc agt tca aat aaa aac cta aca		1440
His Asp Asn Phe Arg Phe Leu Thr Ser Ser Ser Asn Lys Lys Leu Thr		
465	470	475 480
aca aat tta cta ctt aag aat ttg acg ggt cta aat cac aac ctc aat		1488
Thr Asn Leu Leu Leu Lys Asn Leu Thr Gly Leu Asn His Lys Leu Asn		
485	490	495
caa cct gat ttt gtg gag att caa tta act tta ttt tac ttg agt tta		1536
Gln Pro Asp Phe Val Gln Ile Gln Leu Thr Leu Phe Tyr Leu Ser Leu		
500	505	510
aaa tta atg act tta aag gaa ggg gac caa gat ttg aag aaa gag gat		1584
Lys Leu Met Thr Leu Lys Glu Gly Asp Gln Asp Leu Lys Lys Glu Asp		
515	520	525

atc tog tta gag ata ttg too ctu tan ttt tta att ctt aca gat gac	1632
Ile Ser Leu Glu Ile Ser Ser Ser Tyr Phe Leu Ile Leu Thr Asp Asp	
530 535 540	
tct aat aat gat gat aat caa cag tta caa cca cag caa sta aat ctg	1680
Ser Asn Asn Asp Asp Asn Gln Gln Leu Gln Pro Gln Gln Leu Asn Leu	
545 550 555 560	
tac cat ttt acg ccc ttc aat agt atc gac att att gac ttc tgt tta	1728
Tyr His Phe Thr Pro Phe Asn Ser Ile Asp Ile Ile Asp Leu Cys Leu	
565 570 575	
aac aat tta aac aat tgg tca tta tca ctt aaa tac gaa agt ggt caa	1776
Asn Asn Leu Asn Asn Trp Ser Leu Ser Leu Lys Tyr Glu Ser Gly Gln	
580 585 590	
aac cag ccc cac tca agt aaa ata aag ttt gaa aaa ttt caa aac ttt	1824
Asn Gln Pro His Ser Ser Lys Ile Lys Phe Glu Lys Phe Gln Asn Phe	
595 600 605	
tta aat cac tgg tgt cca ata tgg tac tat gat gaa ttt tcc aac aac	1872
Leu Asn His Thr Cys Pro Ile Thr Tyr Tyr Asp Glu Phe Ser Thr Asn	
610 615 620	
ccg tct tta caa atc ctg aac ctg aat ttc aaa tta ctt cct ttt gag	1920
Pro Phe Leu Gln Ile Leu Lys Ile Asn Phe Lys Leu Leu Pro Phe Glu	
625 630 635 640	
aca atc cat tac tca caa gaa gag cca cga ttg tta ata agt ttg aat	1968
Thr Ile His Tyr Ser Cln Glu Glu Gln Arg Leu Leu Ile Ser Leu Asn	
645 650 655	
aaa ttg aga tat ttg gat gcc gla tgg agc ttt aat tca agt tca gtc	2016
Lys Leu Arg Tyr Leu Asp Ala Val Ser Ser Phe Asn Ser Ser Ser Val	
660 665 670	
aag tgg aac ttc gcg tct aag gtc aat aac cag cta aac ctt ttg caa	2064
Lys Ser Asn Phe Ala Ser Lys Val Asn Thr Gln Leu Asn Leu Leu Gln	
675 680 685	
cac tgg agt tct aac tcc aat ttc cta gat gcg tca cca tac gat ttt	2112

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His Ser Ser Ser Asn Ser Asn Phe Leu Asp Ala Ser Pro Tyr Asp Phe
    690                695                700

aat aaa att ttt atg aac aac ttt gaa aac Lal gac Lac gaa aca gat    2160
Asn Lys Ile Phe Met Asn Asn Phe Gln Asn Tyr Asp Tyr Gln Thr Asp
    705                710                715                720

gaa gga tat gag gaa gat gat gat gaa gag gat agt gac agt gac aat    2208
Glu Gly Tyr Ala Glu Asp Asp Asp Glu Gln Asp Ser Asp Ser Asp Asn
                725                730                735

agc tta cca cta gaa att cct ttt aaa aaa agt aaa aat aaa tgc gag    2256
Ser Leu Pro Leu Glu Ile Pro Phe Lys Lys Ser Lys Asn Lys Cys Lys
                740                745                750

aat aag aat aaa gag ctt tca cca agg tta tcc cta ttt gaa aac aga    2304
Asn Arg Asn Lys Glu Leu Ser Gln Arg Leu Ser Leu Phe Gln Asn Arg
                755                760                765

gat agc aat tgg gln gat ttc aac aca gat aca aat tta aat tta aac    2352
Asp Ser Asn Ser Val Asp Phe Asn Thr Asp Thr Asn Leu Asn Leu Asn
                770                775                780

cct gat tgg cca tca gtt acg tct tct aag aaa aaa tat tta gat ccl    2400
Pro Asp Ser Pro Ser Val Thr Ser Ser Lys Lys Lys Tyr Leu Asp His
    785                790                795                800

att att tta gat aac cga gac abc gtr agc aac aat gac tcc agt aaa    2440
Ile Ile Leu Asp Asn Arg Asp Ile Val Ser Asn His Asp Ser Ser Lys
                805                810                815

caa aaa ttc aag atc cag aat att ttg aac tgg acc ttc taa    2490
Gln Lys Phe Lys Ile Gln Asn Ile Leu Asn Ser Thr Phe
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<210> 107

<211> 829

<212> PRT

<213> Saccharomyces cerevisiae

<400> 107

Seq. ID No. 1: 1-160 amino acids

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Ser Cys Ser Asn Lys Val Leu Ile Val Pro Thr Gly Gln Ser Ser Ser
20 25 30

Asn Ala Ile Thr Asp Phe Ser Val Arg Lys Ala His Ala Cys Asp Arg
35 40 45

Cys Arg Leu Lys Lys Ile Lys Cys Asp Gly Leu Lys Pro Asn Cys Ser
50 55 60

Asn Cys Ala Lys Ile Asp Phe Pro Cys Lys Thr Ser Asp Lys Leu Ser
65 70 75 80

Arg Arg Gly Leu Pro Lys Gly Tyr Thr Glu Leu Leu Glu Lys Glu Val
85 90 95

Val Arg Leu Thr Asn Met Asn Ala Ser Ser Ser Ala Asn Ala Asn Ser
100 105 110

Asn Leu Pro Phe Ile Asn Asp Thr Phe Tyr Cys Phe Asp Asn Tyr Asn
115 120 125

Thr Gln Ser Glu Asn Gln Arg Phe Leu Gly His Leu Thr Trp Asn Ile
130 135 140

Leu Thr Asn Thr Phe Pro Thr Glu Lys Ala Val Val Phe Thr Asp Asp
145 150 155 160

Arg Asn Asn Ile Asp Leu Gln Leu Gln Leu Leu Thr Asn Phe Leu Asn

FIG. 12: Amino acid sequence of the protein

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165	170	175
Leu Asn Gly Asp Phe Asn His Leu Pro Asn Phe Leu Leu Leu Lys Tyr		
180	185	190
Asp Tyr Asn Leu Gln Phe Leu Lys Asn Leu Leu Ser Val Ile Ile Lys		
195	200	205
Asp Phe Phe Lys Arg Gln Asn Ser Leu Leu Leu Leu Leu Tyr Pro Thr		
210	215	220
Asn Leu Trp Lys Asn Leu Leu Leu Asn Lys Ile Asn Ser Thr Ala Met		
225	230	235
Thr Gly Glu Pro Ile Thr Leu Leu Ala Leu Leu Tyr Ile Ile Gln Phe		
245	250	255
Thr Trp Ser Cys Phe Asp Asp Phe Lys Leu Phe Lys Val Thr Lys Leu		
260	265	270
Ile Val Ser Leu Thr Thr Asn Ser Lys Leu Asp Leu Lys Val Leu Gln		
275	280	285
Leu Val Asn Leu Ser Ile Phe Tyr Phe Met Gly Ala Ser Val Asp Ser		
290	295	300
Cys Lys Ser Lys Ser Ser Leu Thr Glu His Ser Asn Val Asn Ser Val		
305	310	315
Ile Trp Thr Asn Asp Leu Leu Asn Leu Asn Phe Thr Asn Ile Leu Asn		
325	330	335

Met Gly Leu Tyr Ile Asn Pro Lys Asn Leu Ile Pro Ile Ser Gly Asx
340 345 350

Asn Asn Asn Asn Lys Ser Asn Gln Glu Asp Asp Arg Ile Val Thr Phe
355 360 365

Trp Cys Phe Gln Phe Leu Ser Ser Trp Trp Ser Leu Ile Gln Gly Leu
370 375 380

Pro Lys Ser Asn Phe Leu Thr Glu Glu Phe Gln Pro Lys Ser Ile Ser
385 390 395 400

Val Leu Glu Ile Pro Arg Leu Lys Pro Phe Glu Ile Leu Leu Asn Phe
405 410 415

Ile Ile Tyr Ser Leu Asp Gly Cys Asn Leu Leu Asn Ile Ser Ser Leu
420 425 430

Asn Val Ser Asp Pro Asn Phe Gln Phe Phe Gln Asn Glu Leu Glu Ser
435 440 445

Phe Lys Lys Asn Leu Leu Leu Trp Asn Leu Tyr His Asn Leu Ser Asp
450 455 460

His Asp Asn Phe Arg Phe Leu Thr Ser Ser Ser Asn Lys Lys Leu Thr
465 470 475 480

Thr Asn Leu Leu Leu Lys Asn Leu Thr Gly Leu Asn His Lys Leu Asn
485 490 495

Seq. ID: 1 (Continued)

Gln Pro Asp Phe Val Glu Ile Gln Leu Thr Leu Phe Tyr Leu Ser Leu
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Lys Leu Met Thr Leu Lys Glu Gly Asp Gln Asp Leu Lys Lys Glu Asn
515 520 525

Ile Ser Val Glu Ile Leu Ser Leu Tyr Phe Leu Ile Leu Thr Asp Asp
530 535 540

Ser Asn Asn Asp Asp Asn Gln Gln Leu Gln Pro Gln Gln Leu Asn Leu
545 550 555 560

Tyr His Phe Thr Pro Phe Asn Ser Ile Asp Ile Ile Asp Leu Cys Leu
565 570 575

Asn Asn Leu Asn Asn Trp Ser Leu Ser Leu Lys Tyr Glu Ser Gly Gln
580 585 590

Asn Gln Pro His Ser Ser Lys Ile Lys Phe Glu Lys Phe Gln Asn Phe
595 600 605

Leu Asn His Trp Cys Pro Ile Trp Tyr Tyr Asp Glu Phe Ser Thr Asn
610 615 620

Pro Phe Leu Gln Ile Leu Lys Ile Asn Phe Lys Leu Leu Pro Phe Glu
625 630 635 640

Thr Ile His Tyr Ser Gln Gln Glu Gln Arg Leu Leu Ile Ser Leu Asn
645 650 655

Lys Leu Arg Tyr Leu Asp Ala Val Ser Ser Phe Asn Ser Ser Ser Val
660 665 670

Lys Ser Asn Phe Ala Ser Lys Val Asn Thr Gln Leu Asn Leu Leu Gln
675 680 685

His Ser Ser Ser Asn Ser Asn Phe Leu Asp Ala Ser Pro Tyr Asp Phe
690 695 700

Asn Lys Ile Phe Met Asn Asn Phe Gln Asn Tyr Asp Tyr Glu Thr Asp
705 710 715 720

Glu Gly Tyr Ala Glu Asp Asp Asp Gln Glu Asp Ser Asp Ser Asp Asn
725 730 735

Ser Leu Pro Leu Glu Ile Pro Phe Lys Lys Ser Lys Asn Lys Cys Lys
740 745 750

Asn Arg Asn Lys Glu Leu Ser Gln Arg Leu Ser Leu Phe Glu Asn Arg
755 760 765

Asp Ser Asn Ser Val Asp Phe Asn Thr Asp Thr Asn Leu Asn Leu Asn
770 775 780

Pro Asp Ser Pro Ser Val Thr Ser Ser Lys Lys Lys Tyr Leu Asp His
785 790 795 800

Ile Ile Leu Asp Asn Arg Asp Ile Val Ser Asn His Asp Ser Ser Lys
805 810 815

Gln Lys Phe Lys Ile Gln Asn Ile Leu Asn Ser Thr Phe
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Seq. ID No. 1

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<211> 1731

<212> DNA

<213> *Saccharomyces cerevisiae*

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<222> 11) .. (1731)

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agg cag aga gcc ttt att agt gga ata gtt gcc ctt att atc atc ggc 86

Arg His Arg Ala Phe Ile Ser Gly Ile Val Ala Leu Ile Ile Ile Gly

20 25 30

acc ttc ttc ctc act tcc ggt ctc cac cca gca cca cct cat gag gca 144

Thr Phe Phe Leu Thr Ser Gly Leu His Pro Ala Pro Pro His Glu Ala

35 40 45

aag cgt cca cag cat gga aaa ggt ccc atg cac tca ccc aaa tgt gag 192

Lys Arg Pro His His Gly Lys Gly Pro Met His Ser Pro Lys Cys Glu

50 55 60

aag att gan cca tta agt cca tca ttc aaa cat tcc gtc gac aca att 240

Lys Ile Glu Pro Leu Ser Pro Ser Phe Lys His Ser Val Asp Thr Ile

65 70 75 80

ctc cat gac cct gcc ttt aga aac agc tcc att gag aaa ctg tcc aat 298

Leu His Asp Pro Ala Phe Arg Asn Ser Ser Ile Glu Lys Leu Ser Asn

85 90 95

gct gtt aga atc ccc act gta gtc cca gac aaa aac ccc aac ccc gca 336

Ala Val Arg Ile Pro Thr Val Val Gln Asp Lys Asn Pro Asn Pro Ala

100 105 110

gat gat ccc gat ttc tat aag cat ttt tat gaa cta cac gac tat ttt 384

Asp Asp Pro Asp Phe Tyr Lys His Phe Tyr Glu Leu His Asp Tyr Phe

115 120 125

gag aag act ctc cct aat att cac aag cat ttg aca ttg gag aaa gtc	422
Gln Lys Thr Phe Pro Asn Ile His Lys His Leu Lys Leu Glu Lys Val	
130 135 140	
aat gag ctg ggt ctt cta cac aca tgg gaa ggt tct gat cct gat cta	480
Asn Glu Leu Gly Leu Leu Tyr Thr Trp Glu Gly Ser Asp Pro Asp Leu	
145 150 155 160	
aaa cca tta ctg tta atg gcc cat caa gat gtt gta cct gta aac aac	528
Lys Pro Leu Leu Leu Met Ala His Gln Asp Val Val Pro Val Asn Asn	
165 170 175	
gaa act tta cca tcc tgg aag ttc cct cca ttt tct qgt cac tac gat	576
Glu Thr Leu Ser Ser Trp Lys Phe Pro Pro Phe Ser Gly His Tyr Asp	
180 185 190	
cca gaa aca gat ttt gtt tgg ggg cgt ggt tct aac gat tgt aag aac	624
Pro Glu Thr Asp Phe Val Trp Gly Arg Gly Ser Asn Asp Cys Lys Asn	
195 200 205	
ttg tta att gcc gag ttt gaa gct atc gaa caa ctg ttg ata gat gga	672
Leu Leu Ile Ala Glu Phe Glu Ala Ile Glu Gln Leu Leu Ile Asp Gly	
210 215 220	
ttc aag ccc aac aga act att gtt atg tgg cct ggt ttt gat gaa gaa	720
Phe Lys Pro Asn Arg Thr Ile Val Met Ser Leu Gly Phe Asp Glu Glu	
225 230 235 240	
gca agc ggc acc ctc ggt gct gcc agc tta gcc tca ttt ctt cac gaa	768
Ala Ser Gly Thr Leu Gly Ala Ala Ser Leu Ala Ser Phe Leu His Glu	
245 250 255	
aga tat ggt gat gat ggt att tac agt atc atc gac gag ggt gaa ggt	816
Arg Tyr Gly Asp Asp Gly Ile Tyr Ser Ile Ile Asp Glu Gly Glu Gly	
260 265 270	
atc atg gaa gtc gac aag gat gtc ttt gtt gcc act cca atc aac gcc	864
Ile Met Glu Val Asp Lys Asp Val Phe Val Ala Thr Pro Ile Asn Ala	
275 280 285	
gaa aaa ggc tat gtc gac ttc gaa gtc agt att cta ggc cat ggt ggt	912

Glu Lys Gly Tyr Val Asp Phe Glu Val Ser Ile Leu Gly His Gly Gly	
290 295 300	
cat tcc tct gtc cca cct gat cat acc aca alc ggt atc got tca gaa	960
His Ser Ser Val Pro Pro Asp His Thr Thr Ile Gly ile Ala Ser Glu	
305 310 315 320	
ctg atc act gaa ttt gaa gcc aac cca ttt gac tac gaa ttt gag ttt	1008
Leu Ile Thr Glu Phe Glu Ala Asn Pro Phe Asp Tyr Glu Phe Glu Phe	
325 330 335	
gac aat cca atc tat gga ttg ttg aca tgt got got gaa cat tct aaa	1056
Asp Asn Pro Ile Tyr Gly Leu Leu Thr Cys Ala Ala Glu His Ser Lys	
340 345 350	
tct tta agt aag gat gtg aag aag aca att ttg ggc gca aca ttc tgt	1104
Ser Leu Ser Lys Arg Val Lys Lys Thr Ile Leu Gly Ala Pro Phe Cys	
355 360 365	
cct aga agt aag gac aag ctc gtt gag tac att tcc aac cca tta cat	1152
Pro Arg Arg Lys Asp Lys Leu Val Glu Tyr Ile Ser Asn Gln Ser His	
370 375 380	
ttg cgc agc tta ata aga aca uca caa got gtt gat acc alc aat ggt	1200
Leu Arg Ser Leu Ile Arg Thr Thr Gln Ala Val Asp Ile Ile Asn Gly	
385 390 395 400	
ggt got aaa got aat got ctg ccc gaa aac acc aga ctc ttg atc aat	1248
Gly Val Lys Ala Asn Ala Leu Pro Glu Thr Thr Arg Phe Leu Ile Asn	
405 410 415	
cac aga att aat tta cat tct tct gtg gcc gaa gtc ttt gaa aga aac	1296
His Arg Ile Asn Leu His Ser Ser Val Ala Glu Val Phe Glu Arg Asn	
420 425 430	
ata gaa tat gag aaa aag att got gag aag tat gcc tat ggt tta tct	1344
Ile Glu Tyr Ala Lys Lys Ile Ala Glu Lys Tyr Gly Tyr Gly Leu Ser	
435 440 445	
aag aac ggt gac gat tac att atc cct gaa acc gag tta ggt ccc att	1392
Lys Asn Gly Asp Asp Tyr Ile Ile Pro Glu Thr Glu Leu Gly His Ile	
450 455 460	

FIG. 10: Amino acid sequence of the protein.

gac att act ctc ttg aga gaa ttg gaa cca gca cca ctt tgg cca agt 1440
Asp Ile Thr Leu Leu Arg Glu Leu Gln Pro Ala Pro Leu Ser Pro Ser
465 470 475 480

tca ggc cct ggt tgg gac att ttg gca ggt act att caa gat gtt ttt 1488
Ser Gly Pro Val Trp Asp Ile Leu Ala Gly Thr Ile Gln Asp Val Phe
485 490 495

gaa aac ggt gtt cta caa aac aac gaa gag ttc tat glg act act ggt 1536
Glu Asn Gly Val Leu Gln Asn Asn Glu Glu Phe Tyr Val Thr Thr Gly
500 505 510

tta ttc tct ggt aac acc gat act aaa tac tac tgg aat ttg tcc aag 1584
Leu Phe Ser Gly Asn Thr Asp Thr Lys Tyr Tyr Trp Asn Leu Ser Lys
515 520 525

aac att tat agg ttt gtt ggc tct atc att gat att gat tta ctg aag 1632
Asn Ile Tyr Arg Phe Val Gly Ser Ile Ile Asp Ile Asp Leu Leu Lys
530 535 540

aca ttg cat tgg gtt aat gaa cac gtg gat gtc cca ggt cat cca cct 1680
Thr Leu His Ser Val Asn Glu His Val Asp Val Pro Gly His Leu Ser
545 550 555 560

gac att ggc ttt gtt tac gag tat atc ggt aat gtt aac gaa tac gct 1728
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565 570 575

taa 1731

<210> 109

<211> 576

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 109

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1

5

10

15

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 20 25 30

Thr Phe Phe Leu Thr Ser Gly Leu His Pro Ala Pro Pro His Glu Ala
 35 40 45

Lys Arg Pro His His Gly Lys Gly Pro Met His Ser Pro Lys Cys Glu
 50 55 60

Lys Ile Glu Pro Leu Ser Pro Ser Phe Lys His Ser Val Asp Thr Ile
 65 70 75 80

Leu His Asp Pro Ala Phe Arg Asn Ser Ser Ile Glu Lys Leu Ser Asn
 85 90 95

Ala Val Arg Ile Pro Thr Val Val Glu Asp Lys Asn Pro Asn Pro Ala
 100 105 110

Asp Asp Pro Asp Phe Tyr Lys His Phe Tyr Glu Leu His Asp Tyr Phe
 115 120 125

Glu Lys Thr Phe Pro Asn Ile His Lys His Leu Lys Leu Glu Lys Val
 130 135 140

Asn Glu Leu Gly Leu Leu Tyr Thr Trp Glu Gly Ser Asp Pro Asp Leu
 145 150 155 160

Lys Pro Leu Leu Leu Met Ala His Gln Asp Val Val Pro Val Asn Asn
 165 170 175

Glu Thr Leu Ser Ser Trp Lys Phe Pro Pro Phe Ser Gly His Tyr Asp

180	185	190
Pro Glu Thr Asp Phe Val Trp Gly Arg Gly Ser Asn Asp Cys Lys Asn		
195	200	205
Leu Leu Ile Ala Glu Phe Glu Ala Ile Glu Gln Leu Leu Ile Asp Gly		
210	215	220
Phe Lys Pro Asn Arg Thr Ile Val Met Ser Leu Gly Phe Asp Glu Glu		
225	230	235
Ala Ser Gly Thr Leu Gly Ala Ala Ser Leu Ala Ser Phe Leu His Gln		
245	250	255
Arg Tyr Gly Asp Asp Gly Ile Tyr Ser Ile Ala Asp Glu Gly Glu Gly		
260	265	270
Ile Met Glu Val Asp Lys Asp Val Phe Val Ala Thr Pro Ile Asn Ala		
275	280	285
Glu Lys Gly Tyr Val Asp Phe Glu Val Ser Ile Leu Gly His Gly Gly		
290	295	300
His Ser Ser Val Pro Pro Asp His Thr Thr Ile Gly Ile Ala Ser Glu		
305	310	315
Leu Ile Thr Glu Phe Glu Ala Asn Pro Phe Asp Tyr Glu Phe Glu Phe		
325	330	335
Asp Asn Pro Ile Tyr Gly Leu Leu Thr Cys Ala Ala Glu His Ser Lys		
340	345	350

Ser Leu Ser Lys Asp Val Lys Lys Thr Ile Leu Gly Ala Pro Phe Cys
 355 360 365

Pro Arg Arg Lys Asp Lys Leu Val Glu Tyr Ile Ser Asn Gln Ser His
 370 375 380

Leu Arg Ser Leu Ile Arg Thr Thr Gln Ala Val Asp Ile Ile Asn Gly
 385 390 395 400

Gly Val Lys Ala Asn Ala Leu Pro Glu Thr Thr Arg Phe Leu Ile Asn
 405 410 415

His Arg Ile Asn Leu His Ser Ser Val Ala Glu Val Phe Glu Arg Asn
 420 425 430

Ile Glu Tyr Ala Lys Lys Ile Ala Glu Lys Tyr Gly Tyr Gly Leu Ser
 435 440 445

Lys Asn Gly Asp Asp Tyr Ile Ile Pro Glu Thr Glu Leu Gly His Ile
 450 455 460

Asp Ile Thr Leu Leu Arg Glu Leu Glu Pro Ala Pro Leu Ser Pro Ser
 465 470 475 480

Ser Gly Pro Val Trp Asp Ile Leu Ala Gly Thr Ile Gln Asp Val Phe
 485 490 495

Glu Asn Gly Val Leu Glu Asn Asn Glu Glu Phe Tyr Val Thr Thr Gly
 500 505 510

Leu Phe Ser Gly Asn Thr Asp Thr Lys Tyr Tyr Trp Asn Leu Ser Lys

515

520

525

Asn Ile Tyr Arg Phe Val Gly Ser Ile Ile Asp Ile Asp Leu Leu Lys
 530 535 540

Thr Leu His Ser Val Asn Glu His Val Asp Val Pro Gly His Leu Ser
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gat tac cca aag gag ttt gtc agt ttc tta aat agc tca cac tct cct 36
 Asp Tyr Pro Lys Glu Phe Val Ser Phe Leu Asn Ser Ser His Ser Pro
 20 25 30

tac cac aca gtt cat aac atc aaa aag cat ctg gtg tca aat ggc ttc 144
 Tyr His Thr Val His Asn Ile Lys Lys His Leu Val Ser Asn Gly Phe
 35 40 45

aaa gag ttg agc gaa cgt gac tgg tgg gct ggc cac gtc gca caa aaa 192
 Lys Glu Leu Ser Glu Arg Asp Ser Trp Ala Gly His Val Ala Gln Lys
 50 55 60

cac gca gaa ctt ttg ggg cta ata gcc aaa gaa ctc gcc att gat aca 729
 His Ala Glu Leu Leu Gly Leu Ile Ala Lys Glu Leu Ala Ile Asp Thr

225	230	235	240	
att gaa gac att gaa gac ttc gaa ttg atc ctt tat gat cat aat gca				768
Ile Glu Asp Ile Glu Asp Phe Glu Leu Ile Leu Tyr Asp His Asn Ala				
245	250	255		
Leu acf cta ggt ggg ttc aac gat gag ttt gtc ttc tct ggt cga ttg				816
Ser Thr Leu Gly Gly Phe Asn Asp Glu Phe Val Phe Ser Gly Arg Leu				
260	265	270		
gat aat ctg aca tct tgt ttc acg tca atg cac ggt tta acg ttg gcg				864
Asp Asn Leu Thr Ser Cys Phe Thr Ser Met His Gly Leu Thr Leu Ala				
275	280	285		
gct gac aca gaa att gac cga gaa tca ggc att aga ttg atg gca tgc				912
Ala Asp Thr Glu Ile Asp Arg Glu Ser Gly Ile Arg Leu Met Ala Cys				
290	295	300		
ttt gat cat gag gag att ggc tca tcc tcc gcc caa ggg gca gat tct				960
Phe Asp His Glu Glu Ile Gly Ser Ser Ser Ala Gln Gly Ala Asp Ser				
305	310	315	320	
aac ttc ttg cct aat ata ttg gaa agg ttg tcc atc ctg aag ggg gac				1008
Asn Phe Leu Pro Asn Ile Leu Glu Arg Leu Ser Ile Leu Tyr Gly Asp				
325	330	335		
ggc tct gat caa act aaa cct ttg ttc cac tct gca ata tct gaa act				1056
Gly Ser Asp Gln Thr Lys Pro Leu Phe His Ser Ala Ile Leu Glu Thr				
340	345	350		
tac gct aag tct tct ttc ctt tca tct gat gct gct cat gca gtt cac				1104
Ser Ala Lys Ser Phe Phe Leu Ser Ser Asp Val Ala His Ala Val His				
355	360	365		
cca aac tat gca aac aca tac gaa agc caa cac aaa ccc ttc ttg ggt				1152
Pro Asn Tyr Ala Asn Lys Tyr Glu Ser Gln His Lys Pro Leu Leu Gly				
370	375	380		
ggt ggt ccc gta atc aag att aac ggc aat caa cgt tac atg acc aat				1200
Gly Gly Pro Val Ile Lys Ile Asn Ala Asn Gln Arg Tyr Met Thr Asn				
385	390	395	400	

Sequence of the protein

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cct ttg aac ttg ttt gtc gta gct aac gac tca cca tgc ggt tct aac	1296
Pro Leu Gln Leu Phe Val Val Ala Asn Asp Ser Pro Cys Gly Ser Thr	
420 425 430	

atc ggc ccc att ttg gcc tca aag aca ggt att aga act cta gac ttg	1344
Ile Gly Pro Ile Leu Ala Ser Lys Thr Gly Ile Arg Thr Leu Arg Leu	
435 440 445	

ggc aac ccc ggg ttg agt atg cat tgc att aga gag aac ggt ggt tct	1392
Gly Asn Pro Val Leu Ser Met His Ser Ile Arg Glu Thr Gly Gly Ser	
450 455 460	

gca gac ctg gag ttc caa atc aag tta ttt aag gaa ttt ttt gaa cgc	1440
Ala Asp Leu Glu Phe Gln Ile Lys Leu Phe Lys Glu Phe Phe Glu Arg	
465 470 475 480	

lac act tcc ala gaa tct gaa att gtt gtc taa	1473
Tyr Thr Ser Ile Glu Ser Glu Ile Val Val	
485 490	

<310> 111
 <311> 490
 <312> FRT
 <313> *Saccharomyces cerevisiae*

<400> 111

Met Phe Arg Ile Gln Leu Arg Thr Met Ser Ser Lys Thr Cys Lys Ser
1 5 10 15

Asp Tyr Pro Lys Gln Phe Val Ser Phe Leu Asn Ser Ser His Ser Pro
20 25 30

Tyr His Thr Val His Asn Ile Lys Lys His Leu Val Ser Asn Gly Phe
35 40 45

Lys Glu Leu Ser Glu Arg Asp Ser Trp Ala Gly His Val Ala Gln Lys
50 55 60

Gly Lys Tyr Phe Val Thr Arg Asn Gly Ser Ser Ile Ile Ala Phe Ala
65 70 75 80

Val Gly Gly Lys Trp Glu Pro Gly Asn Pro Ile Ala Ile Thr Gly Ala
85 90 95

His Thr Asp Ser Pro Ala Leu Arg Ile Lys Pro Ile Ser Lys Arg Val
100 105 110

Ser Glu Lys Tyr Leu Glu Val Gly Val Glu Thr Tyr Gly Gly Ala Ile
115 120 125

Trp His Ser Trp Phe Arg Lys Asp Leu Gly Val Ala Gly Arg Val Phe
130 135 140

Val Lys Asp Ala Lys Thr Gly Lys Ser Ile Ala Arg Leu Val Asp Leu
145 150 155 160

Asn Arg Pro Leu Leu Lys Ile Pro Thr Leu Ala Ile His Leu Asp Arg
165 170 175

Asp Val Asn Gln Lys Phe Glu Phe Asn Arg Glu Thr Gln Leu Leu Pro
180 185 190

Ile Gly Gly Leu Gln Glu Asp Lys Thr Glu Ala Lys Thr Gln Lys Glu
195 200 205

Protein Data Bank (PDB) Entry: 1A2A

Ile Asn Asn Gly Glu Phe Thr Ser Ile Lys Thr Ile Val Gln Arg His
210 215 220

His Ala Glu Leu Leu Gly Leu Ile Ala Lys Glu Leu Ala Ile Asp Thr
225 230 235 240

Ile Glu Asp Ile Glu Asp Phe Glu Leu Ile Leu Tyr Asp His Asn Ala
245 250 255

Ser Thr Leu Gly Gly Phe Asn Asp Glu Phe Val Phe Ser Gly Arg Leu
260 265 270

Asp Asn Leu Thr Ser Cys Phe Thr Ser Met His Gly Leu Thr Leu Ala
275 280 285

Ala Asp Thr Glu Ile Asp Arg Glu Ser Gly Ile Arg Leu Met Ala Cys
290 295 300

Phe Asp His Gln Glu Ile Gly Ser Ser Ser Ala Gln Gly Ala Asp Ser
305 310 315 320

Asn Phe Leu Pro Asn Ile Leu Glu Arg Leu Ser Ile Leu Lys Gly Asp
325 330 335

Gly Ser Asp Gln Thr Lys Pro Leu Phe His Ser Ala Ile Leu Glu Thr
340 345 350

Ser Ala Lys Ser Phe Phe Leu Ser Ser Asp Val Ala His Ala Val His
355 360 365

Pro Asn Tyr Ala Asn Lys Tyr Glu Ser Gln His Lys Pro Leu Leu Gly
370 375 380

Gly Gly Pro Val Ile Lys Ile Asn Ala Asn Gln Arg Tyr Met Thr Asn
 305 320 335 400

Ser Pro Gly Leu Val Leu Val Lys Arg Leu Ala Glu Ala Ala Lys Val
 405 410 415

Pro Leu Gln Leu Phe Val Val Ala Asn Asp Ser Pro Cys Gly Ser Thr
 420 425 430

Ile Gly Pro Ile Leu Ala Ser Lys Thr Gly Ile Arg Thr Leu Asp Leu
 435 440 445

Gly Asn Pro Val Leu Ser Met His Ser Ile Arg Glu Thr Gly Gly Ser
 450 455 460

Ala Asp Leu Glu Phe Gln Ile Lys Leu Phe Lys Glu Phe Phe Glu Arg
 465 470 475 480

Tyr Thr Ser Ile Glu Ser Glu Ile Val Val
 485 490

<210> 112
 <211> 570
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(570)

<400> 112
 atg gat gat aag aaa aca tgg agt aca gtc aat ttg aga acc ttc aat

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Met	Asp	Asp	Lys	Lys	Thr	Trp	Ser	Thr	Val	Thr	Leu	Arg	Thr	Phe	Asn		
1			5						10					15			
cag	ctg	gta	acg	tct	tgg	tta	att	gga	tac	tca	aaa	aag	atg	gal	agc		96
Gln	Leu	Val	Thr	Ser	Ser	Leu	Ile	Gly	Tyr	Ser	Lys	Lys	Met	Asp	Ser		
			20					25					30				
atg	aat	cac	aag	atg	gaa	gga	aat	ggg	ggc	cac	gac	cac	agt	gat	atg		144
Met	Asn	His	Lys	Met	Glu	Gly	Asn	Ala	Gly	His	Asp	His	Ser	Asp	Met		
			35				40					45					
cat	atg	gga	gat	gga	gat	gat	acc	tgt	tgg	atg	aat	atg	cta	ttt	tgg		192
His	Met	Gly	Asp	Gly	Asp	Asp	Thr	Cys	Ser	Met	Asn	Met	Leu	Phe	Ser		
			50				55					60					
tgg	tca	tac	aag	aat	acg	tgt	gtc	gtc	ttt	gaa	tgg	tgg	cat	atc	aag		240
Trp	Ser	Tyr	Lys	Asn	Thr	Cys	Val	Val	Phe	Glu	Trp	Trp	His	Ile	Lys		
65					70					75				80			
acc	ctg	act	gga	acg	att	tta	agt	tgt	tta	gca	att	ttt	ggg	cta	gac		288
Thr	Leu	Pro	Gly	Leu	Ile	Leu	Ser	Cys	Leu	Ala	Ile	Phe	Gly	Leu	Ala		
				85					90					95			
tac	ctc	tat	gag	tac	tta	aag	tac	tgt	gtc	cat	aag	aga	caa	tta	tcc		336
Tyr	Leu	Tyr	Glu	Tyr	Leu	Lys	Tyr	Cys	Val	His	Lys	Arg	Gln	Leu	Ser		
			100					105					110				
cag	aga	gta	ttg	tta	cca	aat	aga	tct	ctg	acc	aag	atc	aac	caa	gcc		384
Gln	Arg	Val	Leu	Leu	Pro	Asn	Arg	Ser	Leu	Thr	Lys	Ile	Asn	Gln	Ala		
			115				120					125					
gac	aaa	gtg	tcc	aat	agt	att	cta	tat	ggg	ttg	caa	gtg	gga	ttc	tca		432
Asp	Lys	Val	Ser	Asn	Ser	Ile	Leu	Tyr	Gly	Leu	Gln	Val	Gly	Phe	Ser		
			130				135				140						
ttc	atg	ctc	atg	ctt	gta	tcc	atg	act	tat	aat	ggg	tgg	tta	atg	tta		480
Phe	Met	Leu	Met	Leu	Val	Phe	Met	Thr	Tyr	Ser	Gly	Trp	Leu	Met	Leu		
145					150					155				160			
gat	gtc	gtg	tgt	ggg	gca	ata	tgg	ggg	aat	tac	agc	tgg	tgt	act	tgg		528
Ala	Val	Val	Cys	Gly	Ala	Ile	Trp	Gly	Asn	Tyr	Ser	Trp	Cys	Thr	Ser		
				165				170					175				

tat agt cct gag ata gat gac agc tcc ctc gcc tgc cat taa 570
 Tyr Ser Pro Glu Ile Asp Asp Ser Ser Leu Ala Cys His
 190 185

<210> 113
 <211> 163
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 113

Met Asp Asp Lys Lys Thr Trp Ser Thr Val Thr Leu Arg Thr Phe Asn
 1 5 10 15

Gln Leu Val Thr Ser Ser Leu Ile Gly Tyr Ser Lys Lys Met Asp Ser
 20 25 30

Met Asn His Lys Met Glu Gly Asn Ala Gly His Asp His Ser Asp Met
 35 40 45

His Met Gly Asp Gly Asp Asp Thr Cys Ser Met Asn Met Leu Phe Ser
 50 55 60

Trp Ser Tyr Lys Asn Thr Cys Val Val Phe Glu Trp Trp His Phe Lys
 65 70 75 80

Thr Leu Pro Gly Leu Ile Leu Ser Cys Leu Ala Ile Phe Gly Leu Ala
 85 90 95

Tyr Leu Tyr Glu Tyr Leu Lys Tyr Cys Val His Lys Arg Gln Leu Ser
 100 105 110

Gln Arg Val Leu Leu Pro Asn Arg Ser Leu Thr Lys Ile Asn Gln Ala

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115

120

125

Asp Lys Val Ser Asn Ser Ile Leu Tyr Gly Leu Gln Val Gly Phe Ser
 130 135 140

Phe Met Leu Met Leu Val Phe Met Thr Tyr Asn Gly Trp Leu Met Leu
 145 150 155 160

Ala Val Val Cys Gly Ala Ile Trp Gly Asn Tyr Ser Trp Cys Thr Ser
 165 170 175

Tyr Ser Pro Glu Ile Asp Asp Ser Ser Leu Ala Cys His
 180 185

<210> 114
 <211> 585
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(585)

<400> 114
 atg att cat gca gtt cta ata ttc aat aag aaa tgc caa cca aga tta 48
 Met Ile His Ala Val Leu Ile Phe Asn Lys Lys Cys Gln Pro Arg Leu
 1 5 10 15
 gtg aaa ttc tac acg ccg gtc gac ctt cca aag caa aaa ctg cta tta 96
 Val Lys Phe Tyr Thr Pro Val Asp Leu Pro Lys Gln Lys Leu Leu Leu
 20 25 30
 gag caa gla tac gaa ttg att tct caa agg aat agc gat ttt caa agt 144
 Glu Gln Val Tyr Gln Leu Ile Ser Gln Arg Asn Ser Asp Phe Gln Ser
 35 40 45

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tct ttt tta gtc aag cca cca cag ctt ctg tta agc aat gaa aat aat Ser Phe Leu Val Thr Pro Pro Ser Leu Leu Leu Ser Asn Glu Asn Asn 50 55 60	192
aat gat gag gta aac aat gaa gat att caa atc atc tat aaa aac tac Asn Asp Glu Val Asn Asn Glu Asp Ile Gln Ile Ile Tyr Lys Asn Tyr 65 70 75 80	240
gct aca cta tat ttc act ttc atc gtc gat gat caa gaa tca gaa ctg Ala Thr Leu Tyr Phe Thr Phe Ile Val Asp Asp Gln Glu Ser Glu Leu 85 90 95	288
gcc ata tta gat ctg atc caa act tct ggc gaa tca ttg gac cgt cgt Ala Ile Leu Asp Leu Ile Gln Thr Phe Val Glu Ser Leu Asp Arg Cys 100 105 110	336
ttt act gaa gtc aat gaa ctt gat ttg att ttc aac tgg caa act ttg Phe Thr Glu Val Asn Glu Leu Asp Leu Ile Phe Asn Trp Gln Thr Leu 115 120 125	384
gaa agt gtc tta gaa gaa atc gtg cag qgg ggc atg ctc att gaa aca Glu Ser Val Leu Glu Gln Ile Val Gln Gly Gly Met Val Ile Glu Thr 130 135 140	432
aac gtc aac aga ata gtt gct tat gtt gac gaa ctc aac aac gct ggc Asn Val Asn Arg Ile Val Ala Ser Val Asp Gln Leu Asn Lys Ala Ala 145 150 155 160	480
gag tcc aca gat agt aaa att gga aga cta aag tcc act gga ttt gga Glu Ser Thr Asp Ser Lys Ile Gly Arg Leu Thr Ser Thr Gly Phe Gly 165 170 175	528
agc gca cta caa gag ttt gct caa ggc gga ttt gca caa tgg gca aag Ser Ala Leu Gln Ala Phe Ala Gln Gly Gly Phe Ala Gln Trp Ala Thr 180 185 190	576
ggg caa taa Gly Gln	585

<211> 194

<212> PPT

<213> *Saccharomyces cerevisiae*

<400> 115

Met Ile His Ala Val Leu Ile Phe Asn Lys Lys Cys Glu Pro Arg Leu
1 5 10 13

Val Lys Phe Tyr Thr Pro Val Asp Leu Pro Lys Gln Lys Leu Leu Leu
30 35 38

Glu Gln Val Tyr Glu Leu Ile Ser Gln Arg Asn Ser Asp Phe Gln Ser
35 40 45

Ser Phe Leu Val Thr Pro Pro Ser Leu Leu Leu Ser Asn Glu Asn Asn
50 55 60

Asn Asp Glu Val Asn Asn Glu Asp Ile Gln Ile Ile Tyr Lys Asn Tyr
65 70 75 80

Ala Thr Leu Tyr Phe Thr Phe Ile Val Asp Asp Gln Glu Ser Glu Leu
85 90 95

Ala Ile Leu Asp Leu Ile Gln Thr Phe Val Glu Ser Leu Asp Arg Cys
100 105 110

Phe Thr Glu Val Asn Glu Leu Asp Leu Ile Phe Asn Trp Gln Thr Leu
115 120 125

Gln Ser Val Leu Glu Glu Ile Val Gln Gly Gly Met Val Ile Glu Thr
130 135 140

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Asn Val Asn Arg Ile Val Ala Ser Val Asp Glu Leu Asn Lys Ala Ala
 145 150 155 160

Glu Ser Thr Asp Ser Lys Ile Gly Arg Leu Thr Ser Thr Gly Phe Gly
 165 170 175

Ser Ala Leu Gln Ala Phe Ala Gln Gly Gly Phe Ala Gln Trp Ala Thr
 180 185 190

Gly Gln

<210> 116
 <211> 1038
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1038)

<400> 116
 atg gaa gca cat aac caa ttt ttg aag act ttc caa aaa gaa cgt cat 48
 Met Glu Ala His Asn Gln Phe Leu Lys Thr Phe Gln Lys Gln Arg His
 1 5 10 15
 gat atg aaa gaa gct gaa aag gat gaa atc ctt ttg atg gaa aac agc 96
 Asp Met Lys Glu Ala Glu Lys Asp Glu Ile Leu Leu Met Glu Asn Ser
 20 25 30
 cgt aga ttc gtg atg ttc cct atc aaa tac cac gaa atc tgg gct gct 144
 Arg Arg Phe Val Met Phe Pro Ile Lys Tyr His Gln Ile Trp Ala Ala
 35 40 45
 tac aag aag gtt gaa gcc tcc ttc tgg act gcg gaa gaa atc gaa ttg 192
 Tyr Lys Lys Val Glu Ala Ser Phe Trp Thr Ala Glu Glu Ile Glu Leu
 50 55 60

gct aag gac act gaa gat ttc caa aaa ttg act gat gac cag aag acc	240
Ala Lys Asp Thr Glu Asp Phe Gln Lys Leu Thr Asp Asp Gln Lys Thr	
65 70 75 80	
tac atc ggt aac ttg tta gcc ttg tcc att tct tct gac aac ctt gtc	388
Tyr Ile Gly Asn Leu Leu Ala Leu Ser Ile Ser Ser Asp Asn Leu Val	
85 90 95	
aac aag tac ttg atc gaa aac ttt tct gcc caa ttg caa aac cct gaa	336
Asn Lys Tyr Leu Ile Glu Asn Phe Ser Ala Gln Leu Gln Asn Pro Glu	
100 105 110	
ggt aag agt ttc tac ggg ttc cag att atg atg gaa aac atc tac tct	384
Gly Lys Ser Phe Tyr Gly Phe Gln Ile Met Met Glu Asn Ile Tyr Ser	
115 120 125	
gaa ggt tac tcc atg atg gtt gat gcc ttc ttc aag gac cct aag aac	432
Glu Val Tyr Ser Met Met Val Asp Ala Phe Phe Lys Asp Pro Lys Asn	
130 135 140	
atc cct cta ttc aag gaa att gcc aat ttg cct gaa gtc aag cat aag	480
Ile Pro Leu Phe Lys Glu Ile Ala Asn Leu Pro Glu Val Tyr His Lys	
145 150 155 160	
gct gcc ttc atc gag aga tgg att tcc aac gal gac ayc ttg tat gct	538
Ala Ala Phe Ile Glu Arg Trp Ile Ser Asn Asp Asp Ser Leu Tyr Ala	
165 170 175	
gaa aga cta gta gca ttt gct gca aag gaa ggt att ttc caa gct ggt	576
Glu Arg Leu Val Ala Phe Ala Ala Lys Glu Gly Ile Phe Gln Ala Gly	
180 185 190	
aac cat gct tct atg ttc tgg ttg act gac aaa aag att atg cca ggt	624
Asn Tyr Ala Ser Met Phe Trp Leu Thr Asp Lys Lys Ile Met Pro Gly	
195 200 205	
tta gca atg gcc aac aga aac atc tgt aga gaa aga ggt gaa lac act	672
Leu Ala Met Ala Asn Arg Asn Ile Cys Arg Asp Arg Gly Ala Tyr Thr	
210 215 220	
gac ttt tca tcc ttg cta ttc gcc cat ttg aga acc aag cca aac ccc	720

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Asp	Phe	Ser	Cys	Leu	Leu	Phe	Ala	His	Leu	Arg	Thr	Lys	Pro	Asp	Pro		
225					230					235					240		
aag	atc	att	gaa	aaa	atc	att	acc	gaa	gcc	gtg	gaa	att	gaa	aag	gaa		768
Lys	Ile	Ile	Glu	Lys	Ile	Ile	Thr	Glu	Ala	Val	Glu	Ile	Glu	Lys	Glu		
				245					250					255			
tac	tac	tca	aac	tct	ttg	cca	gtc	gaa	aaa	ttt	ggc	atg	gac	ttg	aag		816
Tyr	Tyr	Ser	Asn	Ser	Leu	Pro	Val	Glu	Lys	Phe	Gly	Met	Asp	Leu	Lys		
			260				265						270				
agg	atc	cac	acc	tac	ata	gaa	ttt	gtc	gct	gac	ggc	cta	Gla	caa	ggc		864
Ser	Ile	His	Thr	Tyr	Ile	Glu	Phe	Val	Ala	Asp	Gly	Leu	Leu	Gln	Gly		
		275					280						285				
ttc	ggc	aac	gaa	aaa	tac	tac	aac	gcc	gtc	aac	cca	ttc	gaa	ttc	atg		912
Phe	Gly	Asn	Glu	Lys	Tyr	Tyr	Asn	Ala	Val	Asn	Pro	Phe	Glu	Phe	Met		
	290						295					300					
gag	gac	gtc	gct	acc	gct	ggc	aag	acc	acc	ttc	ttt	gaa	aag	aag	gtt		960
Glu	Asp	Val	Ala	Thr	Ala	Gly	Lys	Thr	Thr	Phe	Phe	Glu	Lys	Lys	Val		
305				310					315					320			
tcc	gac	tac	caa	aag	gcc	agt	gac	atg	tct	aag	tcc	gct	acc	cca	tcc		1008
Ser	Asp	Tyr	Gln	Lys	Ala	Ser	Asp	Met	Ser	Lys	Ser	Ala	Thr	Pro	Ser		
				325				330					335				
aag	gaa	att	aac	ttt	gat	gat	gac	ttc	taa								1038
Lys	Glu	Ile	Asn	Phe	Asp	Asp	Asp	Phe									
			340				345										

<210> 117

<211> 345

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 117

Met Glu Ala His Asn Gln Phe Leu Lys Thr Phe Gln Lys Gln Arg His

1

5

10

15

Asp Met Lys Glu Ala Glu Lys Asp Glu Ile Leu Leu Met Glu Asn Ser
30 25 30

Arg Arg Phe Val Met Phe Pro Ile Lys Tyr His Glu Ile Trp Ala Ala
35 40 45

Tyr Lys Lys Val Glu Ala Ser Phe Trp Thr Ala Glu Glu Ile Glu Leu
50 55 60

Ala Lys Asp Thr Glu Asp Phe Gln Lys Leu Thr Asp Asp Gln Lys Thr
65 70 75 80

Tyr Ile Gly Asn Leu Leu Ala Leu Ser Ile Ser Ser Asp Asn Leu Val
85 90 95

Asn Lys Tyr Leu Ile Glu Asn Phe Ser Ala Glu Leu Gln Asn Pro Glu
100 105 110

Gly Lys Ser Phe Tyr Gly Phe Gln Ile Met Met Glu Asn Ile Tyr Ser
115 120 125

Glu Val Tyr Ser Met Met Val Asp Ala Phe Phe Lys Asp Pro Lys Asn
130 135 140

Ile Pro Leu Phe Lys Glu Ile Ala Asn Leu Pro Glu Val Lys His Lys
145 150 155 160

Ala Ala Phe Ile Glu Arg Trp Ile Ser Asn Asp Asp Ser Leu Tyr Ala
165 170 175

Glu Arg Leu Val Ala Phe Ala Ala Lys Glu Gly Ile Phe Gln Ala Gly

	180	185	190
Asn Tyr Ala Ser Met Phe Trp Leu Thr Asp Lys Lys Ile Met Pro Gly			
	195	200	205
Leu Ala Met Ala Asn Arg Asp Ile Cys Arg Asp Arg Gly Ala Tyr Thr			
	210	215	220
Asp Phe Ser Cys Leu Leu Phe Ala His Leu Arg Thr Lys Pro Asn Pro			
	225	230	235
			240
Lys Ile Ile Glu Lys Ile Ile Thr Glu Ala Val Glu Ile Glu Lys Glu			
	245	250	255
Tyr Tyr Ser Asn Ser Leu Pro Val Glu Lys Phe Gly Met Asp Leu Lys			
	260	265	270
Ser Ile His Thr Tyr Ile Glu Phe Val Ala Asp Gly Leu Leu Gln Gly			
	275	280	285
Phe Gly Asn Glu Lys Tyr Tyr Asn Ala Val Asn Pro Phe Glu Phe Met			
	290	295	300
Glu Asp Val Ala Thr Ala Gly Lys Thr Thr Phe Phe Glu Lys Lys Val			
	305	310	315
			320
Ser Asp Tyr Gln Lys Ala Ser Asp Met Ser Lys Ser Ala Thr Pro Ser			
	325	330	335
Lys Glu Ile Asn Phe Asp Asp Asp Phe			
	340	345	

<210> 118

<211> 330

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(330)

<400> 118

atg tca cag ata gca caa gaa atg aca gly agc tta aga aac gcc agg 48

Met Ser Gln Ile Ala Gln Gln Met Thr Val Ser Leu Arg Asn Ala Arg

1 5 10 15

aca caa ttg gat atg gtc aat cag cag cta gca tat ttg gac aga caa 96

Thr Gln Leu Asp Met Val Asn Gln Gln Leu Ala Tyr Leu Asp Arg Gln

20 25 30

gaa aag ctt gct gaa ttg aca aag aaa gaa cta gag tct tat cca aag 144

Glu Lys Leu Ala Gln Leu Thr Lys Lys Glu Leu Glu Ser Tyr Pro Thr

35 40 45

gac aca gta aag aga tct agc ggt aaa tgg ttt atc tta cag gat aac 192

Asp Lys Val Trp Arg Ser Lys Gly Lys Ser Phe Ile Leu Gln Asp Lys

50 55 60

tcc aaa tac gtt aat gat tta tca cat gcc gaa act gtt ctt atg gat 240

Ser Lys Tyr Val Asn Asp Leu Ser His Ala Gln Thr Val Leu Leu Asp

65 70 75 80

caa aga aaa aca tta aag ala aag aag aac tat tta gaa act act gtt 288

Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Glu Thr Thr Val

85 90 95

gaa aaa aca ata gac aat cta aag gca ttg atg aag aat taa 330

Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn

100 105

<210> 119

<211> 109

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 119

Met Ser Gln Ile Ala Gln Gln Met Thr Val Ser Leu Arg Asn Ala Arg
1 5 10 15

Thr Gln Leu Asp Met Val Asn Gln Gln Leu Ala Tyr Leu Asp Arg Gln
20 25 30

Glu Lys Leu Ala Gln Leu Thr Lys Lys Glu Leu Glu Ser Tyr Pro Thr
35 40 45

Asp Lys Val Trp Arg Ser Cys Gly Lys Ser Phe Ile Leu Gln Asp Lys
50 55 60

Ser Lys Tyr Val Asn Asp Leu Ser His Ala Glu Thr Val Leu Leu Asp
65 70 75 80

Gln Arg Lys Thr Leu Lys Ile Lys Lys Asn Tyr Leu Gln Thr Thr Val
85 90 95

Glu Lys Thr Ile Asp Asn Leu Lys Ala Leu Met Lys Asn
100 105

<210> 120

<211> 648

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (648)

<400> 120

atg aat gga att caa gtg gac atc aat cgt ttg aaa aag ggg gaa gtc 48
Met Asn Gly Ile Gln Val Asp Ile Asn Arg Leu Lys Lys Gly Glu Val

1 5 10 15

agt tta ggt acc tca att atg gac gtg aca ttt aag gat agt gtc ata 96
Ser Leu Gly Thr Ser Ile Met Ala Val Thr Phe Lys Asp Gly Val Ile

20 25 30

cta ggt gct gat tca cgt acc acc act ggt ggc tac ata gct aac cgt 144
Leu Gly Ala Asp Ser Arg Thr Thr Thr Gly Ala Tyr Ile Ala Asn Arg

35 40 45

gtg aca gat aaa tta acg aga gta cat gac aaa att tgg tgt tgt agg 192
Val Thr Asp Lys Leu Thr Arg Val His Asp Lys Ile Trp Cys Cys Arg

50 55 60

tcc ggt tct gca gca gac aag cag ggc att gcc gac att gtt aag tac 240
Ser Gly Ser Ala Ala Asp Thr Gln Ala Ile Ala Asp Ile Val Gln Tyr

65 70 75 80

cat ttg gaa tta tat act tcc caa tat ggt acc ccc tcc aca gag act 288
His Leu Glu Leu Tyr Thr Ser Gln Tyr Gly Thr Pro Ser Thr Glu Thr

85 90 95

gct gcc tgg gtg ttc aaa gaa tta tgt tac gaa aat aaa gat aac ctg 336
Ala Ala Ser Val Phe Lys Glu Leu Cys Tyr Glu Asn Lys Asp Asn Leu

100 105 110

act gct ggt ata att gtg gct ggt tac gat gac aaa aac aaa ggg gaa 384
Thr Ala Gly Ile Ile Val Ala Gly Tyr Asp Asp Lys Asn Lys Gly Glu

115 120 125

gta tat act att cca ttg ggt ggc tcc gtc cat aag ctg cct tct ggc 432
Val Tyr Thr Ile Pro Leu Gly Gly Ser Val His Lys Leu Pro Tyr Ala

130 135 140

ata gca gga tct ggc tct act ttc ata tat ggg tat tgt gat aac aac 480
Ile Ala Gly Ser Gly Ser Thr Phe Ile Tyr Gly Tyr Cys Asp Lys Asn

145 150 155 160

UUU AGA GAA AAT AUG UCA AAG GAA GAA ACC GTA GAT TTC ATA AAG CAT 528
 Phe Arg Glu Asn Met Ser Lys Glu Glu Thr Val Asp Phe Ile Lys His
 165 170 175

UCG CTA UCG CAA GCC ATT AAA UGG GAC GGA TGT TCC GGT GGT GTT ATA 576
 Ser Leu Ser Gln Ala Ile Lys Trp Asp Gly Ser Ser Gly Gly Val Ile
 180 185 190

AGA ATG GTT GTT TTG ACA GCT GCT GGT GTG GAA CGT TTG ATA TTC TAC 624
 Arg Met Val Val Leu Thr Ala Ala Gly Val Glu Arg Leu Ile Phe Tyr
 195 200 205

CCT GAT GAA TAT GAA CAA CTA TAA 648
 Pro Asp Glu Tyr Glu Glu Leu
 210 215

<210> 121
 <211> 215
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 121

MET ASN GLY ILE GLN VAL ASP ILE ASN ARG LEU LYS LYS GLY GLU VAL
 1 5 10 15

SER LEU GLY THR SER ILE MET ALA VAL THR PHE LYS ASP GLY VAL ILE
 20 25 30

LEU GLY ALA ASP SER ARG THR THR THR GLY ALA TYR ILE ALA ASN ARG
 35 40 45

VAL THR ASP LYS LEU THR ARG VAL HIS ASP LYS ILE TRP CYS CYS ARG
 50 55 60

SER GLY SER ALA ALA ASP THR GLN ALA ILE ALA ASP ILE VAL GLN TYR

65

70

75

80

His Leu Gln Leu Tyr Thr Ser Gln Tyr Gly Thr Pro Ser Thr Glu Thr
 85 90 95

Ala Ala Ser Val Phe Lys Gln Leu Cys Tyr Glu Asn Lys Asp Asn Leu
 100 105 110

Thr Ala Gly Ile Ile Val Ala Gly Tyr Asp Asp Lys Asn Lys Gly Glu
 115 120 125

Val Tyr Thr Ile Pro Leu Gly Gly Ser Val His Lys Leu Pro Tyr Ala
 130 135 140

Ile Ala Gly Ser Gly Ser Thr Phe Ile Tyr Gly Tyr Cys Asp Lys Asn
 145 150 155 160

Phe Arg Glu Asn Met Ser Lys Glu Glu Thr Val Asp Phe Ile Lys His
 165 170 175

Ser Leu Ser Gln Ala Ile Lys Trp Asp Gly Ser Ser Gly Gly Val Ile
 180 185 190

Arg Met Val Val Leu Thr Ala Ala Gly Val Glu Arg Leu Ile Phe Tyr
 195 200 205

Pro Asp Glu Tyr Glu Gln Leu
 210 215

<210> 122

<211> 990

<212> DNA

<213> *Saccharomyces cerevisiae* .

<220>

<221> CDS

<222> (1)..(990)

<400> 132

atg tgc agt agg ata ctc ttg tcc ggt tta gtc gga ctg ggt gct ggt 48

Met Cys Ser Arg Ile Leu Leu Ser Gly Leu Val Gly Leu Gly Ala Gly

1 5 10 15

act ggc tta acc tat ctt ctt ttg aac aaa cat tct cca acg caa aac 96

Thr Gly Leu Thr Tyr Leu Leu Leu Asn Lys His Ser Pro Thr Gln Ile

20 25 30

att gag aca cct tat cca cct acc cag aaa cct aat agt aat att caa 144

Ile Glu Thr Pro Tyr Pro Pro Thr Gln Lys Pro Asn Ser Asn Ile Gln

35 40 45

tct cac tct ttc aac gtc gat cct tcc ggg ttc ttc aag tat ggt ttt 192

Ser His Ser Phe Asn Val Asp Pro Ser Gly Phe Phe Lys Tyr Gly Phe

50 55 60

cct ggt ccg att cat gct ctg cag caa cgg gaa gag ttt atc tca tgt 240

Pro Gly Pro Ile His Asp Leu Gln Asn Arg Glu Glu Phe Ile Ser Cys

65 70 75 80

cac aac aga cca act caa aat cct tat tgg gtc ctg gaa cat ata acg 288

Tyr Asn Arg Gln Thr Gln Asn Pro Tyr Trp Val Leu Gln His Ile Thr

85 90 95

cca gaa tca ttg gct gca agg aat gct gac aga aua aat tcc ttt ttc 336

Pro Glu Ser Leu Ala Ala Arg Asn Ala Asp Arg Lys Asn Ser Phe Phe

100 105 110

aag gaa gat gaa gta att cca gaa aag ttt aga ggt aaa cta aga gac 384

Lys Glu Asp Glu Val Ile Pro Glu Lys Phe Arg Gly Lys Leu Arg Asp

115 120 125

cac ttt agg tcc ggc tat gat cga ggc cat caa gcc cca gct gca gac 432

Tyr Phe Arg Ser Gly Tyr Asp Arg Gly His Gln Ala Pro Ala Ala Asp

130	135	140	
gca aca ttt tct caa cag gcc atg gat gat aca ttc tac tta tcc aat			480
Ala Lys Phe Ser Gln Gln Ala Met Asp Asp Thr Phe Tyr Leu Ser Asn			
145	150	155	160
atg tgc cct caa gta cga gaa ggt ttc aat aga gac tat tgg gcg cat			528
Met Cys Pro Gln Val Gly Glu Gly Phe Asn Arg Asp Tyr Trp Ala His			
	165	170	175
ctg gag cac ctt tgc agg gga ttg aat aag aaa tat aag agt gta aga			576
Leu Gln Tyr Phe Cys Arg Gly Leu Thr Lys Lys Tyr Lys Ser Val Arg			
	180	185	190
atc gtg act ggt cca ttg tat cta ccc aac aag gat ccc ata gat aat			624
Ile Val Thr Gly Pro Leu Tyr Leu Pro Lys Lys Asp Pro Ile Asp Asn			
	195	200	205
aaa ttc agg gtt aat tat gaa gtt att gcc aat cca ccc agt att gct			672
Lys Phe Arg Val Asn Tyr Glu Val Ile Gly Asn Pro Pro Ser Ile Ala			
	210	215	220
gtt cca acg cac ttt ttt aaa ttg att gtc gca gaa gca cca aca gcc			720
Val Pro Thr His Phe Phe Lys Leu Ile Val Ala Glu Ala Pro Thr Ala			
225	230	235	240
aat ccc gct aga gag gat att gct gtc gcg gca ttt gta ttg cca aac			768
Asn Pro Ala Arg Glu Asp Ile Ala Val Ala Ala Phe Val Leu Pro Asn			
	245	250	255
gac cag ata tca aat gag acg aaa ttg act gac ttt gaa gtt cct ata			816
Glu Pro Ile Ser Asn Glu Thr Lys Leu Thr Asp Phe Glu Val Pro Ile			
	260	265	270
gat gct tta gag aga agt act ggg cta gaa ctt ctg caa aaa gta cca			864
Asp Ala Leu Glu Arg Ser Thr Gly Leu Glu Leu Leu Gln Lys Val Pro			
	275	280	285
cct tca aag aag aag gca tta tgc aaa gag gta aat tgt caa att gta			912
Pro Ser Lys Lys Lys Ala Leu Cys Lys Glu Val Asn Cys Gln Ile Val			
	290	295	300

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gtg aga gat ttc tct aac gcg gcg atc aac caa tcc aaa gat gtg aaa 260
 Val Arg Asp Phe Ser Asn Ala Ala Ile Lys Gln Ser Lys Asp Val Lys
 305 310 315 320

tgg tta cct cct cca aaa aaa agg aat tga 290
 Leu Leu Pro Pro Pro Lys Lys Arg Asn
 325

<210> 123

<211> 329

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 123

Met Cys Ser Arg Ile Leu Leu Ser Gly Leu Val Gly Leu Gly Ala Gly
 1 5 10 15

Thr Gly Leu Thr Tyr Leu Leu Leu Asn Lys His Ser Pro Thr Gln Ile
 20 25 30

Ile Glu Thr Pro Tyr Pro Pro Thr Gln Lys Pro Asn Ser Asn Ile Gln
 35 40 45

Ser His Ser Phe Asn Val Asp Pro Ser Gly Phe Phe Lys Tyr Gly Phe
 50 55 60

Pro Gly Pro Ile His Asp Leu Gln Asn Arg Glu Glu Phe Ile Ser Cys
 65 70 75 80

Tyr Asn Arg Gln Thr Gln Asn Pro Tyr Trp Val Leu Glu His Ile Thr
 85 90 95

Pro Gln Ser Leu Ala Ala Arg Asn Ala Asp Arg Lys Asn Ser Thr Phe
 100 105 110

Lys Glu Asp Glu Val Ile Pro Glu Lys Phe Arg Gly Lys Leu Arg Asp
115 120 125

Tyr Phe Arg Ser Gly Tyr Asp Arg Gly His Glu Ala Pro Ala Ala Asp
130 135 140

Ala Lys Phe Ser Glu Gln Ala Met Asp Asp Thr Phe Tyr Leu Ser Asn
145 150 155 160

Met Cys Pro Gln Val Gly Glu Gly Phe Asn Arg Asp Tyr Trp Ala His
165 170 175

Leu Glu Tyr Phe Cys Arg Gly Leu Thr Lys Lys Tyr Lys Ser Val Arg
180 185 190

Ile Val Thr Gly Pro Leu Tyr Leu Pro Lys Lys Asp Pro Ile Asp Asn
195 200 205

Lys Phe Arg Val Asn Tyr Glu Val Ile Gly Asn Pro Pro Ser Ile Ala
210 215 220

Val Pro Thr His Phe Phe Lys Leu Ile Val Ala Glu Ala Pro Thr Ala
225 230 235 240

Asn Pro Ala Arg Glu Asp Ile Ala Val Ala Ala Phe Val Leu Pro Asn
245 250 255

Glu Pro Ile Ser Asn Gln Thr Lys Leu Thr Asp Phe Glu Val Pro Ile
260 265 270

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Asp Ala Leu Glu Arg Ser Thr Gly Leu Glu Leu Leu Gln Lys Val Pro
 275 280 285

Pro Ser Lys Lys Lys Ala Leu Cys Lys Glu Val Asn Cys Gln Ile Val
 290 295 300

Val Arg Asp Phe Ser Asn Ala Ala Ile Lys Glu Ser Lys Asp Val Lys
 305 310 315 320

Leu Leu Pro Pro Pro Lys Lys Arg Asn
 325

<210> 124
 <211> 360
 <212> CNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (360)

<400> 124
 atg cag cat tta gcc gcc gaa gag cat acg tgg cat ccg cat att tca 48
 Met Pro His Leu Ala Ala Glu Ala His Thr Trp Pro Pro His Ile Ser
 1 5 10 15
 cat tta aca ctt tgg att ccg cat cca acc ccg gaa cac cgg cac gta 52
 His Ser Thr Leu Ser Ile Pro His Pro Thr Pro Glu His Arg His Val
 20 25 30
 ttt cat aaa aag gac gtg aag aac aaa agg aac gaa gaa aaa ggc aat 144
 Phe His Lys Lys Asp Val Lys Asn Lys Arg Asn Glu Glu Lys Gly Asn
 35 40 45
 aat tta ctc tat gtg tta ttt aga act ccg gtg ata aag agc tgg ttc 192
 Asn Leu Leu Tyr Val Leu Phe Arg Thr Thr Val Ile Lys Ser Ser Phe
 50 55 60

cga tca cta agt acg gcc gga agu gag atg ttg ttt gtt gtc cat caa 240
 Arg Ser Leu Ser Thr Ala Gly Arg Glu Leu Leu Phe Val Val His Gln
 55 70 75 80

ggg cac atc ggc acc ggc ctc atc gtc ttc atc ata tgc tgg agg ctg 288
 Gly His Ile Gly Thr Gly Leu Ile Val Phe Ile Ile Cys Trp Arg Leu
 85 90 95

tgc ttg aga ttc ctc tgc agg gtg agc ttc cag gtc acg gtc tac ggc 336
 Cys Leu Arg Phe Leu Cys Arg Val Ser Phe Gln Val Thr Val Tyr Gly
 100 105 110

ggg cgc agt cgc atg tct gag tga 360
 Gly Arg Ser Arg Met Ser Ala
 115

<210> 125
 <211> 119
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 125

Met Pro His Leu Ala Ala Glu Ala His Thr Trp Pro Pro His Ile Ser
 1 5 10 15

His Ser Thr Leu Ser Ile Pro His Pro Thr Pro Gln His Arg His Val
 20 25 30

Phe His Lys Lys Asp Val Lys Asn Lys Arg Asn Glu Gln Lys Gly Asn
 35 40 45

Asn Leu Leu Tyr Val Leu Phe Arg Thr Thr Val Ile Lys Ser Ser Phe
 50 55 60

Arg Ser Leu Ser Thr Ala Gly Arg Glu Leu Leu Phe Val Val His Gln

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65 70 75 80
 Gly His Ile Gly Thr Gly Leu Ile Val Phe Ile Ile Cys Trp Arg Leu
 85 90 95
 Cys Leu Arg Phe Leu Cys Arg Val Ser Phe Gln Val Thr Val Tyr Gly
 100 105 110
 Gly Arg Ser Arg Met Ser Ala
 115

<210> 126
 <211> 1071
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1071)

<400> 126
 atg tta aaa gtt cct ttg agt gat gtc ctt tca cag aag atg ctg ttt 48
 Met Leu Lys Val Pro Leu Ser Asp Val Leu Ser Gln Lys Met Leu Phe
 1 5 10 15
 tta aaa agt ttt aga tat ttt cat tgc aca aaa tac ttc agc aga gac 96
 Leu Lys Ser Phe Arg Tyr Phe His Cys Thr Lys Tyr Phe Ser Arg Asp
 20 25 30
 aat gca tca tct acc aca gat ata ttt cgc aac gca atg aaa cgt aaa 144
 Asn Ala Ser Ser Thr Thr Asp Ile Phe Arg Asn Ala Met Lys Arg Lys
 35 40 45
 cgt gag ctg gca aat ctt aac gag caa agt cat gga aat gtg gca aga 192
 Arg Glu Leu Ala Asn Leu Lys Glu Gln Ser His Gly Asn Val Ala Arg
 50 55 60

290762

aat	gct	gct	ttt	cct	aaa	gag	tat	att	aag	cgc	cgc	aaa	caa	gtg	cca	240
Asn	Ala	Ala	Phe	Pro	Lys	Gln	Tyr	Ile	Lys	Arg	Pro	Gys	Gln	Val	Pro	
65					70					75				80		
agg	aat	gct	act	aac	agg	aaa	aaa	atc	ctg	att	act	tgg	agc	acc	ggg	288
Arg	Asn	Ala	Thr	Asn	Arg	Lys	Lys	Ile	Leu	Ile	Thr	Trp	Ser	Thr	Gly	
				85					90					95		
aca	gat	cga	gct	aaa	cag	gca	gct	aat	tca	gll	git	agt	cag	ata	ttc	336
Thr	Asp	Arg	Ala	Lys	Gln	Ala	Ala	Asn	Ser	Val	Val	Ser	Gln	Ile	Phe	
				100				105						110		
aaa	aaa	aac	cac	aag	gga	aac	atc	aaa	gtc	gig	gat	ccc	acg	acc	cac	384
Lys	Lys	Asn	His	Lys	Gly	Asn	Ile	Lys	Val	Val	Asp	Pro	Thr	Thr	His	
				115				120						125		
cga	atc	gaa	gca	tcc	aat	att	egg	tat	ttt	goc	aag	ggc	att	gai	ctc	432
Arg	Ile	Glu	Ala	Ser	Asn	Ile	Arg	Tyr	Phe	Ala	Lys	Gly	Ile	Asp	Leu	
				130				135						140		
gat	aaa	gtt	gga	ctc	agt	att	gtt	aac	gta	gag	caa	atc	gal	aat	gaa	480
Asp	Lys	Val	Gly	Leu	Ser	Ile	Val	Asn	Val	Glu	Glu	Ile	Asp	Asn	Glu	
				145				150						155		160
aat	caa	att	cca	ctt	gtt	aag	ata	gtc	gaa	agt	cgt	gta	gac	tta	aaa	528
Asn	Gln	Ile	Pro	Leu	Val	Lys	Ile	Val	Glu	Ser	Arg	Val	Ala	Leu	Lys	
				165				170						175		
aaa	tat	tca	gac	ttt	ctg	gct	aaa	aaa	aag	gaa	aag	gaa	ctg	atg	gaa	576
Lys	Tyr	Ser	Asp	Phe	Leu	Ala	Lys	Lys	Lys	Gln	Lys	Glu	Leu	Met	Glu	
				180				185						190		
ttg	gga	gta	ctg	aat	aag	tct	tac	aag	aat	ttg	gtg	act	gat	aaa	aaa	624
Leu	Gly	Val	Leu	Asn	Lys	Ser	Tyr	Lys	Asn	Leu	Val	Thr	Asp	Lys	Lys	
				195				200						205		
gaa	gat	aac	ttg	aag	cac	att	aaa	ata	tca	tgg	cag	att	gaa	agc	gat	672
Glu	Asp	Asn	Leu	Lys	His	Ile	Lys	Ile	Ser	Trp	Gln	Ile	Glu	Ser	Asp	
				210				215						220		
gal	lla	aaa	agg	cag	aag	gct	cac	gaa	ata	gtt	tcc	cta	ttg	aaa	aaa	720
Asp	Leu	Lys	Arg	Gln	Lys	Ala	His	Glu	Ile	Val	Ser	Leu	Leu	Lys	Lys	

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225	230	235	240	
ggg aat aaa gta acg tta tat ctt gat gac aag aat aac ata aat tca	768			
Gly Asn Lys Val Thr Leu Tyr Leu Asp Asp Lys Asn Asn Ile Asn Ser				
245	250	255		
aac aat tgg ctt gaa aat ttc gag gag ctc gac agc tct cca aac ggt	816			
Asn Asn Trp Leu Glu Asn Phe Glu Glu Leu Asp Arg Ser Gln Lys Gly				
260	265	270		
gaa cca ccc agg cta cca gaa tca gtt ttc cag aaa aga gct gct gtc	864			
Glu Pro Pro Arg Leu Pro Glu Ser Val Phe Gln Lys Arg Ala Ala Val				
275	280	285		
ttg gag aca ttg aaa gag ata gtt agc gaa tat gct aat gat cct gtc	912			
Leu Gln Thr Leu Lys Glu Ile Val Ser Glu Tyr Ala Asn Asp Pro Val				
290	295	300		
ctg cta ggt aac atg aac tgg aac atg ata atg aac ctt ata cca aag	960			
Leu Leu Gly Asn Met Asn Ser Lys Met Ile Met Lys Leu Ile Pro Lys				
305	310	315	320	
gac gct aaa cca cca aac aac gat aag agg gcg cta aag gaa ttg aga	1008			
Asp Val Tyr Pro Gln Asn Asn Asp Lys Arg Ala Leu Lys Glu Leu Arg				
325	330	335		
aag aag gag agg caa gaa aca ttg caa aaa agg att cag aga aca aca	1056			
Lys Lys Glu Arg Gln Glu Lys Leu Gln Lys Arg Ile Gln Arg Lys Lys				
340	345	350		
atg aat gaa atg tan	1071			
Met Asn Glu Met				
355				

<210> 127

<211> 356

<212> PRT

<213> Saccharomyces cerevisiae

<400> 127

Met Leu Lys Val Pro Leu Ser Asp Val Leu Ser Gln Lys Met Leu Phe
1 5 10 15

Leu Lys Ser Phe Arg Tyr Phe His Cys Thr Lys Tyr Phe Ser Arg Asp
20 25 30

Asn Ala Ser Ser Thr Thr Asp Ile Phe Arg Asn Ala Met Lys Arg Lys
35 40 45

Arg Gln Leu Ala Asn Leu Lys Glu Gln Ser His Gly Asn Val Ala Arg
50 55 60

Asn Ala Ala Phe Pro Lys Glu Tyr Ile Lys Arg Pro Lys Gln Val Pro
65 70 75 80

Arg Asn Ala Thr Asn Arg Lys Lys Ile Leu Ile Thr Trp Ser Thr Gly
85 90 95

Thr Asp Arg Ala Lys Gln Ala Ala Asn Ser Val Val Ser Gln Ile Phe
100 105 110

Lys Lys Asn His Cys Gly Asn Ile Lys Val Val Asp Pro Thr Thr His
115 120 125

Arg Ile Gln Ala Ser Asn Ile Arg Tyr Phe Ala Lys Gly Ile Asp Leu
130 135 140

Asp Lys Val Gly Leu Ser Ile Val Asn Val Gln Gln Ile Asp Asn Glu
145 150 155 160

Asn Gln Ile Pro Leu Val Lys Ile Val Glu Ser Arg Val Ala Leu Lys
165 170 175

Lys Tyr Ser Asp Phe Leu Ala Lys Lys Lys Glu Lys Glu Leu Met Glu
180 185 190

Leu Gly Val Leu Asn Lys Ser Tyr Lys Asn Leu Val Thr Asp Lys Lys
195 200 205

Glu Asp Asn Leu Lys His Ile Lys Ile Ser Trp Gln Ile Glu Ser Asp
210 215 220

Asp Leu Lys Arg Gln Lys Ala His Glu Ile Val Ser Leu Leu Lys Lys
225 230 235 240

Gly Asn Lys Val Thr Leu Tyr Leu Asp Asp Lys Asn Asn Ile Asn Ser
245 250 255

Asn Asn Trp Leu Glu Asn Phe Glu Glu Leu Asp Arg Ser Gln Lys Gly
260 265 270

Glu Pro Pro Arg Leu Pro Glu Ser Val Phe Gln Lys Arg Ala Ala Val
275 280 285

Leu Gln Thr Leu Lys Glu Ile Val Ser Glu Tyr Ala Asn Asp Pro Val
290 295 300

Leu Leu Gly Asn Met Asn Ser Lys Met Ile Met Lys Leu Ile Pro Lys
305 310 315 320

Asp Val Lys Pro Gln Asn Asn Asp Lys Arg Ala Leu Lys Glu Leu Arg
325 330 335

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Lys Lys Glu Arg Glu Glu Lys Leu Glu Lys Arg Ile Glu Arg Lys Lys
 340 345 350

Met Asn Glu Met
 355

<210> 128
 <211> 402
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (402)

<400> 128
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 Met Asp Arg Asp His Ile Asn Asp His Asp His Arg Met Ser Tyr Ser
 1 5 10 15
 atc aac aag gac gac ttg ttg tta atg gtt ttg gag gtc ttc att ccc 84
 Ile Asn Lys Asp Asp Leu Leu Leu Met Val Leu Ala Val Phe Ile Pro
 20 25 30
 cca gag gcc gtc tgg aag cgt aag ggt atg ttc aac agg gat aca cta 144
 Pro Val Ala Val Trp Lys Arg Lys Gly Met Phe Asn Arg Asp Thr Leu
 35 40 45
 ttg aac tta ctt ctc ttc cta ctg tta ttc ttc cca gca atc att cac 192
 Leu Asn Leu Leu Leu Phe Leu Leu Leu Phe Phe Pro Ala Ile Ile His
 50 55 60
 gct tgc cac gtt gta tat gaa acg agt agt gaa cgt tgg tac gat ctt 240
 Ala Cys Tyr Val Val Tyr Glu Thr Ser Ser Glu Arg Ser Tyr Asp Leu
 65 70 75 80
 tca cgc aga cat gag act gag ccc gcc gta gac cgt gac ctg gaa gct 288
 Ser Arg Arg His Ala Thr Ala Pro Ala Val Asp Arg Asp Leu Glu Ala
 85 90 95

cac cct gca gag gaa tct caa gca cag cct cca gca tat gat gaa gac 336
 His Pro Ala Glu Glu Ser Gln Ala Glu Pro Pro Ala Tyr Asp Glu Asp
 100 105 110

gat gag gcc ggt gcc cat gtg ccc ttg atg gac nac aaa caa cag ctg 384
 Asp Glu Ala Gly Ala Asp Val Pro Leu Met Asp Asn Lys Gln Gln Leu
 115 120 125

tct tcc ggc cgt act tag 402
 Ser Ser Gly Arg Thr
 130

<210> 125
 <211> 153
 <212> FRT
 <213> *Saccharomyces cerevisiae*

<400> 129

Met Asp Arg Asp His Ile Asn Asp His Asp His Arg Met Ser Tyr Ser
 1 5 10 15

Ile Asn Lys Asp Asp Leu Leu Leu Met Val Leu Ala Val Phe Ile Pro
 20 25 30

Pro Val Ala Val Trp Lys Arg Lys Gly Met Phe Asn Arg Asp Thr Leu
 35 40 45

Leu Asn Leu Leu Leu Phe Leu Leu Leu Phe Phe Pro Ala Ile Ile His
 50 55 60

Ala Cys Tyr Val Val Tyr Glu Thr Ser Ser Glu Arg Ser Tyr Asp Leu
 65 70 75 80

Ser Arg Arg His Ala Thr Ala Pro Ala Val Asp Arg Asp Leu Glu Ala

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85

90

95

His Pro Ala Glu Glu Ser Gln Ala Gly Pro Pro Ala Tyr Asp Glu Asp
100 105 110

Asp Glu Ala Gly Ala Asp Val Pro Leu Met Asp Asn Lys Gln Gln Leu
115 120 125

Ser Ser Gly Arg Thr
130

<210> 130

<211> 768

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(768)

<400> 130

atg gct gtc gga aag aat aag aga cta tcc aag ggt aag aaa ggt caa 18
Met Ala Val Gly Lys Asn Lys Arg Leu Ser Tyr Gly Tyr Tyr Gly Gln
1 5 10 15

aag aag aga gtc gtt gac cca ttt acc aga aag gaa tgg ttc gac att 36
Lys Lys Arg Val Val Asp Pro Phe Thr Arg Lys Glu Trp Phe Asp Ile
20 25 30

aaa gct cca tcc act ttt gaa aac aga aat gtt ggt aag act tca gtt 144
Lys Ala Pro Ser Thr Phe Glu Asn Arg Asn Val Gly Lys Thr Leu Val
35 40 45

aac aag tcc act ggt ttg aag agt gct tca gat gct ttg aaa ggt aga 192
Asn Lys Ser Thr Gly Leu Lys Ser Ala Ser Asp Ala Leu Lys Gly Arg
50 55 60

gtt gtc gaa gtt tgc ttg gct gac tta cag ggt tct gaa gac cac tct	240
Val Val Glu Val Cys Leu Ala Asp Leu Gln Gly Ser Glu Asp His Ser	
65 70 75 80	
ttc aga aaa atc aac tta aga gtt gac gaa gtc caa ggt aag aat tta	288
Phe Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu	
85 90 95	
ttg acc aac ttc cac ggt atg gac ttc act act gat aaa ttg aga tcc	336
Leu Thr Asn Phe His Gly Met Asp Phe Thr Thr Asp Lys Leu Arg Ser	
100 105 110	
arg gtc aga aag tgg caa act ttg atc gaa gct aac gtt act gtt aag	384
Met Val Arg Lys Trp Gln Thr Leu Ile Glu Ala Asn Val Thr Val Lys	
115 120 125	
act tct gat gat tac gtt ttg aga atc ttt gct atc gcc ttc acc aga	432
Thr Ser Asp Asp Tyr Val Leu Arg Ile Phe Ala Ile Ala Phe Thr Arg	
130 135 140	
aag caa gct acc caa gtt aag aga cac tct tac gct caa tct tac cac	480
Lys Gln Ala Asn Gln Val Lys Arg His Ser Tyr Ala Glu Ser Ser His	
145 150 155 160	
atc aga gct atc aga aag gtt att tcc gaa atc ttg act aag gaa gtc	528
Ile Arg Ala Ile Arg Lys Val Ile Ser Glu Ile Leu Thr Lys Glu Val	
165 170 175	
caa gga tct acc ttg gcc caa ttg acc tcc aag ttg att caa gaa gtc	576
Gln Gly Ser Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val	
180 185 190	
atc aac aag gaa att gaa aac gcc acc aag gac att ttc caa cta caa	624
Ile Asn Lys Glu Ile Glu Asn Ala Thr Lys Asp Ile Phe Pro Leu Gln	
195 200 205	
aac atc cat gtt aga aag gtt aag ttg ttg aaa caa cca aag ttc gat	672
Asn Ile His Val Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp	
210 215 220	
gtc ggt gct ttg atg gct ttg cac ggt gaa ggt tct ggt gaa gaa aag	720
Val Gly Ala Leu Met Ala Leu His Gly Glu Gly Ser Gly Glu Glu Lys	

225	230	235	240	
ggf aag aag ggt acc ggt ttc aag gac gaa gtc ttg gaa act gtg taa				768
Gly Lys Lys Val Thr Gly Phe Lys Asp Glu Val Leu Glu Thr Val				
245	250	255		

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<210> 131
<211> 255
<212> PRT
<213> Saccharomyces cerevisiae
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4905 131

Met Ala Val Gly Lys Asn Pys Arg Leu Ser Lys Gly Lys Lys Gly Gln
1 5 10 15

Lys Lys Arg Val Val Asp Pro Phe Thr Arg Lys Glu Trp Phe Asp Ile
 20 25 30

Lys Ala Pro Ser Thr Phe Gln Asn Arg Asn Val Gly Tyr Thr Leu Val
35 40 45

Asn Lys Ser Thr Gly Leu Lys Ser Ala Ser Asp Ala Leu Lys Gly Arg
50 55 60

Val	Val	Glu	Val	Cys	Leu	Ala	Asp	Leu	Gln	Gly	Ser	Glu	Asp	His	Ser
65					70					75					80

Phe Arg Lys Ile Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Leu
 05 90 95

Leu	Thr	Asn	Phe	His	Gly	Met	Asp	Phe	Thr	Thr	Asp	Iys	Leu	Arg	Ser
			100					105					110		

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Met Val Arg Lys Trp Gln Thr Leu Ile Gly Ala Asn Val Thr Val Lys
115 120 125

Thr Ser Asp Asp Tyr Val Leu Arg Ile Phe Ala Ile Ala Phe Thr Arg
130 135 140

Lys Gln Ala Asn Gln Val Lys Arg His Ser Tyr Ala Gln Ser Ser His
145 150 155 160

Ile Arg Ala Ile Arg Lys Val Ile Ser Glu Ile Leu Thr Lys Glu Val
165 170 175

Gln Gly Ser Thr Leu Ala Gln Leu Thr Ser Lys Leu Ile Pro Glu Val
180 185 190

Ile Asn Lys Glu Ile Glu Asn Ala Thr Lys Asp Ile Phe Pro Leu Gln
195 200 205

Asn Ile His Val Arg Lys Val Lys Leu Leu Lys Gln Pro Lys Phe Asp
210 215 220

Val Gly Ala Leu Met Ala Leu His Gly Gln Gly Ser Gly Glu Glu Lys
225 230 235 240

Gly Lys Lys Val Thr Gly Phe Lys Asp Glu Val Leu Glu Thr Val
245 250 255

<210> 132

<211> 339

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (339)

<400> 132

atg tat ctc agt ggc cag ctt atg aga act gtc aca ggc tcc cac ttg	48
Met Tyr Leu Ser Ala Gln Leu Met Arg Thr Val Thr Ala Ser His Leu	
1 5 10 15	

acc ctc aga ggc ctc tcc act cnc ccc ctc ttt caa cat cgc cag ata	96
Thr Leu Arg Ala Leu Ser Thr Pro Pro Leu Phe Gln His Arg Gln Ile	
20 25 30	

gac gac gtt gaa tgg tgc ggg aca acc cgg cat ggc ctg gcc agg caa	144
Ala Ala Val Glu Trp Cys Gly Thr Thr Arg Pro Gly Leu Ala Arg Gln	
35 40 45	

aaa agg acg cag cac gcc tgg agc gtc att tcc aaa tgg ggc gta cta	192
Lys Arg Thr Gln His Ala Ser Ser Val Ile Ser Lys Ser Gly Val Leu	
50 55 60	

cca gcc aag ccc agc tgg gtc ttt tta gag ctt ctc gta gga aca ttg	240
Ser Ala Lys Pro Ser Ser Val Phe Leu Ala Ile Ile Ala Gly Lys Leu	
65 70 75 80	

gct gag aag tat ata tac ggc aga atg ttg ctc ttc cat gtc tca gta	288
Ala Glu Lys Tyr Ile Tyr Ala Arg Met Leu Leu Phe His Val Ser Val	
85 90 95	

gtc aat gag tgt cca gtc ggc ttt cat tct gga cca gtt gat tgg aag	336
Val Asn Glu Cys Pro Val Val Phe His Ser Gly Pro Val Val Trp Lys	
100 105 110	

tag	339
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<210> 133

<211> 112

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 133

Met Tyr Leu Ser Ala Gln Leu Met Arg Thr Val Thr Ala Ser His Leu
 1 5 10 15

Thr Leu Arg Ala Leu Ser Thr Pro Pro Leu Phe Gln His Arg Gln Ile
 20 25 30

Ala Ala Val Glu Trp Cys Gly Thr Thr Arg Pro Gly Leu Ala Arg Gln
 35 40 45

Lys Arg Thr Gln His Ala Ser Ser Val Ile Ser Lys Ser Gly Val Leu
 50 55 60

Ser Ala Tyr Pro Ser Ser Val Phe Leu Ala Leu Leu Ala Gly Lys Leu
 65 70 75 80

Ala Glu Lys Tyr Ile Tyr Ala Arg Met Leu Leu Phe His Val Ser Val
 85 90 95

Val Asn Glu Cys Pro Val Val Phe His Ser Gly Pro Val Val Trp Cys
 100 105 110

<315> 134
 <311> 1422
 <312> DNA
 <313> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1422)

<400> 134
 atg ggt gga gaa att att act ttg caa gca ggt caa tgc ggg aac cac 48
 Met Gly Gly Gln Ile Ile Thr Leu Gln Ala Gly Gln Cys Gly Asn His

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1	5	10	15	
gtt ggt aag ttc ctc tgg tct caa ttg gcg aaa gaa cac gct ata ggc				96
Val Gly Lys Phe Leu Trp Ser Gln Leu Ala Lys Glu His Ala Ile Gly				
	20	25	30	
acc gat ggg cta tct cag ctt cct gat tcc agt aag gaa aga gat gat				144
Thr Asp Gly Leu Ser Gln Leu Pro Asp Ser Ser Thr Gln Arg Asp Asp				
	35	40	45	
gac aca aag cct ttc ttc cgc gaa aac agt agg aat aag ttt acg cca				192
Asp Thr Lys Pro Phe Phe Arg Glu Asn Ser Arg Asn Lys Phe Trp Pro				
	50	55	60	
agg gat att atg atg gat tcc gag cct agt glc atc gcc gac gtg gag				240
Arg Ala Ile Met Met Asp Ser Glu Pro Ser Val Phe Ala Asp Val Glu				
	65	70	75	80
aac aca ttt cgt ggg ttt ttc gac cca aga aat acc tgg gta gct tct				288
Asn Thr Phe Arg Gly Phe Phe Asp Pro Arg Asn Thr Trp Val Ala Ser				
	85	90	95	
gat ggc gct agc gat ggt aat tct tgg gcc aat ggg tat gat ata gga				336
Asp Gly Ala Ser Ala Gly Asn Ser Trp Ala Asn Gly Tyr Asp Ile Gly				
	100	105	110	
act cat aac cag gat gat att ctt aac aag atc gcc aag gag att gat				384
Thr Arg Asn Gln Asp Asp Ile Leu Asn Lys Ile Asp Lys Glu Ile Asp				
	115	120	125	
tct acc gac aat ttc gaa ggt ttc cag ttg ctg cac tca gta gcc gga				432
Ser Thr Asp Asn Phe Glu Gly Phe Gln Leu Leu His Ser Val Ala Gly				
	130	135	140	
ggg acc ggt tca ggg ctc gga tcc aac atc tta gaa gcg ctg tgt gat				480
Gly Thr Gly Ser Gly Leu Gly Ser Asn Leu Leu Glu Ala Leu Cys Asp				
	145	150	155	160
cga tat cct aca aca ata atc acg aca tat tct gtg ttc cct gca aga				528
Arg Tyr Pro Lys Lys Ile Leu Thr Thr Tyr Ser Val Phe Pro Ala Arg				
	165	170	175	

tet lel gag gtt gtt gtt caa tct tat aac act atk ctg gct ttg aga	576
Ser Ser Glu Val Val Val Gln Ser Tyr Asn Thr Ile Leu Ala Leu Arg	
180 185 190	
aga ctg ala gaa gat agc gat gca acg gtg gtg ttt gat aac gct tgg	624
Arg Leu Ile Glu Asp Ser Asp Ala Thr Val Val Phe Asp Asn Ala Ser	
195 200 205	
ttg ctg aat att tcc ggt aaa gtg tll aga aat cgg aac atc gat tta	672
Leu Leu Asn Ile Ser Gly Lys Val Phe Arg Asn Pro Phe Ile Asp Leu	
210 215 220	
caa cac acg aat caa ttg ata tgg acc ata ala tct tca gta acg aac	720
Gln His Thr Asn Gln Leu Ile Ser Thr Ile Ile Ser Ser Val Thr Asn	
225 230 235 240	
agt ata cgg ttt cgg agt tac atg tat tca tcc atg tcc agt att taa	768
Ser Ile Arg Phe Pro Ser Tyr Met Tyr Ser Ser Met Ser Ser Ile Tyr	
245 250 255	
tct acc ttg att cct tct cct gaa ctt cat ttc cta agc cct agt ttc	816
Ser Thr Leu Ile Pro Ser Pro Glu Leu His Phe Leu Ser Pro Ser Phe	
260 265 270	
act caa ttt aca cca gat tat att cac gat gat ata gcg cat aac ggc	864
Thr Pro Phe Thr Ser Asp Tyr Ile His Asp Asp Ile Ala His Lys Gly	
275 280 285	
cat tcc agt tat gac gtc atg llu gat tta tta gac cct tcc aat tct	912
His Ser Ser Tyr Asp Val Met Leu Asp Leu Leu Asp Pro Ser Asn Ser	
290 295 300	
ctt gtc tct acc gag atg aac aat cca acc tat ttt aac gtt tat aat	960
Leu Val Ser Thr Ala Met Asn Asn Pro Thr Tyr Phe Asn Val Tyr Asn	
305 310 315 320	
aca atc att ggt aat gta gaa cct cgt cag ata tgg cgt gct atg acc	1008
Thr Ile Ile Gly Asn Val Glu Pro Arg Gln Ile Ser Arg Ala Met Thr	
325 330 335	
aaa tta caa caa cgc atc aaa ttc ccc tca tgg acc tct tct gag atg	1056
Lys Leu Gln Gln Arg Ile Lys Phe Pro Ser Trp Ser Ser Ser Ala Met	

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340	345	350	
cac gtt aac att gga aga aga tgg cca tac ttg cct tta caa cca aat			1104
His Val Asn Ile Gly Arg Arg Ser Pro Tyr Leu Pro Leu Gln Pro Asn			
355	360	365	
gaa aac gaa gtt agc ggc atg atg tta agc aat atg tct acc gtg gtg			1152
Glu Asn Glu Val Ser Gly Met Met Leu Ser Asn Met Ser Thr Val Val			
370	375	380	
aac gtc ttt gag aat ggc tgc aat act ttt gac aaa gta ttt gcc aag			1200
Asn Val Phe Glu Asn Ala Cys Asn Thr Phe Asp Lys Val Phe Ala Lys			
385	390	395	400
ggc gca ttt tta aat aat tat aat gta ggc gac ttg ttc caa tca atg			1248
Gly Ala Phe Leu Asn Asn Tyr Asn Val Gly Asp Leu Phe Gln Ser Met			
405	410	415	
cag aac gtt caa gat gaa ttc gcc gag tca agc gaa gta gta caa agc			1296
Gln Asn Val Gln Asp Glu Phe Ala Glu Ser Arg Glu Val Val Gln Ser			
420	425	430	
ctg atg gag gat tat gta gct gca gaa caa gat tgg taa ttg gac gat			1344
Leu Met Glu Asp Tyr Val Ala Ala Glu Gln Asp Ser Tyr Leu Asp Asp			
435	440	445	
cta cct gtt gal gat gaa aat atg gtt ggc gag ttg gaa gag gac ctg			1392
Val Leu Val Asp Asp Glu Asn Met Val Gly Glu Leu Gln Glu Asp Leu			
450	455	460	
gat ggc gac ggt gat cat aaa tta gta taa			1422
Asp Ala Asp Gly Asp His Lys Leu Val			
465	470		

<210> 135

<211> 473

<212> PRT

<213> Saccharomyces cerevisiae

<400> 135

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Met Gly Gly Glu Ile Ile Thr Leu Gln Ala Gly Gln Cys Gly Asn His
1 5 10 15

Val Gly Lys Phe Leu Trp Ser Gln Leu Ala Lys Glu His Ala Ile Gly
20 25 30

Thr Asp Gly Leu Ser Gln Leu Pro Asp Ser Ser Thr Glu Arg Asp Asp
35 40 45

Asp Thr Lys Pro Phe Phe Arg Glu Asn Ser Arg Asn Lys Phe Thr Pro
50 55 60

Arg Ala Ile Met Met Asp Ser Glu Pro Ser Val Ile Ala Asp Val Glu
65 70 75 80

Asn Thr Phe Arg Gly Phe Phe Asp Pro Arg Asn Thr Trp Val Ala Ser
85 90 95

Asp Gly Ala Ser Ala Gly Asn Ser Trp Ala Asn Gly Tyr Asp Ile Gly
100 105 110

Thr Arg Asn Gln Asp Asp Ile Leu Asn Lys Ile Asp Lys Glu Ile Asp
115 120 125

Ser Thr Asp Asn Phe Glu Gly Phe Gln Leu Leu His Ser Val Ala Gly
130 135 140

Gly Thr Gly Ser Gly Leu Gly Ser Asn Leu Leu Glu Ala Leu Cys Asp
145 150 155 160

Arg Tyr Pro Lys Lys Ile Leu Thr Thr Tyr Ser Val Phe Pro Ala Arg
165 170 175

Ser Ser Glu Val Val Val Gln Ser Tyr Asn Thr Ile Leu Ala Leu Arg
180 185 190

Arg Leu Ile Glu Asp Ser Asp Ala Thr Val Val Phe Asp Asn Ala Ser
195 200 205

Leu Leu Asn Ile Ser Gly Lys Val Phe Arg Asn Pro Asn Ile Asp Leu
210 215 220

Gln His Thr Asn Gln Leu Ile Ser Thr Ile Ile Ser Ser Val Thr Asn
225 230 235 240

Ser Ile Arg Phe Pro Ser Tyr Met Tyr Ser Ser Met Ser Ser Ile Tyr
245 250 255

Ser Thr Leu Ile Pro Ser Pro Gln Leu His Phe Leu Ser Pro Ser Phe
260 265 270

Thr Pro Phe Thr Ser Asp Tyr Ile His Asp Asp Ile Ala His Lys Gly
275 280 285

His Ser Ser Tyr Asp Val Met Leu Asp Leu Leu Asp Pro Ser Asn Ser
290 295 300

Leu Val Ser Thr Ala Met Asn Asn Pro Thr Tyr Phe Asn Val Tyr Asn
305 310 315 320

Thr Ile Ile Gly Asn Val Gln Pro Arg Gln Ile Ser Arg Ala Met Thr
325 330 335

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Lys Leu Gln Gln Arg Ile Lys Phe Pro Ser Trp Ser Ser Ser Ala Met
 340 345 350

His Val Asn Ile Gly Arg Arg Ser Pro Tyr Leu Pro Leu Gln Pro Asn
 355 360 365

Glu Asn Gln Val Ser Gly Met Met Leu Ser Asn Met Ser Thr Val Val
 370 375 380

Asn Val Phe Glu Asn Ala Cys Asn Thr Phe Asp Lys Val Phe Ala Lys
 385 390 395 400

Gly Ala Phe Leu Asn Asn Tyr Asn Val Gly Asp Leu Phe Gln Ser Met
 405 410 415

Gln Asn Val Gln Asp Glu Phe Ala Glu Ser Arg Gln Val Val Gln Ser
 420 425 430

Leu Met Glu Asp Tyr Val Ala Ala Glu Gln Asp Ser Tyr Leu Asp Asp
 435 440 445

Val Leu Val Asp Asp Glu Asn Met Val Gly Gln Leu Glu Glu Asp Leu
 450 455 460

Asp Ala Asp Gly Asp His Lys Leu Val
 465 470

<210> 136

<211> 615

<212> DNA

<213> *Saccharomyces cerevisiae*

<400> 136

atgggtgctt acaaatattt ggaaguattg caaagaaga agcaatctga tgttttgaga 60
 ttcttgcaaa gactcagagt ctgggaatac agacaaaga atgtcattca cagagccgct 120
 agaccaacta gaccagacaa ggcLagaaga ttgggttaca aagctaagca aggttttggt 180
 atctaccgtg tcagagttag acgtggtaac agaaagagac ctgttccaaa ggggtgctact 240
 tccggtaagc caactaacca aggtgtcaal gaatcgaaat acaaaagata cttagagagct 300
 aacgctgaag aagagtttgg tcttctgtgc gctaactga gactcttgaa ctctactgg 360
 gtaaccaag attctactta caagtacttc gaagttatct tggtagaccc taacacaaag 420
 gctatcagaa gagatgctcg ttacaactgg atctgtgacc cagttcaca gacccgtgaa 480
 gctagaggtt tgactgcac tcgtaagaaa tccagaggta tcaacaaggg tcacaaaltc 540
 aacacccca aggtctgtag aagaagagac tggaaagagac aaaaactttt gtaactgtgg 600
 agatacagaa aataa 615

<210> 137
 <211> 801
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(801)

<400> 137
 atg ttg aac gtg cta ttg aga agg aag gcc ttt tgt ttg gtg aag aag 48
 Met Leu Asn Val Leu Ieu Arg Arg Lys Ala Phe Cys Leu Val Thr Lys
 1 5 10 15
 aag ggt atg got acl gcc aca aca got gcc got aag cat acc ccc aga 96
 Lys Gly Met Ala Thr Ala Thr Thr Ala Ala Ala Thr His Thr Pro Arg
 20 25 30

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ttg aaa act ttt aaa gtt tac aga tgg aat cca gac gag cca agt gct	144
Leu Lys Thr Phe Lys Val Tyr Arg Trp Asn Pro Asp Glu Pro Ser Ala	
35 40 45	
aaa cct cat tta caa tca tat caa gtc gat ctg aat gac tgt ggg ccc	192
Lys Pro His Leu Gln Ser Tyr Gln Val Asp Leu Asn Asp Cys Gly Pro	
50 55 60	
atg gta ctt gat ggc ctg tta aag atc aaa gac gaa cag gat tct acc	240
Met Val Leu Asp Ala Phe Leu Lys Phe Tyr Asp Glu Gln Asp Ser Thr	
65 70 75 80	
cta act ttt aga aga tca tgt aga gaa ggt atc tgc ggt tca tgt gcc	288
Leu Thr Phe Arg Arg Ser Cys Arg Gln Gly Ile Cys Gly Ser Cys Ala	
85 90 95	
atg aac att ggc ggt aga aac acg cta gct tgt ata tgt aag atc gac	336
Met Asn Ile Gly Gly Arg Asn Thr Leu Ala Cys Ile Cys Lys Ile Asp	
100 105 110	
cag aac gaa tcc aaa caa ctc aag atc tat cca tta ccc aac atg tta	384
Gln Asn Glu Ser Lys Gln Leu Lys Ile Tyr Pro Leu Pro His Met Phe	
115 120 125	
att gtc aaa gat ttg gta cct gat tta act aac ttc tac caa caa tac	432
Ile Val Lys Asp Leu Val Pro Asp Leu Thr Asn Phe Tyr Gln Gln Tyr	
130 135 140	
aaa cct atc caa cct tca tta cag aga tca tgc ttt cca aag gat gga	480
Lys Ser Ile Gln Pro Tyr Leu Gln Arg Ser Ser Phe Pro Lys Asp Gly	
145 150 155 160	
acg gaa gtg cta caa agt att gaa gat cgt aag aaa ctg gat ggt ctt	528
Thr Glu Val Leu Gln Ser Ile Glu Asp Arg Lys Lys Leu Asp Gly Leu	
165 170 175	
tac gaa tgt att ctg tgt gca tgc tgc tct act tca tgt cca tgc tac	576
Tyr Glu Cys Ile Leu Cys Ala Cys Cys Ser Thr Ser Cys Pro Ser Tyr	
180 185 190	
lyg lyg aac caa gaa cag tat ttg ggc cct gcc gtg cta atg caa gcc	624
Trp Trp Asn Gln Gln Gln Tyr Leu Gly Pro Ala Val Leu Met Gln Ala	

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195	200	205	
taa agt tgg cta att gag tct aga gac caa gcc acc aag acg aga aag			672
Tyr Arg Trp Leu Ile Asp Ser Arg Asp Gln Ala Thr Lys Thr Arg Lys			
210	215	220	
gcc atg cta aac aac tcc atg tca ttg tac aga tgt cac acc atc atg			720
Ala Met Leu Asn Asn Ser Met Ser Leu Tyr Arg Cys His Thr Ile Met			
225	230	235	240
aaa tgt act aga act tgt cca aag gcc ttg aat cct ggt ttg gct att			768
Asn Cys Thr Arg Thr Cys Pro Lys Gly Leu Asn Pro Gly Leu Ala Ile			
	245	250	255
gct gaa att aag aaa tct ttg gca ttt gcc aag			801
Ala Glu Ile Lys Lys Ser Leu Ala Phe Ala			
	260	265	
<210> 138			
<211> 266			
<212> FRT			
<213> <i>Saccharomyces cerevisiae</i>			
<400> 138			
Met Leu Asn Val Leu Leu Arg Arg Lys Ala Phe Cys Leu Val Thr Lys			
1	5	10	15
Lys Gly Met Ala Thr Ala Thr Thr Ala Ala Ala Thr His Thr Pro Arg			
	20	25	30
Leu Lys Thr Phe Lys Val Tyr Arg Trp Asn Pro Asp Glu Pro Ser Ala			
	35	40	45
Lys Pro His Leu Gln Ser Tyr Gln Val Asp Leu Asn Asp Cys Gly Pro			
	50	55	60

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Met Val Ile Asp Ala Leu Leu Lys Ile Lys Asp Gln Gln Asp Ser Thr
65 70 75 80

Leu Thr Phe Arg Arg Ser Cys Arg Gln Gly Ile Cys Gly Ser Cys Ala
85 90 95

Met Asn Ile Gly Gly Arg Asn Thr Leu Ala Cys Ile Cys Tyr Ile Asp
100 105 110

Gln Asn Glu Ser Lys Gln Leu Lys Ile Tyr Pro Leu Pro His Met Phe
115 120 125

Ile Val Lys Asp Leu Val Pro Asp Leu Thr Asn Phe Tyr Gln Gln Tyr
130 135 140

Lys Ser Ile Gln Pro Tyr Leu Cln Arg Ser Ser Phe Pro Lys Asp Gly
145 150 155 160

Thr Glu Val Leu Gln Ser Ile Glu Asp Arg Lys Lys Leu Asp Gly Leu
165 170 175

Tyr Glu Cys Ile Leu Cys Ala Cys Cys Ser Thr Ser Cys Pro Ser Tyr
180 185 190

Trp Trp Asn Gln Glu Gln Tyr Leu Gly Pro Ala Val Leu Met Gln Ala
195 200 205

Tyr Arg Trp Leu Ile Asp Ser Arg Asp Gln Ala Thr Lys Thr Arg Lys
210 215 220

Ala Met Leu Asn Asn Ser Met Ser Leu Tyr Arg Cys His Thr Ile Met
225 230 235 240

Asn Cys Thr Arg Thr Cys Pro Lys Gly Leu Asn Pro Gly Leu Ala Ile
 245 250 255

Ala Glu Ile Lys Lys Ser Leu Ala Phe Ala
 260 265

<210> 139
 <211> 1134
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<230>
 <221> CDS
 <222> (1)..(1134)

<400> 139
 atg tct aaa ggg agg gtc aat cag aag agt tac aag tat cct ctt cca 45
 Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro
 1 5 10 15
 att cac ccc gta gat gac ctt cca gag tta atc ctt cat aat cag tta 96
 Ile His Pro Val Asp Asp Leu Pro Gln Leu Ile Leu His Asn Pro Leu
 20 25 30
 tct tgg cta tat tgg gca tac cgc tat tac aag agt aag aac gca ctg 144
 Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu
 35 40 45
 aac gat aaa gta cat gta gat ttt ata gga gat acc act ctt cac atc 192
 Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Phe Leu His Ile
 50 55 60
 acg gll caa gat gac aag caa atg cta tat ctt tgg aat aat gga ttt 240
 Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe
 65 70 75 80
 ttt ggc act ggt caa ttt agc agg agt gag cct aca tgg aaa gcl aga 288

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Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg	
85 90 95	
aca gag gcc aga ctg cgt ctc aat gat act ccc etc cac aat cgg gga	336
Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly	
100 105 110	
gga aca aag agt aat act gaa aag gag atg act cca gag aag etc aca	384
Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr	
115 120 125	
caa cag agg aga tta caa aga tta gag ttc aag aaa gaa cgt cgg aag	432
Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys	
130 135 140	
tta gaa aga gaa tta cta gaa tta aga aaa aaa ggt ggt cat atc gal	480
Leu Glu Arg Glu Leu Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp	
145 150 155 160	
gag gaa aac atc etc ctt gag aac cac cga gaa tca tta aga aaa ttt	528
Gln Gln Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe	
165 170 175	
aaa cta aaa caa aca gaa gaa gag ggc atc gtt gca caa cag caa gac	576
Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp	
180 185 190	
att tcc gaa tca aat tta aga gat gaa gac aac aat ctt ctt gat gag	624
Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu	
195 200 205	
aac ggt gat ctt ttg cca cta gag tca cta gaa cta atg cca gtg gaa	672
Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Glu Leu Met Pro Val Glu	
210 215 220	
gct atg ttt tta act ttt gca ctt cct gcc ctt gac ata tct ccc gag	720
Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala	
225 230 235 240	
tgc ccg gca ggg aaa ctg ttt caa ttc gat gcc aac tat aaa gat att	768
Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile	
245 250 255	

cac tcc ttt gtc aga tca tuc gtt ata tac cat cnc tac aga tca cac 816
 His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
 260 265 270

ggc tgg lyc gta aga tct ggt ata aaa ttc ggc tgc gat tat tta tta 864
 Gly Trp Cys val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
 275 280 285

tat aag aga ggg cca cca ttt caa cac gct gaa ttt tgt gtt atg ggt 912
 Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Gln Phe Cys Val Met Gly
 290 295 300

ctt gac cac gac gtc tct aaa gat tat aag tgg tat tct agc ata gcc 960
 Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
 305 310 315 320

cgt gtt gtg ggc ggc gca aag aag acg ttt gtg tta tgc tac gtg gag 1038
 Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Gln
 325 330 335

aga cta atc tgg gaa cag gag gcg ala gca cta tgg aat tca aac aac 1098
 Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn
 340 345 350

ttt act aac tgg ttc aat agt ttt caa gtt ggc gaa gta tgg tat aag 1164
 Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Gln Val Leu Tyr Lys
 355 360 365

aga tgg gtt ccc gga aga aat aga gac tag 1234
 Arg Trp Val Pro Gly Arg Asn Arg Asp
 370 375

<210> 140

<211> 377

<212> PRT

<213> Saccharomyces cerevisiae

<400> 140

Met Ser Lys Gly Arg Val Asn Gln Lys Arg Tyr Lys Tyr Pro Leu Pro

1	5	10	15
Ile His Pro Val Asp Asp Leu Pro Glu Leu Ile Leu His Asn Pro Leu	20	25	30
Ser Trp Leu Tyr Trp Ala Tyr Arg Tyr Tyr Lys Ser Thr Asn Ala Leu	35	40	45
Asn Asp Lys Val His Val Asp Phe Ile Gly Asp Thr Thr Leu His Ile	50	55	60
Thr Val Gln Asp Asp Lys Gln Met Leu Tyr Leu Trp Asn Asn Gly Phe	65	70	75
Phe Gly Thr Gly Gln Phe Ser Arg Ser Glu Pro Thr Trp Lys Ala Arg	85	90	95
Thr Glu Ala Arg Leu Gly Leu Asn Asp Thr Pro Leu His Asn Arg Gly	100	105	110
Gly Thr Lys Ser Asn Thr Glu Thr Glu Met Thr Leu Glu Lys Val Thr	115	120	125
Gln Gln Arg Arg Leu Gln Arg Leu Glu Phe Lys Lys Glu Arg Ala Lys	130	135	140
Leu Glu Arg Gln Asn Leu Glu Leu Arg Lys Lys Gly Gly His Ile Asp	145	150	155
Glu Glu Asn Ile Leu Leu Glu Lys Gln Arg Glu Ser Leu Arg Lys Phe	165	170	175

Lys Leu Lys Gln Thr Glu Asp Val Gly Ile Val Ala Gln Gln Gln Asp
 180 185 190

Ile Ser Glu Ser Asn Leu Arg Asp Glu Asp Asn Asn Leu Leu Asp Glu
 195 200 205

Asn Gly Asp Leu Leu Pro Leu Glu Ser Leu Gln Leu Met Pro Val Gln
 210 215 220

Ala Met Phe Leu Thr Phe Ala Leu Pro Val Leu Asp Ile Ser Pro Ala
 225 230 235 240

Cys Leu Ala Gly Lys Leu Phe Gln Phe Asp Ala Lys Tyr Lys Asp Ile
 245 250 255

His Ser Phe Val Arg Ser Tyr Val Ile Tyr His His Tyr Arg Ser His
 260 265 270

Gly Trp Cys Val Arg Ser Gly Ile Lys Phe Gly Cys Asp Tyr Leu Leu
 275 280 285

Tyr Lys Arg Gly Pro Pro Phe Gln His Ala Glu Phe Cys Val Met Gly
 290 295 300

Leu Asp His Asp Val Ser Lys Asp Tyr Thr Trp Tyr Ser Ser Ile Ala
 305 310 315 320

Arg Val Val Gly Gly Ala Lys Lys Thr Phe Val Leu Cys Tyr Val Gln
 325 330 335

Arg Leu Ile Ser Glu Gln Glu Ala Ile Ala Leu Trp Lys Ser Asn Asn

340

345

350

Phe Thr Lys Leu Phe Asn Ser Phe Gln Val Gly Glu Val Leu Tyr Lys
 355 360 365

Arg Trp Val Pro Gly Arg Asn Arg Asp
 370 375

<210> 141

<211> 1162

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1162)

<400> 141

atg tca tca aga ata att gtc ggc agt gca gca ttg gca gct gcc atc 40
 Met Ser Ser Arg Ile Ile Val Gly Ser Ala Ala Leu Ala Ala Ala Ile
 1 5 10 15

aca gct agc atc atg gtc aga gaa cag aag gcc aag ggt cag aga aga 95
 Thr Ala Ser Ile Met Val Arg Glu Gln Lys Ala Lys Gly Gln Arg Arg
 20 25 30

gag ggc aac gtc tcc gct tac tac aac ggc cag gag tac gcc agt tca 144
 Glu Gly Asn Val Ser Ala Tyr Tyr Asn Gly Gln Gln Tyr Gly Ser Ser
 35 40 45

gca ccc cca cag ttg gga aag cta cat aac ata aag caa gcc ata aag 192
 Ala Pro Pro Gln Leu Gly Lys Leu His Asn Ile Lys Gln Gly Ile Lys
 50 55 60

gaa gat gcc ttg tgg tta aag gac gag ctt ctg gcc gta tct caa aag 240
 Glu Asp Ala Leu Ser Leu Lys Asp Ala Leu Leu Gly Val Ser Gln Lys
 65 70 75 80

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gct agg gaa gag gct cca aag gta act aag cgt glg ata tca aag gaa	238
Ala Arg Glu Glu Ala Pro Lys Val Thr Lys Arg Val Ile Ser Pro Glu	
85 90 95	
 gag gat gct cag aca cgc aag cag cta ggc caa aaa gcc aag gat tct	336
Glu Asp Ala Glu Thr Arg Lys Glu Leu Gly Glu Lys Ala Lys Asp Ser	
100 105 110	
 tcc tgg caa agc acc ttc aat tgg ggg ttt agt gag gct gaa aga agg	384
Ser Ser Gln Ser Ile Phe Asn Trp Gly Phe Ser Glu Ala Glu Arg Arg	
115 120 125	
 aaa gcc ata gcc atc ggg gaa ttt gat act gct aag aag cgt ttc gaa	432
Lys Ala Ile Ala Ile Gly Glu Phe Asp Thr Ala Lys Lys Arg Phe Glu	
130 135 140	
 gag gaa gtg gat cgt aat gag aag gag ctc ttg tcc acg gtg atg aga	480
Glu Ala Val Asp Arg Asn Glu Lys Glu Leu Leu Ser Thr Val Met Arg	
145 150 155 160	
 gag aag aag gcc gct ctg gac aga gca tcc att gag tac gaa agg tac	528
Glu Lys Lys Ala Ala Leu Asp Arg Ala Ser Ile Glu Tyr Glu Arg Tyr	
165 170 175	
 ggg aag gcc aga gac ttt aat gag ctt tgg gac aag cta gac caa cag	576
Gly Arg Ala Arg Asp Phe Asn Glu Leu Ser Asp Lys Leu Asp Gln Glu	
180 185 190	
 gaa agg aac agt aat cct ttg aaa cgc ctg ttg aag act aac acg ggt	624
Glu Arg Asn Ser Asn Pro Leu Lys Arg Leu Leu Lys Asn Asn Thr Gly	
195 200 205	
 gac gct aat act gaa gaa gcc gct gca aga agt gtc caa ggc tgg ggt	672
Asp Ala Asn Thr Glu Glu Ala Ala Ala Arg Ser Val Gln Gly Trp Gly	
210 215 220	
 gat acg gca cag gag ttt ggt aga gaa gag ttg gag gaa gcc aag aga	720
Asp Thr Ala Gln Glu Phe Gly Arg Glu Glu Leu Glu Glu Ala Lys Arg	
225 230 235 240	
 aat gct tcc leu gag cca agc gag ggc cna aaa cgt ctc gac gag ctg	768
Asn Ala Ser Ser Gln Pro Ser Gln Ala Gln Lys Arg Leu Asp Glu Leu	

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245	250	255	
aag aag atc aag gaa aag ggc tgg ttt ggt tac aac aaa ggg gag caa			816
Lys Lys Ile Lys Glu Lys Gly Trp Phe Gly Tyr Asn Lys Gly Glu Gln			
240	245	250	
agc gag caa cag att gct gaa cgg gta gcc aga ggt tta gaa gga tgg			864
Ser Glu Gln Gln Ile Ala Glu Arg Val Ala Arg Gly Leu Glu Gly Trp			
275	280	285	
ggc gaa aca gcc gct caa ctt tcc aag gac gaa atg gac gat tta aga			912
Gly Gln Thr Ala Ala Gln Leu Ser Lys Asp Glu Met Asp Asp Leu Arg			
290	295	300	
tgg aac tat gag aat tca aag aaa caa ctg gat aag aac gtg tcc gac			960
Trp Asn Tyr Glu Asn Ser Lys Lys Gln Leu Asp Lys Asn Val Ser Asp			
305	310	315	320
gcc atg gac cag tta tct aag gcc aag gag gac ttg aac cag tac gcc			1008
Ala Met Asp Ser Leu Ser Lys Ala Lys Glu Asp Leu Lys Gln Tyr Gly			
325	330	335	
agc cac tgg tgg tct gga tgg act tcc aag gtc gac aat gac aag cag			1056
Ser His Trp Trp Ser Gly Trp Thr Ser Lys Val Asp Asn Asp Lys Gln			
340	345	350	
gct tta aaa gat gag gcc caa aag aag tac gat gaa gcc ttg aaa aag			1104
Ala Leu Lys Asp Glu Ala Glu Lys Lys Tyr Asp Glu Ala Leu Lys Lys			
355	360	365	
tac gat gaa gcc cag aac aaa ttc aaa gaa tgg aat gat aag ggt gac			1152
Tyr Asp Glu Ala Lys Asn Lys Phe Lys Glu Trp Asn Asp Lys Gly Asp			
370	375	380	
ggc aaa ttc tgg agc tgc aaa aag gac tag			1182
Gly Lys Phe Trp Ser Ser Lys Lys Asp			
385	390		

<210> 143

<211> 393

<212> PRT

<213> *Saccharomyces cerevisiae*

<406> 142

Met Ser Ser Arg Ile Ile Val Gly Ser Ala Ala Leu Ala Ala Ala Ile
1 5 10 15

Thr Ala Ser Ile Met Val Arg Glu Gln Lys Ala Lys Gly Gln Arg Arg
20 25 30

Glu Gly Asn Val Ser Ala Tyr Tyr Asn Gly Glu Glu Tyr Gly Ser Ser
35 40 45

Ala Pro Pro Gln Leu Gly Lys Leu His Asn Ile Lys Gln Gly Ile Lys
50 55 60

Glu Asp Ala Leu Ser Leu Lys Asp Ala Leu Leu Gly Val Ser Gln Lys
65 70 75 80

Ala Arg Glu Gln Ala Pro Lys Val Thr Lys Arg Val Ile Ser Pro Glu
85 90 95

Glu Asp Ala Gln Thr Arg Lys Gln Leu Gly Gln Lys Ala Lys Asp Ser
100 105 110

Ser Ser Gln Ser Ile Phe Asn Trp Gly Phe Ser Glu Ala Glu Arg Arg
115 120 125

Lys Ala Ile Ala Ile Gly Glu Phe Asp Thr Ala Lys Lys Arg Phe Glu
130 135 140

Glu Ala Val Asp Arg Asn Glu Lys Glu Leu Leu Ser Thr Val Met Arg
145 150 155 160

Glu Lys Lys Ala Ala Leu Asp Arg Ala Ser Ile Glu Tyr Glu Arg Tyr
165 170 175

Gly Arg Ala Arg Asp Phe Asn Glu Leu Ser Asp Lys Leu Asp Glu Gln
180 185 190

Glu Arg Asn Ser Asn Pro Leu Lys Arg Leu Leu Lys Asn Asn Thr Gly
195 200 205

Asp Ala Asn Thr Glu Glu Ala Ala Ala Arg Ser Val Gln Gly Trp Gly
210 215 220

Asp Thr Ala Glu Glu Phe Gly Arg Glu Glu Leu Glu Glu Ala Lys Arg
225 230 235 240

Asn Ala Ser Ser Glu Pro Ser Glu Ala Gln Lys Arg Ser Asp Glu Leu
245 250 255

Lys Lys Ile Lys Glu Lys Gly Trp Phe Gly Tyr Asn Lys Gly Glu Gln
260 265 270

Ser Glu Gln Gln Ile Ala Glu Arg Val Ala Arg Gly Leu Glu Gly Trp
275 280 285

Gly Glu Thr Ala Ala Gln Leu Ser Lys Asp Glu Met Asp Asp Leu Arg
290 295 300

Trp Asn Tyr Glu Asn Ser Lys Lys Gln Leu Asp Lys Asn Val Ser Asp
305 310 315 320

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Ala Met Asp Ser Leu Ser Lys Ala Lys Glu Asp Leu Lys Gln Tyr Gly
 325 330 335

Ser His Trp Trp Ser Gly Trp Thr Ser Lys Val Asp Asn Asp Lys Gln
 340 345 350

Ala Leu Lys Asp Glu Ala Gln Lys Lys Tyr Asp Glu Ala Leu Lys Tyr
 355 360 365

Tyr Asp Glu Ala Lys Asn Lys Phe Lys Glu Trp Asn Asp Lys Gly Asp
 370 375 380

Gly Lys Phe Trp Ser Ser Lys Lys Asp
 385 390

<210> 143
 <211> 1063
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> (108)
 <222> (1)..(1083)

<400> 143
 atg tcc tca caa gaa tat aca act ttt ata gat ata cca gtg aca aga 48
 Met Ser Ser Gln Glu Tyr Thr Thr Phe Ile Asp Ile Pro Val Thr Arg
 1 5 10 15
 gcg cag gtt gaa caa tgg tct tac tgg ttt tgg tcc tca ctg tat ccc 96
 Ala Gln Val Gln His Cys Ser Tyr Ser Phe Trp Ser Ser Leu Tyr Pro
 20 25 30
 aaa tat gtg cca aaa tcc ata gtg tta aaa tcc tta ccg aaa aaa ttt 144
 Lys Tyr Val Pro Lys Ser Ile Val Leu Lys Ser Leu Pro Lys Lys Phe
 35 40 45

atc caa tat ttg gaa caa gac ggt atc aag cta ccc caa gag gaa aac Ile Gln Tyr Leu Glu Gln Asp Gly Ile Lys Leu Pro Gln Glu Glu Asn 50 55 60	192
ccc agg tct gtc tac acc gag gaa ata ata aga aat gaa gat aat gac Ser Arg Ser Val Tyr Thr Glu Glu Ile Ile Arg Asn Glu Asp Asn Asp 65 70 75 80	240
tat agt gat tgg gag gac gat gag gat acc gcc acc gaa ttt gtc caa Tyr Ser Asp Trp Glu Asp Asp Glu Asp Thr Ala Thr Glu Phe Val Gln 85 90 95	288
caa gtt gag cca ttg ata gat ttt cca gaa tta cnc cag aaa tta aag Glu Val Glu Pro Leu Ile Asp Phe Pro Glu Leu His Gln Lys Leu Lys 100 105 110	336
gat gct ttg aac gaa tta ggt gca gtg gct ccc aag tta aac tgg tct Asp Ala Leu Asn Glu Leu Gly Ala Val Ala Pro Lys Leu Asn Trp Ser 115 120 125	384
gca ccc aga gac gct ccc tgg att ttc ccg aat aac act atg cag tgt Ala Pro Arg Asp Ala Thr Trp Ile Leu Pro Asn Asn Thr Met Lys Cys 130 135 140	432
aac gag gta aat gag ctt cac cta ttg ttg aac gca tcc aat tac ata Asn Glu Val Asn Glu Leu Tyr Leu Leu Leu Asn Ala Ser Asn Tyr Tle 145 150 155 160	480
atg cat gac ctt caa aga gca ttt aac gcc tgc gtc gac ggg gat gat Met His Asp Leu Gln Arg Ala Phe Lys Gly Cys Val Asp Gly Asp Asp 165 170 175	528
ata aac gga ttg aaa ttt gac ttg gta ctt aga caa tgg tgt gat atg Ile Lys Gly Leu Lys Phe Asp Leu Val Leu Arg Gln Trp Cys Asp Met 180 185 190	576
aat ccg gca ctc gaa ttt agg gtc ttc gtc aag aat ggc cat atc gtt Asn Pro Ala Leu Glu Phe Arg Val Phe Val Lys Asn Ala His Ile Val 195 200 205	624
ggg gcc acc cag cgt gat tta aat tat tat gac tat tta gat gag ttc 210	672

Gly Ala Thr Gln Arg Asp Leu Asn Tyr Tyr Asp Tyr Leu Asp Glu Leu	
210 215 220	
tea gat acc tcc aag gac ctt att gal gaa ata gtt cat gat glc gtc	720
Ser Asp Thr Phe Lys Asp Leu Ile Asp Glu Ile Val His Asp Val Val	
225 230 235 240	
ctg ccc aag ttt cct gat aaa agl ltc gtt ccc gac gtt tat att cca	768
Leu Pro Lys Phe Pro Asp Lys Ser Phe Val Leu Asp Val Tyr Ile Pro	
245 250 255	
aga cct ttc aat aaa atc ttc att gtt gat ata aat ccg ttt gcc agg	816
Arg Pro Phe Asn Lys Ile Phe Ile Val Asp Ile Asn Pro Phe Ala Arg	
260 265 270	
aag aca gat tct ttg cta ttt tca tgg aac gag att gct gag ala gca	864
Lys Thr Asp Ser Leu Leu Phe Ser Trp Asn Glu Ile Ala Ala Ile Ala	
275 280 285	
cct ccg aag aat gat gtt gaa gat tat gaa tta agg tta gtg acc agg	912
Pro Pro Lys Asn Asp Val Glu Asp Tyr Glu Leu Arg Leu Val Thr Arg	
290 295 300	
cat aac acg ggg agc ttc gct tca aaa gag cac tcc gaa aat cat gtt	960
His Asn Thr Gly Arg Phe Ala Ser Lys Glu His Ser Glu Asn His Val	
305 310 315 320	
cca cag gat ctg gta gaa gct agt tta aat cct gaa gca atc cga gag	1008
Pro Gln Asp Leu Val Glu Ala Ser Leu Asn Pro Glu Ala Ile Arg Gln	
325 330 335	
ctc act caa aaa tgg aaa gaa cta ctg tct caa cag gca aag gaa gaa	1056
Leu Thr Gln Lys Trp Lys Glu Leu Leu Ser Gln Gln Ala Lys Glu Gln	
340 345 350	
agc agt gat agt gag aat gaa act lag	1083
Ser Ser Asp Ser Glu Asn Glu Thr	
355 360	

<210> 144

<211> 360

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 144

Met Ser Ser Gln Glu Tyr Thr Thr Phe Ile Asp Ile Pro Val Thr Arg
1 5 10 15

Ala Gln Val Glu His Cys Ser Tyr Ser Phe Trp Ser Ser Leu Tyr Pro
20 25 30

Lys Tyr Val Pro Lys Ser Ile Val Leu Lys Ser Leu Pro Lys Lys Phe
35 40 45

Ile Gln Tyr Leu Glu Gln Asp Gly Ile Lys Leu Pro Gln Glu Glu Asn
50 55 60

Ser Arg Ser Val Tyr Thr Glu Glu Ile Ile Arg Asn Glu Asp Asn Asp
65 70 75 80

Tyr Ser Asp Trp Glu Asp Asp Glu Asp Thr Ala Thr Glu Phe Val Gln
85 90 95

Glu Val Glu Pro Leu Ile Asp Phe Pro Glu Leu His Gln Lys Leu Lys
100 105 110

Asp Ala Leu Asn Glu Leu Gly Ala Val Ala Pro Lys Leu Asn Trp Ser
115 120 125

Ala Pro Arg Asp Ala Thr Trp Ile Leu Pro Asn Asn Thr Met Lys Cys
130 135 140

Asn Glu Val Asn Glu Leu Tyr Leu Leu Leu Asn Ala Ser Asn Tyr Ile

145	150	155	160
Met His Asp Leu Gln Arg Ala Phe Lys Gly Cys Val Asp Gly Asp Asp			
	165	170	175
Ile Lys Gly Leu Lys Phe Asp Leu Val Leu Arg Gln Trp Cys Asp Met			
	180	185	190
Asn Pro Ala Leu Gln Phe Arg Val Phe Val Lys Asn Ala His Ile Val			
	195	200	205
Gly Ala Thr Gln Arg Asp Leu Asn Tyr Tyr Asp Tyr Leu Asp Glu Leu			
210	215	220	
Ser Asp Thr Phe Lys Asp Leu Ile Asp Glu Ile Val His Asp Val Val			
225	230	235	240
Leu Pro Lys Phe Pro Asp Lys Ser Phe Val Leu Asp Val Tyr Ile Pro			
	245	250	255
Arg Pro Phe Asn Lys Ile Phe Ile Val Asp Ile Asn Pro Phe Ala Arg			
	260	265	270
Lys Thr Asp Ser Leu Leu Phe Ser Trp Asn Glu Ile Ala Ala Ile Ala			
275	280	285	
Pro Pro Lys Asn Asp Val Glu Asp Tyr Gln Leu Arg Leu Val Thr Arg			
290	295	300	
His Asn Thr Gly Arg Phe Ala Ser Lys Glu His Ser Gln Asn His Val			
305	310	315	320

Pro Gln Asp Leu Val Glu Ala Ser Leu Asn Pro Glu Ala Ile Arg Glu
 325 330 335

Leu Thr Gln Lys Trp Lys Glu Leu Leu Ser Gln Gln Ala Lys Glu Glu
 340 345 350

Ser Ser Asp Ser Glu Asn Glu Thr
 355 360

<210> 145
 <211> 1281
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1281)

<400> 145
 atg tgg cac caa aac cag ctt atg cgc caa ggt tat att tct aac ttt 48
 Met Ser His Gln Asn Gln Leu Ile Pro Gln Ala Tyr Ile Ser Asn Phe
 1 5 10 15
 cat aac aga ttg aca aac gaa gat gat ggt atc ccc atc ttt aca atg 96
 His Asn Arg Leu Thr Asn Glu Asp Asp Gly Phe Pro Ile Phe Thr Met
 20 25 30
 gct caa caa aca agg cag cat aaa agg gct aaa gtg gtc aac tat gcg 144
 Ala Gln Gln Thr Arg Gln His Lys Arg Ala Lys Val Val Asn Tyr Ala
 35 40 45
 gaa tat gac aac gat ctc ttt gat gaa ttc aat atg aac ggt tct aat 192
 Glu Tyr Asp Asn Asp Leu Phe Asp Glu Phe Asn Met Asn Gly Ser Asn
 50 55 60
 ttg aac aat gct gat aca cgc tat aaa gat aat cca gtg tct cat gaa 240
 Phe Asn Asn Ala Asp Thr His Tyr Lys Asp Asn Ala Val Ser His Glu

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65	70	75	80	
aat act cag gca att aca aat ggt gtt acc atg gac ggt tcc gaa tac				288
Asn Thr Pro Ala Leu Thr Asn Gly Val Thr Met Asp Gly Ser Glu Tyr				
	85	90	95	
aat gtc cta gag aac atg aat gga gct gat agt att atc tct aac aac				336
Asn Val Leu Glu Asn Met Asn Gly Ala Asp Ser Ile Ile Ser Asn Asn				
	100	105	110	
aaa tuc gat gag ggt tca aac atg gtt gtg gaa tct tta tcc ggt ttg				384
Lys Tyr Asp Ala Gly Ser Asn Met Val Val Glu Ser Leu Ser Gly Leu				
	115	120	125	
aat agc aat aac aac gcc agc aac ggt cag agc aac aaa gag cag gca				432
Asn Ser Asn Asn Asn Ala Ser Asn Gly Pro Ser Asn Lys Ala Glu Ala				
	130	135	140	
cag gat att gga aac gcc gtt cta cag gat ctg caa gac caa ttc cca				480
Gln Asp Ile Gly Asn Ala Val Leu Pro Asp Leu Gln Asp Gln His His				
	145	150	155	160
aac ccc ttc aac ata ttg aga tac ccc aac ata aga gat act ttc att				528
Asn Pro Phe Asn Ile Leu Arg Tyr Pro Lys Ile Arg Asp Thr Phe Ile				
	165	170	175	
aac gga aac gtg gtg tct cca tat aga ctc aac act gat caa gaa acg				576
Asn Gly Lys Val Val Ser Pro Tyr Arg Leu Asn Thr Asp Gln Glu Thr				
	180	185	190	
cag gca aac gcc aat tct gga gag gca atc atg ata cca att act ttg				624
Lys Ala Asn Ala Asn Ser Gly Glu Ala Ile Met Ile Pro Ile Thr Leu				
	195	200	205	
gat ata gaa cat atg ggt cat acc ata aaa gac cag ttt ctc tgg aac				672
Asp Ile Glu His Met Gly His Thr Ile Lys Asp Gln Phe Leu Trp Asn				
	210	215	220	
lac aat gac gac tcc ata tct cag gag gaa ttt gcc tct ata tcc tgt				720
Tyr Asn Asp Asp Ser Ile Ser Pro Glu Glu Phe Ala Ser Ile Tyr Cys				
	225	230	235	240

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aaa gat ctt gat atg act tcc gct acc tta caa acg caa att gcg aat	768
Lys Asp Leu Asp Met Thr Ser Ala Thr Leu Gln Thr Gln Ile Ala Asn	
345 250 255	
ata ata aaa gag cag ttg aaa gac ctc gaa aat att gca gcc act gag	816
Ile Ile Lys Glu Gln Leu Lys Asp Leu Glu Asn Ile Ala Ala Thr Glu	
260 265 270	
ata atg tct gac ctc cac gtg ata atc aac cta acc tgc aac tta caa	864
Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Gln	
275 280 285	
gac aga ttt ttt gaa gat aac ttc cag tgg aac tly aac gac aaa tca	912
Asp Arg Phe Phe Glu Asp Asn Phe Gln Trp Asn Leu Asn Asp Lys Ser	
290 295 300	
ctt act cca gaa aga ttt gct aca tcc att gta cag gac ctt ggc tta	960
Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Gln Asp Leu Cys Leu	
305 310 315 320	
aca aga gag ttc atc ccc tta ata tct caa tgg ctt cat gaa acg atc	1008
Thr Arg Glu Phe Ile Pro Leu Ile Ser Gln Ser Leu His Glu Thr Ile	
325 330 335	
ttg aag ata aag acg gac tgg gta gat ggc cac atg att cag gac cat	1056
Leu Lys Ile Lys Tyr Asp Trp Val Asp Gly His Leu Ile Gln Asp His	
340 345 350	
gic caa aac gat gcc gca ttt ggg tac tta tct ggt ata agg atg gat	1104
Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp	
355 360 365	
att gat gaa atg ggc tcc aat tgg tgc cca aag gtg gaa ata tta aca	1152
Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Glu Ile Leu Thr	
370 375 380	
aaa gaa gaa ata caa aag aga gaa att gaa aaa gaa aga aac tta aga	1200
Lys Glu Glu Ile Gln Lys Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg	
385 390 395 400	
aga tgg aaa aga gaa act gat aga tta tct aga aag ggc agg aga aga	1248
Arg Leu Lys Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg	

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105

410

415

tta gat gac tta gac acc aca atg aga atg tag

1281

Leu Asp Asp Leu Glu Thr Thr Met Arg Met

420

425

<210> 146

<211> 426

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 146

Met Ser His Gln Asn Gln Leu Ile Pro Gln Ala Tyr Ile Ser Asn Phe

1

5

10

15

His Asn Arg Leu Thr Asn Glu Asp Asp Gly Ile Pro Ile Phe Thr Met

20

25

30

Ala Gln Gln Thr Arg Gln His Lys Arg Ala Lys Val Val Asn Tyr Ala

35

40

45

Glu Tyr Asp Asn Asp Leu Phe Asp Glu Phe Asn Met Asn Gly Ser Asn

50

55

60

Phe Asn Asn Ala Asp Thr His Tyr Lys Asp Asn Ala Val Ser His Glu

65

70

75

80

Asn Thr Pro Ala Leu Thr Asn Gly Val Thr Met Asp Gly Ser Glu Tyr

85

90

95

Asn Val Leu Glu Asn Met Asn Gly Ala Asp Ser Ile Ile Ser Asn Asn

100

105

110

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Lys Tyr Asp Ala Gly Ser Asn Met Val Val Glu Ser Leu Ser Gly Leu
115 120 125

Asn Ser Asn Asn Asn Ala Ser Asn Gly Pro Ser Asn Lys Ala Gln Ala
130 135 140

Gln Asp Ile Gly Asn Ala Val Leu Pro Asp Leu Gln Asp Gln His His
145 150 155 160

Asn Pro Phe Asn Ile Leu Arg Tyr Pro Lys Ile Arg Asp Thr Phe Ile
165 170 175

Asn Gly Lys Val Val Ser Pro Tyr Arg Leu Asn Thr Asp Gln Glu Thr
180 185 190

Lys Ala Asn Ala Asn Ser Gly Glu Ala Ile Met Thr Pro Ile Thr Leu
195 200 205

Asp Ile Glu His Met Gly His Thr Ile Lys Asp Gln Phe Leu Trp Asn
210 215 220

Tyr Asn Asp Asp Ser Ile Ser Pro Glu Glu Phe Ala Ser Ile Tyr Cys
225 230 235 240

Lys Asp Leu Asp Met Thr Ser Ala Thr Leu Gln Thr Gln Ile Ala Asn
245 250 255

Ile Ile Lys Glu Gln Leu Lys Asp Leu Glu Asn Ile Ala Ala Thr Glu
260 265 270

Ile Met Ser Asp Leu His Val Ile Ile Asn Leu Thr Cys Asn Leu Gln
275 280 285

Asp Arg Phe Phe Glu Asp Asn Phe Gln Trp Asn Leu Asn Asp Lys Ser
 290 295 300

Leu Thr Pro Glu Arg Phe Ala Thr Ser Ile Val Gln Asp Leu Gly Leu
 305 310 315 320

Thr Arg Glu Phe Ile Pro Leu Ile Ser Gln Ser Leu His Glu Thr Ile
 325 330 335

Asp Lys Ile Lys Lys Asp Trp Val Asp Gly His Leu Ile Gln Asp His
 340 345 350

Val Pro Asn Asp Ala Ala Phe Gly Tyr Leu Ser Gly Ile Arg Leu Asp
 355 360 365

Ile Asp Glu Leu Gly Ser Asn Trp Cys Pro Arg Val Gln Tle Leu Thr
 370 375 380

Lys Glu Glu Ile Glu Cys Arg Glu Ile Glu Lys Glu Arg Asn Leu Arg
 385 390 395 400

Arg Leu Lys Arg Glu Thr Asp Arg Leu Ser Arg Arg Gly Arg Arg Arg
 405 410 415

Leu Asp Asp Leu Glu Thr Thr Met Arg Met
 420 425

<210> 147

<211> 462

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(462)

<400> 147

atg ggt aag aaa aac act aaa ggt ggt aaa aaa ggt agu aga ggt aag 48

Met Gly Lys Lys Asn Thr Lys Gly Gly Lys Lys Gly Arg Arg Gly Lys

1 5 10 15

aac gac tct gac ggt cca aag cgt gaa ctt att tat aag gaa gaa ggc 96

Asn Asp Ser Asp Gly Pro Lys Arg Glu Leu Ile Tyr Lys Glu Glu Gly

20 25 30

caa gaa tat gaa caa atc acc aag atg ttg ggt aat gga aga gtc gaa 144

Gln Glu Tyr Ala Gln Ile Thr Lys Met Leu Gly Asn Gly Arg Val Glu

35 40 45

gcc agt tgc ttc gat ggt aac aag aga atg gcc cat att aga ggt aag 192

Ala Ser Cys Phe Asp Gly Asn Lys Arg Met Ala His Ile Arg Gly Lys

50 55 60

tta agu aag uua gtc tgg atg gga caa ggt gat att att ctt gtt tcc 240

Leu Arg Lys Lys Val Thr Met Gly Gln Gly Asp Ile Ile Leu Val Ser

65 70 75 80

tta aga gat ttc caa gat gac caa tgl gat gtt gtc cac aaa tat aat 288

Leu Arg Asp Phe Gln Asp Asp Glu Cys Asp Val Val His Lys Tyr Asn

85 90 95

tta gat gaa gcc aga aca ctg aaa aac caa ggt gaa ctt cct gaa aac 336

Leu Asp Glu Ala Arg Thr Leu Lys Asn Gln Gly Glu Leu Pro Glu Asn

100 105 110

gcc aac att aat gaa aca gac aac ttt ggt ttc gaa tct gat gaa gac 384

Ala Lys Ile Asn Glu Thr Asp Asn Phe Gly Phe Glu Ser Asp Glu Asp

115 120 125

gtt aac ttt gaa ttt ggt aac gct gat gaa gat gat gag gaa ggt gaa 432

Val Asn Phe Glu Phe Gly Asn Ala Asp Glu Asp Asp Glu Glu Gly Glu

130 135 140

gat gaa gaa ctt gnl att gat gac att taa 462
 Asp Glu Glu Asp Asp Ile Asp Asp Ile

145 150

<210> 140

<211> 153

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 148

Met Gly Lys Lys Asn Thr Lys Gly Gly Lys Lys Gly Arg Arg Gly Lys
 1 5 10 15

Asn Asp Ser Asp Gly Pro Lys Arg Glu Leu Ile Tyr Lys Glu Glu Gly
 20 25 30

Gln Glu Tyr Ala Gln Ile Thr Lys Met Leu Gly Asn Gly Arg Val Glu
 35 40 45

Ala Ser Cys Phe Asp Gly Asn Lys Arg Met Ala His Ile Arg Gly Lys
 50 55 60

Leu Arg Lys Lys Val Trp Met Gly Gln Gly Asp Ile Ile Leu Val Ser
 65 70 75 80

Leu Arg Asp Phe Gln Asp Asp Gln Cys Asp Val Val His Lys Tyr Asn
 85 90 95

Leu Asp Glu Ala Arg Thr Leu Lys Asn Gln Gly Glu Leu Pro Glu Asn
 100 105 110

Ala Lys Ile Asn Glu Thr Asp Asn Phe Gly Phe Glu Ser Asp Glu Asp

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115	120	125	
Val Asn Phe Glu Phe Gly Asn Ala Asp Glu Asp Asp Glu Glu Gly Glu			
130	135	140	
Asp Glu Glu Leu Asp Ile Asp Asp Ile			
145	150		
<210> 140			
<211> 406			
<212> DNA			
<213> Saccharomyces cerevisiae			
<220>			
<221> CDS			
<222> (1)..(486)			
<400> 149			
atg aia aaa gtc gat act tcc gat gca ttg ttg aag aat tgg tta aca	48		
Met Ile Lys Val Asp Thr Ser Asp Ala Leu Leu Lys Asn Ser Leu Thr			
1 5 10 15			
leu ata aag tgg aca tta aat atg ttg gat att tta ttc agt tgc gac	96		
Ser Ile Lys Trp Thr Leu Asn Met Leu Asp Ile Leu Phe Ser Cys Asp			
20 25 30			
att ttt tca tta atc aag gat tcc ata cgt tct ttg ata aca gaa aca	144		
Ile Phe Ser Leu Ile Lys Asp Ser Ile Arg Ser Leu Ile Thr Glu Thr			
35 40 45			
ttt tcc tgg gtg aat acc gtg agt aca tgg aag gta aag cct gta cga	192		
Phe Ser Ser Val Asn Thr Val Ser Thr Ser Thr Val Lys Pro Val Arg			
50 55 60			
tta ttg tgt tgc tta gtt tgt tcc aat agc aag tgg tgn aca ata tct	240		
Leu Leu Cys Cys Leu Val Cys Ser Asn Ser Lys Ser Cys Thr Ile Ser			
65 70 75 80			

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aac ata acc aga gat cct gaa tca gaa tgt gat aag ggg agc aga atc	288
Asn Ile Thr Arg Asp Pro Glu Ser Glu Cys Asp Lys Gly Ser Arg Ile	
85 90 95	

tta gag acg gat cct tct ttt tca aat ggg tat ata act tta aat agg	336
Leu Glu Thr Asp Pro Ser Phe Ser Asn Gly Tyr Ile Thr Leu Asn Arg	
100 105 110	

ttc ctg aaa tat tca tcc ttc atc att tgt ttc ctt tgt tta gta cta	384
Phe Leu Lys Tyr Ser Ser Phe Ile ttc Cys Phe Phe Cys Leu Val Leu	
115 120 125	

aca aac ttg atg aaa cat tca tgg caa aac ttt tcc ttt cta gac tca	432
Thr Asn Leu Met Lys His Ser Ser Glu Asn Phe Ser Phe Leu Asp Ser	
130 135 140	

act gtc gcc gga ttt ctg gca gat gca ggg cac ctc tgg cac tcc atc	480
Thr Val Ala Gly Phe Leu Ala Asp Ala Gly His Leu Trp His Ser Ile	
145 150 155 160	

act tga	486
Thr	

<210> 150
 <211> 161
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 150

Met Ile Lys Val Asp Thr Ser Asp Ala Leu Leu Lys Asn Ser Leu Thr
1 5 10 15

Ser Ile Lys Trp Thr Leu Asn Met Leu Asp Ile Leu Phe Ser Cys Asp
20 25 30

Ile Phe Ser Leu Ile Lys Asp Ser Ile Arg Ser Leu Ile Thr Glu Thr
35 40 45

Phe Ser Ser Val Asn Thr Val Ser Thr Ser Thr Val Lys Pro Val Arg
50 55 60

Leu Leu Cys Cys Leu Val Cys Ser Asn Ser Lys Ser Cys Thr Ile Ser
65 70 75 80

Asn Ile Thr Arg Asp Pro Glu Ser Glu Cys Asp Lys Gly Ser Arg Ile
85 90 95

Leu Glu Thr Asp Pro Ser Phe Ser Asn Gly Tyr Ile Thr Leu Asn Arg
100 105 110

Phe Leu Lys Tyr Ser Ser Phe Ile Ile Cys Phe Leu Cys Leu Val Leu
115 120 125

Thr Asn Leu Met Lys His Ser Ser Glu Asn Phe Ser Phe Leu Asp Ser
130 135 140

Thr Val Ala Gly Phe Leu Ala Asp Ala Gly His Leu Trp His Ser Ile
145 150 155 160

Thr

<210> 151

<211> 690

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(690)

<400> 151

atg act gtt tct act tcc aag acc uua aaa aag aal att aag tat acc 48

Met Thr Val Ser Thr Ser Lys Thr Pro Lys Lys Asn Ile Lys Tyr Thr

1 5 10 15

tta aca cat act tta caa aaa tgg aaa gaa act tta aag aaa att acc 96

Leu Thr His Thr Leu Gln Lys Trp Lys Glu Thr Leu Lys Lys Ile Thr

20 25 30

cac gaa aag ttg agt agt atc gat gac tct agl gga agc gat gaa aua 144

His Glu Thr Leu Ser Ser Ile Asp Asp Ser Ser Gly Ser Asp Glu Lys

35 40 45

ata gag gct ctg ttt act gtg tct cag cct gcc glc gta gcc tcc aag 192

Ile Glu Ala Leu Phe Thr Val Ser Gln Pro Ala Val Val Ala Ser Lys

50 55 60

ggc ata gac aga gal act ggt gct tct atg tgg cag gta gga gga ggt 240

Gly Ile Asp Arg Asp Ser Gly Ala Ser Met Ser Gln Val Gly Gly Gly

65 70 75 80

gtc aat agt aca ttg gag atg aag ctc aca gat gag agt gag gaa tct 288

Val Asn Ser Thr Asn Glu Met Lys Leu Thr Asp Glu Ser Glu Glu Ser

85 90 95

agg tct gct aat aac aag acc aca acc gcc tgg cat act cta tgg aat 336

Ser Ser Ala Asn Asn Thr Thr Thr Thr Ala Ser His Thr Leu Ser Asn

100 105 110

tcg aag aag tct acg cag aac ttt gaa aac tat aac gta gtg gag gaa 384

Ser Lys Lys Ser Thr Gln Asn Phe Glu Asn Tyr Asn Val Val Glu Glu

115 120 125

cgc ata aaa tta gca cag aaa agt aag gcc cgg ttt tgt aac gct gag 432

Arg Ile Lys Leu Ala Gln Lys Ser Lys Ala Pro Phe Cys Asn Ala Glu

130 135 140

aaa atc tgg aaa cga aga cga caa ctc tgg aca caa ccc act gag caa 480

Lys Ile Trp Lys Arg Arg Arg Gln Leu Trp Thr Gln Pro Thr Glu Gln

145 150 155 160

agt gaa agc gcc aac cat gac gga gtt act cga acg qaq att tlc caa 528
 Ser Glu Ser Ala Asn Asn Asp Gly Val Thr Arg Arg Glu Ile Phe Gln
 165 170 175

gct ata cct cag gaa tat tat gct cga gtt tac aag aaa ctg gtg gta 576
 Ala Ile Pro Gln Glu Tyr Tyr Ala Arg Val Tyr Lys Lys Leu Val Val
 180 185 190

gat gat aag cca tlg aga gag cct cta aat ctg gaa gat gct tta caa 624
 Asp Asp Lys Pro Leu Arg Glu Pro Leu Asn Leu Glu Asp Ala Leu Gln
 195 200 205

gtc ata aat gca ggc tgg aag gaa acg aga aag tgg gct aat gct gcc 672
 Val Ile Asn Ala Gly Trp Thr Glu Thr Arg Lys Trp Ala Asn Ala Ala
 210 215 220

aag gca lyc cat gac tga 690
 Lys Ala Cys His Asp
 225

<210> 152
 <211> 329
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 152

Met Thr Val Ser Thr Ser Lys Thr Pro Lys Lys Asn Ile Lys Tyr Thr
 1 5 10 15

Leu Thr His Thr Leu Glu Lys Trp Lys Glu Thr Leu Lys Lys Ile Thr
 20 25 30

His Glu Thr Leu Ser Ser Ile Asp Asp Ser Ser Gly Ser Asp Glu Lys
 35 40 45

Ile Glu Ala Leu Phe Thr Val Ser Gln Pro Ala Val Val Ala Ser Lys

50		55		60
Gly Ile Asp Arg Asp Ser Gly Ala Ser Met Ser Gln Val Gly Gly Gly				
65		70		75
				80
Val Asn Ser Thr Leu Gln Met Lys Leu Thr Asp Gln Ser Gln Gln Ser				
	85		90	
				95
Ser Ser Ala Asn Asn Thr Thr Thr Thr Ala Ser His Thr Leu Ser Asn				
	100		105	
				110
Ser Lys Lys Ser Thr Gln Asn Phe Gln Asn Tyr Asn Val Val Gln Gln				
	115		120	
				125
Arg Ile Lys Leu Ala Gln Lys Ser Lys Ala Pro Phe Cys Asn Ala Gln				
	130		135	
				140
Lys Ile Trp Lys Arg Arg Arg Gln Leu Trp Thr Gln Pro Thr Gln Gln				
	145		150	
				155
				160
Ser Gln Ser Ala Asn Asn Asp Gly Val Thr Arg Arg Gln Ile Phe Gln				
	165		170	
				175
Ala Ile Pro Gln Gln Tyr Tyr Ala Arg Val Tyr Lys Lys Leu Val Val				
	180		185	
				190
Asp Asp Lys Pro Leu Arg Gln Pro Leu Asn Leu Gln Asp Ala Leu Gln				
	195		200	
				205
Val Ile Asn Ala Gly Trp Thr Gln Thr Arg Lys Trp Ala Asn Ala Ala				
	210		215	
				220

Lys Ala Cys His Asp

225

<210> 153

<211> 654

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(654)

<400> 153

atg agt tcc cta tta ata tca tac gaa tct gac ttc aaa aga acc tta	48
Met Ser Ser Leu Leu Ile Ser Tyr Glu Ser Asp Phe Lys Thr Thr Leu	
1 5 10 15	

gaa caa gcc aac gag agc tta gca gag gcc ccc tca caa cag tta tca	96
Glu Gln Ala Lys Ala Ser Leu Ala Glu Ala Pro Ser Gln Pro Leu Ser	
20 25 30	

cag aga aat act aca ctg aag cac gta gaa cag caa caa gat gag ttg	144
Gln Arg Asn Thr Thr Leu Lys His Val Glu Gln Gln Gln Asp Glu Leu	
35 40 45	

ttt gac ctg cta gat cag atg gat gta gaa gtt aat aac agc ata ggc	192
Phe Asp Leu Leu Asp Gln Met Asp Val Glu Val Asn Asn Ser Ile Gly	
50 55 60	

gat gcc tca gaa cgt gat acg tac aag gag aag tta aga gaa tgg aag	240
Asp Ala Ser Glu Arg Ala Thr Tyr Lys Ala Lys Leu Arg Glu Trp Tyr	
65 70 75 80	

aag act ata cag agc gat atc aaa cga cca ctg caa tcc tta gta gac	288
Lys Thr Ile Gln Ser Asp Ile Lys Arg Pro Leu Gln Ser Leu Val Asp	
85 90 95	

tca gcc gat cgt gat aga ctt ttt gga gat ctt aac gca tct aat aat	336
Ser Gly Asp Arg Asp Arg Leu Phe Gly Asp Leu Asn Ala Ser Asn Ile	

	100	105	110	
	gac gal gac caa agg caa cag ttg ttg agc aac cat gca atc tta cag			384
	Asp Asp Asp Gln Arg Gln Gln Leu Leu Ser Asn His Ala Ile Leu Gln			
	115	120	125	
	aaa tgg gga gat aga cta aau gat gcc agt aga ata gca aat gaa aat			432
	Lys Ser Gly Asp Arg Ileu Lys Asp Ala Ser Arg Ile Ala Asn Glu Thr			
	130	135	140	
	gaa gga ata ggg tca caa ala atg atg gat tta agg tca cag aga gaa			480
	Glu Gly ile Gly Ser Gln ile Met Met Asp Leu Arg Ser Gln Arg Glu			
	145	150	155	160
	act tgg gaa aat gca aga cag acc ttg ttt caa gag gat tca tat gtc			528
	Thr Leu Glu Asn Ala Arg Gln Thr Leu Phe Gln Ala Asp Ser Tyr Val			
	165	170	175	
	gat aaa agt ata aag aca cta aaa acc atg act aga agg cta gtt gct			576
	Asp Lys Ser Ile Lys Thr Leu Lys Thr Met Thr Arg Arg Leu Val Ala			
	180	185	190	
	aat aaa ttc ata agc tat gcc att acc gca gtc ctt ata tta ttg att			624
	Asn Lys Phe Ile Ser Tyr Ala ile ile Ala Val Leu ile Leu Leu ile			
	195	200	205	
	ttg cta gtt tgg ttc tca aag ttt aaa taa			654
	Leu Leu Val Leu Phe Ser Lys Phe Lys			
	210	215		

<210> 154

<211> 217

<212> FET

<213> *Saccharomyces cerevisiae*

<400> 151

Met	Ser	Ser	Leu	Leu	Ile	Ser	Tyr	Glu	Ser	Asp	Phe	Lys	Thr	Thr	Leu
1			5					10					15		

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Glu Gln Ala Lys Ala Ser Leu Ala Gln Ala Pro Ser Gln Pro Leu Ser
20 25 30

Gln Arg Asn Thr Thr Leu Lys His Val Glu Gln Gln Gln Asp Glu Leu
35 40 45

Phe Asp Leu Leu Asp Gln Met Asp Val Glu Val Asn Asn Ser Ile Gly
50 55 60

Asp Ala Ser Glu Arg Ala Thr Tyr Lys Ala Lys Leu Arg Glu Trp Lys
65 70 75 80

Lys Thr Ile Gln Ser Asp Ile Lys Arg Pro Leu Gln Ser Leu Val Asp
85 90 95

Ser Gly Asp Arg Asp Arg Leu Phe Gly Asp Asn Asn Ala Ser Asn Ile
100 105 110

Asp Asp Asp Gln Arg Gln Glu Leu Leu Ser Asn His Ala Ile Leu Gln
115 120 125

Lys Ser Gly Asp Arg Leu Lys Asp Ala Ser Arg Ile Ala Asn Glu Thr
130 135 140

Glu Gly Ile Gly Ser Gln Ile Met Met Asp Leu Arg Ser Gln Arg Glu
145 150 155 160

Thr Leu Glu Asn Ala Arg Gln Thr Leu Phe Gln Ala Asp Ser Tyr Val
165 170 175

Asp Lys Ser Ile Lys Thr Leu Lys Thr Met Thr Arg Arg Leu Val Ala
180 185 190

Asn Lys Phe Ile Ser Tyr Ala Ile Ile Ala Val Leu Ile Leu Leu Ile
 195 200 205

Leu Leu Val Leu Phe Ser Lys Phe Lys
 210 215

<210> 155
 <211> 1863
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (3)..(1863)

<400> 155
 atc aca gac tcc aat cat cga tca tta acg tcc aac aag cct ata gta 43
 Met Arg Asp Ser Asn His Arg Ser Leu Thr Ser Asn Lys Pro Ile Val
 1 5 10 15

aca ata aca tct act gtc tat gac cga agc gca ttg gat atc acc tct 96
 Thr Ile Thr Ser Thr Val Tyr Asp Arg Arg Ala Leu Asp Ile Asn Ser
 20 25 30

agt att ccc tca ata aac tcc cta aac tac tta aca tal cta acc tct 144
 Ser Ile Pro Leu Ile Asn Ser Leu Asn Tyr Leu Thr Tyr Leu Thr Ser
 35 40 45

aat tca tca aaa gtt agg gan acg gta gct aac gac ggc gct cta gaa 192
 Asn Ser Ser Lys Val Arg Glu Thr Val Ala Asn Asp Gly Ala Leu Glu
 50 55 60

aga tta gtc tca ata ttg agc agc lgt cat tta agt ttg ttt gag ttg 240
 Arg Leu Val Ser Ile Leu Arg Ser Cys His Leu Ser Leu Phe Glu Leu
 65 70 75 80

ctg gat ttg gat tta gaa aat ttt aat gag cac gaa acc ata aag gat 288

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Leu Asp Leu Asp Leu Glu Asn Phe Asn Glu His Glu Asn Ile Lys Asp	
85 90 95	
cta tgg aag gag aaa cga cta gca cta tgc gct tgg aaa tgg act tta	336
Leu Trp Lys Glu Lys Arg Leu Ala Leu Cys Ala Trp Lys Trp Thr Leu	
100 105 110	
aca ttt cag tgc tta gta ttg aca ggt act aga ggg aca gaa caa att	384
Thr Phe Gln Cys Leu Val Leu Thr Gly Thr Arg Gly Thr Glu Glu Ile	
115 120 125	
cgt aaa aca gtg gta aag tat ggg gtc cta tct gtc ctg gtc aca gta	432
Arg Lys Lys Val Val Met Ser Gly Val Leu Ser Val Leu Val Thr Val	
130 135 140	
ttg gat aac tat tta cta tat tat aaa aat tac gac ttc atc aaa gat	480
Leu Asp Asn Tyr Leu Leu Tyr His Lys Asn Tyr Asp Phe Ile Lys Asp	
145 150 155 160	
caa aca atg acc ttt gac ttc aaa ggg ata aca aag gag aca atg tat	528
Gln Thr Met Thr Phe Asp Phe Lys Gly Ile Thr Thr Glu Thr Met Tyr	
165 170 175	
aaa ttc atg aga aaa gat gag aat gaa aca tat cag cag tat ata gag	576
Lys Phe Met Arg Lys Asp Glu Asn Cln Thr Tyr Cln Cln Tyr Ile Glu	
180 185 190	
ttc att aca ggt cag gat aaa ttg aag ttg tca act gac aaa aat ttt	624
Phe Ile Thr Gly Glu Asp Lys Leu Lys Leu Ser Thr Asp Lys Asn Phe	
195 200 205	
cta aac gaa cga tta gtg gca cag tct atg aca att cca act gat ttt	672
Leu Asn Glu Arg Leu Val Ala Pro Ser Met Thr Ile Pro Thr Asp Phe	
210 215 220	
agt gat ata tgg ggc cag ttt gaa gac cta gct agc aat ttt gaa cct	720
Ser Asp Ile Trp Gly Arg Phe Ala Asp Leu Ala Ser Asn Phe Glu Pro	
225 230 235 240	
gac cag gaa aga cac gac gaa gac att gat att gat agt gaa gta gaa	768
Asp Gln Glu Arg His Asp Asp Asp Ile Asp Ile Asp Ser Glu Val Glu	
245 250 255	

agt gaa aat ttt gat gca cat aag aat ttc ttt tgg caa cca gac att	816
Ser (40) Asn Phe Asp Ala His Lys Asn Phe Phe Ser Gln Pro Asp Ile	
260 265 270	
aat aga cct aca att tcc aat cca cgt gaa ttt ttt ctc gga aga att	864
Asn Arg Pro Thr Ile Ser Thr Pro Arg Glu Phe Phe Leu Gly Arg Ile	
275 280 285	
gtc ccc aaa caa gac gac gtt ata tgg tgg ctt cag tta tta gct ttt	912
Val Pro Lys Gln Asp Asp Val Ile Trp Ser Leu Gln Leu Leu Ala Phe	
290 295 300	
glt tgg aag tat aca tat atg aca tca acc ctt caa aat gtt gag ctg	960
Val Ser Lys Tyr Thr Tyr Met Lys Ser Thr Leu Gln Asn Val Glu Leu	
305 310 315 320	
gtt gaa tcc cta tgg ttc aga agt atg gct tac aaa att aaa cag aga	1008
Val Glu Ser Leu Ser Phe Arg Ser Met Ala Tyr Lys Ile Lys Gln Arg	
325 330 335	
atc tca gaa gag aat gac tca gaa gaa caa gaa aga gac gta act gta	1056
Ile Ser Glu Glu Asn Asp Leu Glu Glu Gln Glu Arg Asp Val Thr Val	
340 345 350	
aaa ttg tct tca tta tat cct tat tta tgg aaa aat cct gaa aac aat	1104
Lys Leu Ser Ser Leu Tyr Pro Tyr Leu Ser Lys Asn Pro Glu Asn Asn	
355 360 365	
tcc aaa gtt aag gcc cta gat act agc aaa atg gat cca ttt ttc aaa	1152
Ser Lys Val Lys Ala Leu Asp Thr Ser Lys Met Asp Pro Phe Phe Lys	
370 375 380	
gaa tta gaa gaa ctc tca aac aga tgt caa caa gaa gaa caa aat gaa	1200
Glu Leu Glu Glu Leu Ser Asn Arg Cys Gln Gln Glu Glu Gln Asn Glu	
385 390 395 400	
ata tgt aat aac cac tgc ccc gtt ctt aat ttg ttt gag cgc tac cgt	1248
Ile Cys Asn Asn His Cys Pro Val Leu Asn Leu Phe Glu Arg Tyr Arg	
405 410 415	
gta cgg aca cct agc gac gac aat gcc tat ggc aac gac aag gaa aga	1296

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Val Pro Lys Pro Ser Asp Asp Asn Ala Tyr Gly Lys Asp Lys Glu Arg	
420 425 430	
att aat tta agg aag caa ata cct gat aac ttt gaa agg cgc tgg agc	1344
Ile Asn Leu Arg Lys Lys Ile Ser Asp Asn Phe Glu Arg Arg Trp Ser	
435 440 445	
tac gat aaa atg aaa aag gaa tta aca aat att gtt tac aaa aac aag	1392
Tyr Asp Lys Met Lys Lys Glu Leu Thr Asn Ile Val Tyr Lys Asn Lys	
450 455 460	
gta cta aca aat gtt gta aac atc ttc ccc tta gtc gaa aaa tat aca	1440
Val Leu Thr Asn Val Val Asn Ile Phe Pro Leu Val Glu Lys Tyr Thr	
465 470 475 480	
gtg agc gca gaa aat aca cat gat gtt ata tat tgg agt tct gtc atc	1488
Val Ser Ala Glu Asn Thr His Asp Val Ile Tyr Trp Ser Ser Val Ile	
485 490 495	
atg aga aat tca tgt cga aaa aat gag atc tta ggt gtg cgt cag tgt	1536
Met Arg Asn Ser Cys Arg Lys Asn Glu Ile Leu Gly Val Arg Gln Cys	
500 505 510	
gcc aat ttt tgg tgc gga aaa tgg gaa gat ttt ccc agc caa ttt gca	1584
Ala Asn Phe Ser Cys Gly Lys Trp Glu Asp Phe Pro Arg Gln Phe Ala	
515 520 525	
aaa tgt cgt cga tgc aaa aga acg aaa tat tgc tca cga aag tgt caa	1632
Lys Cys Arg Arg Cys Lys Arg Thr Lys Tyr Cys Ser Arg Lys Cys Gln	
530 535 540	
tta aaa gca tgg gga tat cat agg tat tgg tgc cac gaa gtt gga tca	1680
Leu Lys Ala Trp Gly Tyr His Arg Tyr Trp Cys His Glu Val Gly Ser	
545 550 555 560	
agt cat atg aga tcc acg aat act acc aca ggt gtc aat acc cca aat	1728
Ser His Met Arg Ser Thr Asn Thr Thr Thr Gly Val Asn Thr Pro Asn	
565 570 575	
gag cct agt tct tta aat gcc acc gct act aca gca gct gat gtt tgg	1776
Glu Pro Ser Ser Leu Asn Ala Thr Ala Thr Thr Ala Ala Asp Val Ser	
580 585 590	

aat tct acc agt aug ttc act cct aat ata tcc acc acc gta cct gat 1824
 Asn Ser Thr Ser Thr Phe Thr Pro Asn Ile Ser Thr Thr Val Pro Asp
 595 600 605

gaa ata agc aat agg gat gaa act agc ata cct gag taa 1863
 Glu Ile Ser Asn Arg Asp Glu Asn Ser Ile Pro Glu
 610 615 620

<210> 156
 <211> 620
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 156

Met Arg Asp Ser Asn His Arg Ser Leu Thr Ser Asn Lys Pro Ile Val
 1 5 10 15

Thr Ile Thr Ser Thr Val Tyr Asp Arg Arg Ala Leu Asp Ile Asn Ser
 20 25 30

Ser Ile Pro Leu Ile Asn Ser Leu Asn Tyr Leu Thr Tyr Leu Thr Ser
 35 40 45

Asn Ser Ser Lys Val Arg Glu Thr Val Ala Asn Asp Gly Ala Leu Glu
 50 55 60

Arg Leu Val Ser Ile Leu Arg Ser Cys His Leu Ser Leu Phe Glu Leu
 65 70 75 80

Leu Asp Leu Asp Leu Glu Asn Phe Asn Glu His Glu Asn Ile Lys Asp
 85 90 95

Leu Trp Lys Glu Lys Arg Leu Ala Leu Cys Ala Trp Lys Trp Thr Leu

100	105	110
Thr Phe Gln Cys Leu Val Leu Thr Gly Thr Arg Gly Thr Glu Gln Ile		
115	120	125
Arg Lys Lys Val Val Met Ser Gly Val Leu Ser Val Leu Val Thr Val		
130	135	140
Leu Asp Asn Tyr Leu Leu Tyr His Lys Asn Tyr Asp Phe Ile Lys Asp		
145	150	155
Gln Thr Met Thr Phe Asp Phe Lys Gly Ile Thr Thr Glu Thr Met Tyr		
165	170	175
Lys Phe Met Arg Lys Asp Glu Asn Gln Thr Tyr Gln Gln Tyr Ile Glu		
180	185	190
Phe Ile Thr Gly Gln Asp Lys Leu Lys Leu Ser Thr Asp Lys Asn Phe		
195	200	205
Leu Asn Glu Arg Leu Val Ala Pro Ser Met Thr Ile Pro Thr Asp Phe		
210	215	220
Ser Asp Ile Tyr Gly Arg Phe Ala Asp Leu Ala Ser Asn Phe Glu Pro		
225	230	235
Asp Gln Glu Arg His Asp Asp Asp Ile Asp Ile Asp Ser Glu Val Glu		
245	250	255
Ser Glu Asn Phe Asp Ala His Lys Asn Phe Phe Ser Gln Pro Asp Ile		
260	265	270

Asn Arg Pro Thr Ile Ser Thr Pro Arg Glu Phe Phe Leu Gly Arg Ile
275 280 285

Val Pro Lys Gln Asp Asp Val Ile Trp Ser Leu Gln Leu Leu Ala Phe
290 295 300

Val Ser Lys Tyr Thr Tyr Met Lys Ser Thr Leu Gln Asn Val Glu Leu
305 310 315 320

Val Glu Ser Leu Ser Phe Arg Ser Met Ala Tyr Lys Ile Lys Gln Arg
325 330 335

Ile Ser Glu Gln Asn Asp Leu Glu Glu Gln Glu Arg Asp Val Thr Val
340 345 350

Lys Leu Ser Ser Leu Tyr Pro Tyr Leu Ser Lys Asn Pro Glu Asn Asn
355 360 365

Ser Lys Val Lys Ala Leu Asp Thr Ser Lys Met Asp Pro Phe Phe Lys
370 375 380

Glu Leu Glu Gln Leu Ser Asn Arg Cys Gln Gln Glu Glu Gln Asn Glu
385 390 395 400

Ile Cys Asn Asn His Cys Pro Val Leu Asn Leu Phe Glu Arg Tyr Arg
405 410 415

Val Pro Lys Pro Ser Asp Asp Asn Ala Tyr Gly Lys Asp Lys Glu Arg
420 425 430

Ile Asn Leu Arg Lys Lys Ile Ser Asp Asn Phe Glu Arg Arg Trp Ser

435	440	445
Tyr Asp Pys Met Lys Lys Glu Leu Thr Asn Ile Val Tyr Lys Asn Lys		
450	455	460
Val Leu Thr Asn Val Val Asn Ile Phe Pro Leu Val Glu Lys Tyr Thr		
465	470	475 480
Val Ser Ala Glu Asn Thr His Asp Val Ile Tyr Trp Ser Ser Val Ile		
485	490	495
Met Arg Asn Ser Cys Arg Lys Asn Glu Ile Leu Gly Val Arg Gln Cys		
500	505	510
Ala Asn Phe Ser Cys Gly Lys Trp Glu Asp Phe Pro Arg Gln Phe Ala		
515	520	525
Lys Cys Arg Arg Cys Lys Arg Thr Lys Tyr Cys Ser Arg Lys Cys Gln		
530	535	540
Leu Lys Ala Trp Gly Tyr His Arg Tyr Trp Cys His Glu Val Gly Ser		
545	550	555 560
Ser His Met Arg Ser Thr Asn Thr Thr Thr Gly Val Asn Thr Pro Asn		
565	570	575
Glu Pro Ser Ser Leu Asn Ala Thr Ala Thr Thr Ala Ala Asp Val Ser		
580	585	590
Asn Ser Thr Ser Thr Phe Thr Pro Asn Ile Ser Thr Thr Val Pro Asp		
595	600	605

Glu Ile Ser Asn Arg Asp Glu Asn Ser Ile Pro Glu
 610 615 620

<210> 157
 <211> 1350
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1350)

<400> 157
 atg cgt cta aaa gaa ttg tta cct nat ttt ttg att gtt cat caa gag 48
 Met Arg Leu Lys Glu Leu Leu Pro Asn Phe Leu Ile Val His Gln Glu
 1 5 10 15
 gtc cct gag gat cct aat gaa ttc aag tcc acc gat aaa aga gag nat 96
 Val Pro Glu Asp Pro Ile Ala Phe Lys Ser Thr Asp Lys Arg Glu Asn
 20 25 30
 gaa aat aaa gag atc acc atc cct gag cta ata gat acc aaa gtt cct 144
 Glu Asn Lys Glu Ile Thr Ile Pro Glu Leu Ile Asp Thr Lys Val Pro
 35 40 45
 gaa tta gct gaa ggt gct act gac act tta tat ggt tta cag gtc aat 192
 Glu Leu Ala Asp Gly Ala Thr Asp Thr Leu Tyr Gly Leu Leu Val Asn
 50 55 60
 ggc cat tta caa act gca tat ggt tcc ttt aga caa ttt gac aat ata 240
 Gly His Leu Gln Thr Ala Tyr Gly Ser Phe Arg His Phe Asp Asn Ile
 65 70 75 80
 tac aaa gtt caa tat aaa aga atg ata atc aaa tac cca cat ggg gga 288
 Tyr Lys Val Gln Tyr Lys Arg Met Ile Ile Lys Tyr Pro His Gly Gly
 85 90 95
 gaa ggg act gtc gat ttt gct gta aat ggt aga agt acc aaa aga aga 336
 Glu Gly Thr Val Asp Phe Ala Val Asn Gly Arg Ser Thr Lys Arg Arg

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100	105	110	
aaa gtg gaa aaa gaa tac gtg cgg aca agt caa cgg gta ttt aac gga			304
Lys Val Glu Lys Glu Tyr Val Pro Thr Ser Gln Pro Val Phe Asn Gly			
115	120	125	
aac ttg aaa cga aga tat cgg tac tat tcc cct gat gat cct aac ttg			432
Asn Leu Lys Arg Arg Tyr Ser Tyr Tyr Ser Pro Asp Asp Pro Lys Leu			
130	135	140	
aac tca gac gat gct aag cct atg ctt att att ctc cat gga tta aca			460
Asn Ser Asp Asp Ala Lys Pro Met Leu Ile Ile Leu His Gly Leu Thr			
145	150	155	160
ggg ggt tgg agg gaa agc tac gtg agg gca ala gll cat gaa atc aac			528
Gly Gly Ser Arg Glu Ser Tyr Val Arg Ala Thr Val His Glu Ile Thr			
165	170	175	
acg aag tac gac ttt gaa gca tgc gtg ttt aat gct aga gga tgt tgt			576
Thr Lys Tyr Asp Phe Glu Ala Cys Val Phe Asn Ala Arg Gly Cys Cys			
180	185	190	
tat tct gca att aca acg cgg cca tta tac aac ggt ggt tgg aac aat			624
Tyr Ser Ala Ile Thr Thr Pro Leu Leu Tyr Asn Gly Gly Trp Thr Asn			
195	200	205	
gat aca aga tal cgl gtt aat gac ttg agg aca aga ttt cgg aat aga			672
Asp Ile Arg Tyr Cys Val Asn Asp Leu Arg Lys Arg Phe Pro Asn Arg			
210	215	220	
aag ttt tat atg atg gga ttt tgg tta ggc gca tcc ata atg aca aat			720
Lys Phe Tyr Met Met Gly Phe Ser Leu Gly Ala Ser Ile Met Thr Asn			
225	230	235	240
tac ttg gga gaa gag tca gat cgt act aca aac gaa tgt gct att tcc			768
Tyr Leu Gly Glu Glu Ser Asp Arg Thr Lys Ile Glu Cys Ala Ile Ser			
245	250	255	
gtg agt aat cca ttt gac atg tac aac tct gca tat ttt att aac agt			816
Val Ser Asn Pro Phe Asp Leu Tyr Asn Ser Ala Tyr Phe Ile Asn Ser			
260	265	270	

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aca cca atg ggg tca cga ttt tat tca cct gct ttg ggt cac aac tta	864
Thr Pro Met Gly Ser Arg Phe Tyr Ser Pro Ala Leu Gly His Asn Leu	
275 280 285	
cta cga atg gtt cga aac cat ctc tct act ctg gaa gaa aac cct gac	912
Leu Arg Met Val Arg Asn His Leu Ser Thr Leu Glu Glu Asn Pro Asp	
290 295 300	
ttc aaa gat gtt atc gag aag cat tta aac aag att cgc act gtg agg	960
Phe Lys Asp Val Ile Glu Lys His Leu Lys Lys Ile Arg Thr Val Arg	
305 310 315 320	
caa ttt gat aac ttg ttg aca ggc cca atg tth gga tat aac aac gca	1008
Gln Phe Asp Asn Leu Leu Thr Gly Pro Met Phe Gly Tyr Lys Asn Ala	
325 330 335	
gag gag tac taa aag aat gct tca tca tat aac aga ata ccc ggg atc	1056
Glu Glu Tyr Tyr Lys Phe Ala Ser Ser Tyr Lys Arg Ile Pro Gly Ile	
340 345 350	
aga act cct ttt ata gct ttg cat gct cag gat gac cca att gtc gga	1104
Arg Thr Pro Phe Ile Ala Leu His Ala Gln Asp Asp Pro Ile Val Tyr	
355 360 365	
ggc gat ctt cct ata gac caa ata aac tcc aat ccc taa act ttg ctt	1152
Gly Asp Leu Pro Ile Asp Gln Ile Lys Ser Asn Pro Tyr Thr Leu Leu	
370 375 380	
cta gaa act tcc acg ggc ggc cat gtt gga tgg ttc aac gac aga tcc	1200
Leu Glu Thr Ser Thr Gly Gly His Val Gly Trp Phe Lys Asp Arg Ser	
385 390 395 400	
ggc aga agg tgg tac gca gaa ccc tca tgc aga ttt ttg aaa ata ttt	1248
Gly Arg Arg Trp Tyr Ala Glu Pro Leu Cys Arg Phe Leu Lys Ile Phe	
405 410 415	
cac gac gaa att act gla aag ggc tta aaa cct gac ttg gaa aat gtt	1296
His Asp Glu Ile Thr Val Lys Gly Leu Lys Pro Asp Leu Glu Asn Val	
420 425 430	
caa ctc cca gat cct aat tgc gaa ccc ata gcc aca acc ttt cgc gag	1344
Gln Leu Pro Asp Pro Asn Cys Glu Pro Ile Ala Thr Thr Phe Arg Ala	

435 440 445 1350

ast tag
Asn

<210> 158
<211> 449
<212> PRT
<213> *Saccharomyces cerevisiae*

<400> 158

Met Arg Leu Lys Glu Leu Leu Pro Asn Phe Leu Ile Val His Gln Glu
1 5 10 15

Val Pro Gln Asp Pro Ile Ala Phe Lys Ser Thr Asp Lys Arg Gln Asn
20 25 30

Glu Asn Lys Glu Ile Thr Ile Pro Gln Leu Ile Asp Thr Lys Val Pro
35 40 45

Glu Leu Ala Asp Gly Ala Thr Asp Thr Leu Tyr Gly Leu Leu Val Asn
50 55 60

Gly His Leu Gln Thr Ala Tyr Gly Ser Phe Arg His Phe Asp Asn Ile
65 70 75 80

Tyr Lys Val Gln Tyr Lys Arg Met Ile Ile Lys Tyr Pro His Gly Gly
85 90 95

Glu Gly Thr Val Asp Phe Ala Val Asn Gly Arg Ser Thr Lys Arg Arg
100 105 110

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Tyr Val Glu Lys Glu Tyr Val Pro Thr Ser Gln Pro Val Phe Asn Gly
115 120 125

Asn Leu Lys Arg Arg Tyr Ser Tyr Tyr Ser Pro Asp Asp Pro Lys Leu
130 135 140

Asn Ser Asp Asp Ala Lys Pro Met Leu Ile Ile Leu His Gly Leu Thr
145 150 155 160

Gly Gly Ser Arg Glu Ser Tyr Val Arg Ala Ile Val His Glu Ile Thr
165 170 175

Thr Lys Tyr Asp Phe Glu Ala Cys Val Phe Asn Ala Arg Gly Cys Cys
180 185 190

Tyr Ser Ala Ile Thr Thr Pro Leu Leu Tyr Asn Gly Gly Trp Thr Asn
195 200 205

Asp Ile Arg Tyr Cys Val Asn Asp Leu Arg Lys Arg Phe Pro Asn Arg
210 215 220

Lys Phe Tyr Met Met Gly Phe Ser Leu Gly Ala Ser Ile Met Thr Asn
225 230 235 240

Tyr Leu Gly Glu Glu Ser Asp Arg Thr Lys Ile Glu Cys Ala Ile Ser
245 250 255

Val Ser Asn Pro Phe Asp Leu Tyr Asn Ser Ala Tyr Phe Ile Asn Ser
260 265 270

Thr Pro Met Gly Ser Arg Phe Tyr Ser Pro Ala Leu Gly His Asn Leu
275 280 285

Leu Arg Met Val Arg Asn His Leu Ser Thr Leu Glu Glu Asn Pro Asp
290 295 300

Phe Lys Asp Val Ile Glu Lys His Leu Lys Lys Ile Arg Thr Val Arg
305 310 315 320

Gln Phe Asp Asn Leu Leu Thr Gly Pro Met Phe Gly Tyr Lys Asn Ala
325 330 335

Glu Glu Tyr Tyr Lys Asn Ala Ser Ser Tyr Lys Arg Ile Pro Gly Ile
340 345 350

Arg Thr Pro Phe Ile Ala Leu His Ala Gln Asp Asp Pro Ile Val Gly
355 360 365

Gly Asp Leu Pro Ile Asp Gln Ile Lys Ser Asn Pro Tyr Thr Leu Leu
370 375 380

Leu Glu Thr Ser Thr Gly Gly His Val Gly Trp Phe Lys Asp Arg Ser
385 390 395 400

Gly Arg Arg Trp Tyr Ala Glu Pro Leu Cys Arg Phe Leu Lys Ile Phe
405 410 415

His Asp Glu Ile Thr Val Lys Gly Leu Lys Pro Asp Leu Glu Asn Val
420 425 430

Gln Leu Pro Asp Pro Asn Cys Glu Pro Ile Ala Thr Thr Phe Arg Ala
435 440 445

Gen

<210> 150

<211> 1000

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1083)

<400> 150

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Met	Ser	Tyr	Pro	Glu	Lys	Phe	Glu	Gly	Ile	Ala	Ile	Gln	Ser	His	Glu	
1				5					10				15			

gat	tgg	aaa	aac	cca	aag	aag	aca	aag	tat	gac	cca	aaa	cca	ttt	tac	36
Asp	Trp	Lys	Asn	Pro	Lys	Lys	Thr	Lys	Tyr	Asp	Pro	Lys	Pro	Phe	Tyr	
			20					25					30			

gat	cat	gac	att	gac	att	aag	atc	gaa	cca	tgt	ggc	gtc	tgc	ggt	agt	144
Asp	His	Asp	Ile	Asp	Ile	Lys	Ile	Glu	Ala	Cys	Gly	Val	Cys	Gly	Ser	
			35				40					45				

gat	atc	cat	tgt	cca	gct	ggc	cat	tgg	ggc	aat	atg	aag	atg	cag	cta	132
Asp	Ile	His	Cys	Ala	Ala	Gly	His	Trp	Gly	Asn	Met	Lys	Met	Pro	Leu	
			50				55					60				

gtc	gta	ggt	cat	gaa	atc	ggt	ggc	aaa	gtt	gtc	aag	cta	ggg	ccc	aag	240
Val	Val	Gly	His	Glu	Ile	Val	Gly	Lys	Val	Val	Lys	Leu	Gly	Pro	Lys	
			65			70				75				80		

tca	aac	agt	ggg	ttg	aaa	gtc	cgt	caa	cgt	gtt	ggc	gta	ggt	gct	caa	288
Ser	Asn	Ser	Gly	Leu	Lys	Val	Gly	Gln	Arg	Val	Gly	Val	Gly	Ala	Gln	
			85					90					95			

gtc	ttt	tca	tgc	ttg	gaa	tgt	gac	cgt	tgt	aag	aat	gat	aat	gaa	cca	336
Val	Phe	Ser	Cys	Leu	Glu	Cys	Asp	Arg	Cys	Lys	Asn	Asp	Asn	Glu	Pro	
				100				105					110			

cac tgc acc aag ttt gtt acc aca lac agt cac cct tat gaa gac ggc	384
Tyr Cys Thr Lys Phe Val Thr Thr Tyr Ser Gln Pro Tyr Glu Asp Gly	
115 120 125	
tat gtg tgc caa ggt ggc tat gca aac tac gtc aga gtt cat gaa cat	432
Tyr Val Ser Gln Gly Gly Tyr Ala Asn Tyr Val Arg Val His Glu His	
130 135 140	
ttt gtg gtg cct atc cca gag aat att cca tca cat ttg gct gct cca	480
Phe Val Val Phe Ile Pro Glu Asn Ile Pro Ser His Leu Ala Ala Pro	
145 150 155 160	
cta tta cgt ggt ggt ttg act gtg tac tct cca ttg gtt cgt aac ggt	528
Leu Leu Cys Gly Gly Leu Thr Val Tyr Ser Pro Leu Val Arg Asn Gly	
165 170 175	
tgc ggt cca ggt aca aaa gtt ggt ata gtt ggt ctt ggt ggt atc ggc	576
Cys Gly Pro Gly Tyr Lys Val Gly Ile Val Gly Leu Gly Gly Ile Gly	
180 185 190	
cgt atg ggt aca ttg att tcc aaa gcc atg ggg gca gag acg cat gtc	624
Ser Met Gly Thr Asn Ile Ser Lys Ala Met Gly Ala Glu Thr Tyr Val	
195 200 205	
att tct cgt tct tgc aga aca aga gaa gat gca atg aag atg ggc gcc	672
Ile Ser Arg Ser Ser Arg Lys Arg Glu Asp Ala Met Lys Met Gly Ala	
210 215 220	
gat cac tac att gct aca tta gaa gaa ggt gat tgg ggt gaa aag tac	720
Asp His Tyr Ile Ala Thr Leu Glu Glu Gly Asp Trp Gly Glu Lys Tyr	
225 230 235 240	
ttt gac acc ttc gac ctg att gta gtc tgc gct tcc tcc ctt acc gac	768
Phe Asp Thr Phe Asp Leu Ile Val Val Cys Ala Ser Ser Leu Thr Asp	
245 250 255	
att gac ttc aac aat atg aca aag gct atg aag gtt ggt ggt aga att	816
Ile Asp Phe Asn Ile Met Pro Cys Ala Met Lys Val Gly Gly Arg Ile	
260 265 270	
gtc tca atc tct ata cca gaa caa cac gaa atg ttc tgc cta aag cca	864

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Val Ser Ile Ser Ile Pro Glu Gln His Glu Met Leu Ser Leu Lys Pro
 275 280 285
 tat ggc tta aag gct gtc tcc att tct tac agt gct tta ggt tcc aic 912
 Tyr Gly Leu Lys Ala Val Ser Ile Ser Tyr Ser Ala Leu Gly Ser Ile
 290 295 300
 asu gaa ttg uac caa ctc ttg aac tta gtc tct gaa aac gat aac aac 960
 Lys Glu Leu Asn Gln Leu Leu Lys Leu Val Ser Glu Lys Asp Ile Lys
 305 310 315 320
 att tgg gtg gaa aca tta cct gtt ggt gaa gcc ggc gtc cat gaa gcc 1008
 Ile Trp Val Glu Thr Leu Pro Val Gly Glu Ala Gly Val His Glu Ala
 325 330 335
 ttc gaa agg atg gaa aag ggt gac gtt aga tat aga ttt acc tta gtc 1056
 Phe Glu Arg Met Glu Lys Gly Asp Val Arg Tyr Arg Phe Thr Leu Val
 340 345 350
 ggc tac gac aac gaa ttt tca gac tag 1082
 Gly Tyr Asp Lys Glu Phe Ser Asp
 355 360

<210> 160
 <211> 360
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 160

Met Ser Tyr Pro Glu Lys Phe Glu Gly Ile Ala Ile Gln Ser His Glu
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Asp Trp Lys Asn Pro Lys Lys Thr Lys Tyr Asp Pro Lys Pro Phe Tyr
 20 25 30

Asp His Asp Ile Asp Ile Lys Ile Glu Ala Cys Gly Val Cys Gly Ser
 35 40 45

Asp Ile His Cys Ala Ala Gly His Trp Gly Asn Met Lys Met Pro Leu
50 55 60

Val Val Gly His Glu Ile Val Gly Lys Val Val Lys Leu Gly Pro Lys
65 70 75 80

Ser Asn Ser Gly Leu Lys Val Gly Gln Arg Val Gly Val Gly Ala Gln
85 90 95

Val Phe Ser Cys Leu Glu Cys Asp Arg Cys Lys Asn Asp Asn Glu Pro
100 105 110

Tyr Cys Thr Lys Phe Val Thr Thr Tyr Ser Gln Pro Tyr Glu Asp Gly
115 120 125

Tyr Val Ser Gln Gly Gly Tyr Ala Asn Tyr Val Arg Val His Glu His
130 135 140

Phe Val Val Pro Ile Pro Glu Asn Ile Pro Ser His Leu Ala Ala Pro
145 150 155 160

Leu Leu Cys Gly Gly Leu Thr Val Tyr Ser Pro Leu Val Arg Asn Gly
165 170 175

Cys Gly Pro Gly Lys Lys Val Gly Ile Val Gly Leu Gly Gly Ile Gly
180 185 190

Ser Met Gly Thr Leu Ile Ser Lys Ala Met Gly Ala Gln Thr Tyr Val
195 200 205

Ile Ser Arg Ser Ser Arg Lys Arg Glu Asp Ala Met Lys Met Cys Ala

210 215 220
Asp His Tyr Ile Ala Thr Leu Glu Gln Gly Asp Trp Gly Glu Lys Tyr
225 230 235 240
Phe Asp Thr Phe Asp Leu Ile Val Val Cys Ala Ser Ser Leu Thr Asp
245 250 255
Ile Asp Phe Asn Ile Met Pro Lys Ala Met Lys Val Gly Gly Arg Ile
260 265 270
Val Ser Ile Ser Ile Pro Glu Gln His Glu Met Leu Ser Leu Lys Pro
275 280 285
Tyr Gly Leu Lys Ala Val Ser Ile Ser Tyr Ser Ala Leu Gly Ser Ile
290 295 300
Lys Glu Leu Asn Gln Leu Leu Lys Leu Val Ser Glu Lys Asp Ile Lys
305 310 315 320
Ile Trp Val Gln Thr Leu Pro Val Gly Glu Ala Gly Val His Glu Ala
325 330 335
Phe Glu Arg Met Glu Lys Gly Asp Val Arg Tyr Arg Phe Thr Leu Val
340 345 350
Gly Tyr Asp Lys Glu Phe Ser Asp
355 360

<210> 161

<211> 858

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(858)

<401> 161

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Met	Arg	Ser	Ser	Val	Tyr	Ser	Glu	Asn	Thr	Tyr	Asn	Cys	Ile	Arg	Thr	
1			5						10					15		

tgg	aag	gag	cac	cta	aca	gaa	aga	agg	agg	gac	gac	atg	gag	cca	atg	96
Ser	Tyr	Glu	His	Leu	Thr	Glu	Arg	Arg	Arg	Val	Ala	Met	Ala	Pro	Met	
			20					25				30				

ttc	caa	cat	ttc	tta	aac	tta	tgc	gtg	gac	aaa	ttt	cct	gaa	ttc	atc	144
Phe	Gln	His	Phe	Leu	Asn	Leu	Cys	Val	Glu	Lys	Phe	Pro	Glu	Ser	Ile	
		35				40					45					

gag	cac	aag	gat	aca	gat	gga	aac	ggc	aac	tgc	acc	acc	gct	att	tta	192
Glu	His	Lys	Asp	Thr	Asp	Gly	Asn	Gly	Asn	Phe	Thr	Thr	Ala	Ile	Leu	
	50					55				60						

gac	agg	gag	att	atc	tac	atc	ccc	gaa	gat	gac	act	gac	agt	att	gac	240
Glu	Arg	Glu	Ile	Ile	Tyr	Ile	Pro	Glu	Asp	Asp	Thr	Asp	Ser	Ile	Asp	
65				70					75					80		

agg	gth	gac	agg	ctc	aag	tgt	ata	aac	tac	aag	ctg	cac	aaa	tct	cgc	288
Ser	Val	Asp	Ser	Leu	Lys	Cys	Ile	Asn	Tyr	Lys	Leu	His	Lys	Ser	Arg	
			85					90					95			

ggc	gac	caa	gtg	ctg	gac	gac	tgt	gtg	caa	tty	ata	gac	aag	cac	ctg	336
Gly	Asp	Gln	Val	Leu	Asp	Ala	Cys	Val	Gln	Leu	Ile	Asp	Lys	His	Leu	
			100				105					110				

ggc	gac	aag	tat	cgc	cgg	gac	tgg	cgc	att	atg	tac	ggc	aac	agg	aaa	384
Gly	Ala	Lys	Tyr	Arg	Arg	Ala	Ser	Arg	Ile	Met	Tyr	Gly	Asn	Arg	Lys	
		115					120				125					

cca	tgg	aag	gca	aac	aaa	ctc	gca	gag	atg	aaa	agc	gac	ggc	ctt	gtg	432
Pro	Trp	Lys	Ala	Asn	Lys	Leu	Ala	Glu	Met	Lys	Ser	Ala	Gly	Leu	Val	

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130	135	140	
tac gtc tgt tac tgg gac aac ggc gtg ctg ggt gca ttt act tca ttc			480
Tyr Val Cys Tyr Trp Asp Asn Gly Val Leu Gly Ala Phe Thr Ser Phe			
145	150	155	160
atg ctt aca gag gag acg ggt ctg gtc gaa ggt gac gct tta cac gag			528
Met Leu Thr Glu Glu Thr Gly Leu Val Glu Gly Asp Ala Leu His Glu			
	165	170	175
gtt agc gtg ccc gtg ata tac ctt tac gaa gta cat gta gct agc gag			576
Val Ser Val Pro Val Ile Tyr Leu Tyr Glu Val His Val Ala Ser Ala			
	180	185	190
cac cgc ggg cal gga atc ggt cgg cgg cta ctg gag cat gca ctg tgc			624
His Arg Gly His Gly Ile Gly Arg Arg Leu Leu Glu His Ala Leu Cys			
	195	200	205
gct ggc gta gct cga cac aac cgc cgc atg tgt gac aat ttc ttc ggt			672
Asp Gly Val Ala Arg His Thr Arg Arg Met Cys Asp Asn Phe Phe Gly			
	210	215	220
gta gca ctg acc gta ttc agt gat aac act cgg gcc cgg cga cta tat			720
Val Ala Leu Thr Val Phe Ser Asp Asn Thr Arg Ala Arg Arg Leu Tyr			
225	230	235	240
gag gag ctt ggg ttc tac cgc gct cgg gga tca ccc gca cca gca tca			768
Glu Ala Leu Gly Phe Tyr Arg Ala Pro Gly Ser Pro Ala Pro Ala Ser			
	245	250	255
ccc aca att cgt cac acg cga cat ggt ggg gga cgt gta gtc gtg ccc			816
Pro Thr Ile Arg His Thr Arg His Gly Gly Gly Arg Val Val Val Pro			
	260	265	270
tgc gat cgg ctg tat tac gta tat tgc ctt cac atg cag tga			864
Cys Asp Pro Leu Tyr Tyr Val Tyr Cys Leu His Met Pro			
	275	280	285

<210> 162

<211> 285

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 162

Met Arg Ser Ser Val Tyr Ser Gln Asn Thr Tyr Asn Cys Ile Arg Thr
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Ser Lys Glu His Leu Thr Glu Arg Arg Arg Val Ala Met Ala Pro Met
20 25 30

Phe Gln His Phe Leu Asn Leu Cys Val Glu Lys Phe Pro Glu Ser Ile
35 40 45

Glu His Lys Asp Thr Asp Gly Asn Gly Asn Phe Thr Thr Ala Ile Leu
50 55 60

Gln Arg Glu Phe Ile Tyr Ile Pro Glu Asp Asp Thr Asp Ser Ile Asp
65 70 75 80

Ser Val Asp Ser Leu Lys Cys Ile Asn Tyr Lys Leu His Lys Ser Arg
85 90 95

Gly Asp Gln Val Leu Asp Ala Cys Val Gln Leu Ile Asp Lys His Leu
100 105 110

Gly Ala Lys Tyr Arg Arg Ala Ser Arg Ile Met Tyr Gly Asn Arg Lys
115 120 125

Pro Trp Lys Ala Asn Lys Leu Ala Gln Met Lys Ser Ala Gly Leu Val
130 135 140

Tyr Val Cys Tyr Trp Asp Asn Gly Val Leu Gly Ala Phe Thr Ser Phe
145 150 155 160

Met. Leu Thr Glu Glu Thr Gly Leu Val Glu Gly Asp Ala Leu His Glu
165 170 175

Val Ser Val Pro Val Ile Tyr Leu Tyr Glu Val His Val Ala Ser Ala
180 185 190

His Arg Gly His Gly Ile Gly Arg Arg Leu Leu Glu His Ala Leu Cys
195 200 205

Asp Gly Val Ala Arg His Thr Arg Arg Met Cys Asp Asn Phe Phe Gly
210 215 220

Val Ala Leu Thr Val Phe Ser Asp Asn Thr Arg Ala Arg Arg Leu Tyr
225 230 235 240

Glu Ala Leu Gly Phe Tyr Arg Ala Pro Gly Ser Pro Ala Pro Ala Ser
245 250 255

Pro Thr Ile Arg His Thr Arg His Gly Gly Gly Arg Val Val Val Pro
260 265 270

Cys Asp Pro Leu Tyr Tyr Val Tyr Cys Leu His Met Pro
275 280 285

<210> 163

<211> 1755

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<232> (1)..(1755)

<400> 16?

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Met	Ser	Arg	Glu	Ala	Phe	Asp	Val	Pro	Asn	Ile	Gly	Thr	Asn	Lys	Phe	
1			5					10						15		
tta	aaa	gtc	aca	cct	aat	tta	ttt	acc	cca	gag	cga	ttg	aat	tta	tat	96
Leu	Lys	Val	Thr	Pro	Asn	Leu	Phe	Thr	Pro	Glu	Arg	Leu	Asn	Leu	Phe	
			20					25					30			
gat	gat	gtc	gaa	cta	tat	gtt	aag	tta	ata	aaa	gca	tcc	aat	tgt	gtc	144
Asp	Asp	Val	Glu	Leu	Tyr	Leu	Thr	Leu	Ile	Lys	Ala	Ser	Lys	Cys	Val	
			35				40						45			
gag	cag	gga	gaa	agg	ctg	cac	aat	ata	agt	tgg	aga	att	ctg	aat	aaa	192
Glu	Gln	Gly	Gln	Arg	Leu	His	Asn	Ile	Ser	Trp	Arg	Ile	Leu	Asn	Lys	
		50					55				60					
gct	gtc	cta	aag	gag	cat	aat	att	aat	cga	tct	aaa	aaa	aga	gac	ggc	240
Ala	Val	Leu	Lys	Glu	His	Asn	Ile	Asn	Arg	Ser	Lys	Lys	Arg	Asp	Gly	
65					70				75				80			
gtg	aag	aac	ata	tat	tat	gtg	tta	aat	cca	aac	aac	aaa	cag	cca	ata	288
Val	Lys	Asn	Ile	Tyr	Tyr	Val	Leu	Asn	Pro	Asn	Asn	Lys	Gln	Pro	Ile	
					85				90				95			
aag	cca	aag	cag	gca	gca	gta	aag	cag	cca	cca	tta	caa	aag	gcc	aat	336
Lys	Pro	Lys	Gln	Ala	Ala	Val	Lys	Gln	Pro	Pro	Leu	Gln	Lys	Ala	Asn	
			100					105				110				
ttg	cct	ccc	aca	acg	gca	aaa	cag	aac	gtt	tta	act	cgg	cca	atg	aca	384
Leu	Pro	Pro	Thr	Thr	Ala	Lys	Gln	Asn	Val	Leu	Thr	Arg	Pro	Met	Thr	
			115					120				125				
tca	cca	gct	ata	gca	cag	ggt	gct	cac	gat	aga	ccc	ctg	gat	aat	cct	432
Ser	Pro	Ala	Ile	Ala	Gln	Gly	Ala	His	Asp	Arg	Ser	Leu	Asp	Asn	Pro	
		130					135				140					
aat	tct	aca	aac	aat	gat	gtg	aaa	aat	gac	gtt	gct	cca	aac	aga	caa	480
Asn	Ser	Thr	Asn	Asn	Asp	Val	Lys	Asn	Asp	Val	Ala	Pro	Asn	Arg	Gln	
145					150				155					160		

tto tcc aaa tct act acg tca ggg ttg ttt tca aat ttt qca gac aaa	528
Phe Ser Lys Ser Thr Thr Ser Gly Leu Phe Ser Asn Phe Ala Asp Lys	
155 170 175	
tat caa aaa atg aaa aat ggg aac cat gtt gct aat aag gaa gaa cca	576
Tyr Gln Lys Met Lys Asn Val Asn His Val Ala Asn Lys Glu Glu Pro	
180 183 190	
caa act att atc acc ggt ttt gat aca agc act gtt ata acc aag aat	624
Gln Thr Ile Ile Thr Gly Phe Asp Thr Ser Thr Val Ile Thr Lys Lys	
195 200 205	
act tta caa tcc aga cgc tca aga tca cct ttc cag cat ata gga gac	672
Pro Leu Gln Ser Arg Arg Ser Arg Ser Pro Phe Gln His Ile Gly Asp	
210 215 220	
atg aac atg aac tgc att gat aat gag act tcc aag agt acc agt cct	720
Met Asn Met Asn Cys Ile Asp Asn Gln Thr Ser Lys Ser Thr Ser Pro	
225 230 235 240	
act att gaa aat atg gga agt aga aaa tcc tot ttt cct cag cag gac	768
Thr Thr Gln Asn Met Gly Ser Arg Lys Ser Ser Phe Pro Gln Lys Gln	
245 250 255	
tot tta ttc gga agg cca agg tot tuc aag aat gac caa aat ggt caa	816
Ser Leu Phe Gly Arg Pro Arg Ser Tyr Lys Asn Asp Gln Asn Gly Gln	
260 265 270	
atg tca ctt tog aaa aca tcc tct aga aaa gga aaa aac aag ata ttt	864
Leu Ser Leu Ser Lys Thr Ser Ser Arg Lys Gly Lys Asn Lys Ile Phe	
275 280 285	
tto agc agt gaa gat gaa gat tcc gat tgg gac agc gtt tog aat gat	912
Phe Ser Ser Glu Asp Glu Asp Ser Asp Trp Asp Ser Val Ser Asn Asp	
290 295 300	
tca gaa ttc taa gct gat gaa gat gat gaa gag tac gat gat tat aat	960
Ser Gln Phe Tyr Ala Asp Glu Asp Asp Gln Gln Tyr Asp Asp Tyr Asn	
305 310 315 320	
gag gaa gaa gca gat cag tac tat aga aga caa tgg gac aag ctt tta	1008

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Glu Glu Glu Ala Asp Gln Tyr Tyr Arg Arg Gln Trp Asp Lys Leu Leu	
325 330 335	
ttt gcc aaa aat caa cag aat ctt gac tca acg aaa tca tct gtt tca	1056
Phe Ala Lys Asn Gln Gln Asn Leu Asp Ser Thr Lys Ser Ser Val Ser	
340 345 350	
tca ggg aac aca atc aac tca aac aca tcc cat gat ccc gta cga aaa	1104
Ser Ala Asn Thr Ile Asn Ser Asn Thr Ser His Asp Pro Val Arg Lys	
355 360 365	
agt tta ctc agt gga cta ctc ctt agt gag gca aat agc aac agt aat	1152
Ser Leu Leu Ser Gly Leu Phe Leu Ser Glu Ala Asn Ser Asn Ser Asn	
370 375 380	
aac cac aat act gca cat agt gaa tac gct tct aaa cac gtt tgg cgg	1200
Asn His Asn Thr Ala His Ser Glu Tyr Ala Ser Lys His Val Ser Pro	
385 390 395 400	
act cct cag tcc tct cat agt aat atc ggt cct caa cgg cag caa aat	1248
Thr Pro Gln Ser Ser His Ser Asn Ile Gly Pro Gln Pro Gln Gln Asn	
405 410 415	
cca cgg agc gct aat ggt ata aaa caa caa aaa cct tct ttg aac aca	1296
Pro Pro Ser Ala Asn Gly Ile Lys Gln Gln Lys Pro Ser Leu Lys Thr	
420 425 430	
agc aac gtg aca gct cta gca tgg cta tct ccc cgg caa caa tcc aac	1344
Ser Asn Val Thr Ala Leu Ala Ser Leu Ser Pro Pro Gln Pro Ser Asn	
435 440 445	
aat gag cgg tta tgg aag gat ata caa aag gac ttc aaa act gat aat	1392
Asn Glu Arg Asn Ser Met Asp Ile Gln Lys Asp Phe Lys Thr Asp Asn	
450 455 460	
gag tcc aat cat tta tat gaa tct aat gct cgg cta act gct caa act	1440
Glu Ser Asn His Leu Tyr Glu Ser Asn Ala Pro Leu Thr Ala Gln Thr	
465 470 475 480	
ata ctg ccc aac gcc tta tct act cac atg ccc cly ccu nat aac att	1488
Ile Leu Pro Thr Ala Leu Ser Thr His Met Phe Leu Pro Asn Asn Ile	
485 490 495	

cac caa caa cga atg gcg att ggc acc ggt agt aat acg cga cat cgt 1536
 His Gln Gln Arg Met Ala Ile Ala Thr Gly Ser Asn Thr Arg His Arg
 500 505 510

ttt tgg agg cgg cag tgg atg gat atc cca tcc aag aac agg aat act 1594
 Phe Ser Arg Arg Gln Ser Met Asp Ile Pro Ser Lys Asn Arg Asn Thr
 515 520 525

ggg ttt ttg aag acc aga atg gag atc tct gag gaa gaa aag atg gla 1632
 Gly Phe Leu Lys Thr Arg Met Glu Ile Ser Glu Glu Glu Lys Met Val
 530 535 540

cgt aca ata tca cgg ctt gac aat acg agt att gca aac agt aat gga 1680
 Arg Thr Ile Ser Arg Leu Asp Asn Thr Ser Ile Ala Asn Ser Asn Gly
 545 550 555 560

aat ggt aat gat gac acc tct aat cag aga acg gaa gca ctg ggg cgt 1728
 Asn Gly Asn Asp Asp Thr Ser Asn Gln Arg Thr Glu Ala Leu Gly Arg
 565 570 575

aag aag cgt aat gga ggg cga ata tga 1755
 Lys Thr Ser Asn Gly Gly Arg Ile
 580

<210> 164

<211> 584

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 164

Met Ser Arg Glu Ala Phe Asp Val Pro Asn Ile Gly Thr Asn Lys Phe
 1 5 10 15

Leu Lys Val Thr Pro Asn Leu Phe Thr Pro Glu Arg Leu Asn Leu Phe
 20 25 30

Asp Asp Val Glu Leu Tyr Leu Thr Leu Ile Lys Ala Ser Lys Cys Val

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35	40	45
Glu Gln Gly Glu Arg Leu His Asn Ile Ser Trp Arg Ile Leu Asn Lys		
50	55	60
Ala Val Leu Lys Glu His Asn Ile Asn Arg Ser Lys Lys Arg Asp Gly		
65	70	75
Val Lys Asn Ile Tyr Tyr Val Leu Asn Pro Asn Asn Lys Gln Pro Ile		
85	90	95
Lys Pro Lys Gln Ala Ala Val Lys Gln Pro Pro Leu Gln Lys Ala Asn		
100	105	110
Leu Pro Pro Thr Thr Ala Lys Gln Asn Val Leu Thr Arg Pro Met Thr		
115	120	125
Ser Pro Ala Ile Ala Gln Gly Ala His Asp Arg Ser Leu Asp Asn Pro		
130	135	140
Asn Ser Thr Asn Asn Asp Val Lys Asn Asp Val Ala Pro Asn Arg Gln		
145	150	155
Phe Ser Lys Ser Thr Thr Ser Gly Leu Phe Ser Asn Phe Ala Asp Lys		
165	170	175
Tyr Gln Lys Met Lys Asn Val Asn His Val Ala Asn Lys Gln Glu Pro		
180	185	190
Gln Thr Ile Ile Thr Gly Phe Asp Thr Ser Thr Val Ile Thr Lys Lys		
195	200	205

Pro Leu Gln Ser Arg Arg Ser Arg Ser Pro Phe Gln His Ile Gly Asp
210 215 220

Met Asn Met Asn Cys Ile Asp Asn Glu Thr Ser Lys Ser Thr Ser Pro
225 230 235 240

Thr Leu Glu Asn Met Gly Ser Arg Lys Ser Ser Phe Pro Gln Lys Glu
245 250 255

Ser Leu Phe Gly Arg Pro Arg Ser Tyr Lys Asn Asp Gln Asn Gly Gln
260 265 270

Leu Ser Leu Ser Lys Thr Ser Ser Arg Lys Gly Lys Asn Lys Ile Phe
275 280 285

Phe Ser Ser Glu Asp Glu Asp Ser Asp Trp Asp Ser Val Ser Asn Asp
290 295 300

Ser Glu Phe Tyr Ala Asp Glu Asp Asp Glu Glu Tyr Asp Asp Tyr Asn
305 310 315 320

Glu Glu Glu Ala Asp Gln Tyr Tyr Arg Arg Gln Trp Asp Lys Leu Leu
325 330 335

Phe Ala Lys Asn Gln Gln Asn Leu Asp Ser Thr Lys Ser Ser Val Ser
340 345 350

Ser Ala Asn Thr Ile Asn Ser Asn Thr Ser His Asp Pro Val Arg Lys
355 360 365

Ser Leu Leu Ser Gly Leu Phe Leu Ser Glu Ala Asn Ser Asn Ser Asn

370.	375	380
Asn His Asn Thr Ala His Ser Glu Tyr Ala Ser Lys His Val Ser Pro		
385	390	395 400
Thr Pro Gln Ser Ser His Ser Asn Ile Gly Pro Gln Pro Gln Gln Asn		
	405	410 415
Pro Pro Ser Ala Asn Gly Ile Lys Gln Gln Lys Pro Ser Leu Lys Thr		
	420	425 430
Ser Asn Val Thr Ala Leu Ala Ser Leu Ser Pro Pro Gln Pro Ser Asn		
	435	440 445
Asn Glu Arg Leu Ser Met Asp Ile Gln Lys Asp Phe Lys Thr Asp Asn		
	450	455 460
Glu Ser Asn His Leu Tyr Glu Ser Asn Ala Pro Leu Thr Ala Gln Thr		
465	470	475 480
Ile Leu Pro Thr Ala Leu Ser Thr His Met Phe Leu Pro Asn Asn Ile		
	485	490 495
His Gln Gln Arg Met Ala Ile Ala Thr Gly Ser Asn Thr Arg His Arg		
	500	505 510
Phe Ser Arg Arg Gln Ser Met Asp Ile Pro Ser Lys Asn Arg Asn Thr		
	515	520 525
Gly Phe Leu Lys Thr Arg Met Glu Ile Ser Glu Glu Glu Lys Met Val		
530	535	540

Arg Thr Ile Ser Arg Leu Asp Asn Thr Ser Ile Ala Asn Ser Asn Gly
 545 550 555 560

Asn Gly Asn Asp Asp Thr Ser Asn Gln Arg Thr Glu Ala Leu Gly Arg
 565 570 575

Lys Thr Ser Asn Gly Gly Arg Ile
 580

<210> 165
 <211> 741
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(741)

<400> 165
 atg gag agl ala ttt ggt ggg ttt gga gat cta gtt gtt cct agg cca 40
 Met Glu Ser Ile Phe Gly Gly Phe Gly Asp Leu Val Val Pro Arg Pro
 1 5 10 15
 aag gag cat cta ggt caa aca gac att tcc ttc ggt gga aaa tta ttg 96
 Lys Glu His Leu Gly Gln Thr Asp Leu Ser Phe Gly Gly Lys Leu Leu
 20 25 30
 cct gaa ttg aaa att tgt gaa gai gga ggt gaa agt ggt tgt ggc ggt 144
 Pro Ala Leu Lys Ile Cys Gln Asp Gly Gly Glu Ser Gly Cys Gly Gly
 35 40 45
 aaa gtc tgg atc gct ggc gaa ctg ttg tgc gag tac ata ctc gag aaa 192
 Lys Val Trp Ile Ala Gly Glu Leu Leu Cys Glu Tyr Ile Leu Glu Lys
 50 55 60
 tca gtt gac cat ctg cta agt aag aag gtc aat ggt aag aaa cca ttt 240
 Ser Val Asp His Leu Leu Ser Lys Thr Val Asn Gly Thr Lys Gln Phe

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65	70	75	80	
aaa aaa gtc tta gaa ttg ggt agt ggt acc ggt tta gtt gga ttg tgc				200
Lys Lys Val Leu Gln Leu Gly Ser Gly Thr Gly Leu Val Gly Leu Cys				
	85	90	95	
gtg ggg ctg ttg gaa aaa aac acc ttc cac gat ggc act aaa gta tat				336
Val Gly Leu Leu Glu Lys Asn Thr Phe His Asp Gly Thr Lys Val Tyr				
	100	105	110	
gtt acg gac att gac aag ttg ata cca cta ttg aaa aga aat ata gaa				384
Val Thr Asp Ile Asp Lys Leu Ile Pro Leu Leu Lys Arg Asn Ile Glu				
	115	120	125	
ctg gac gaa gtt cag tat gaa gll clt gag agg gaa ctt tgg tgg ggt				432
Leu Asp Glu Val Gln Tyr Glu Val Leu Ala Arg Glu Leu Trp Trp Gly				
	130	135	140	
gag cgg ctg tgg gca gat ttc tca cct caa gaa ggt gct atg caa gca				480
Glu Pro Leu Ser Ala Asp Phe Ser Pro Gln Glu Gly Ala Met Gln Ala				
	145	150	155	160
aat aac gtt gat cta gtt tgg gca gct gat tgt gtg tat ctg gag gaa				528
Asn Asn Val Asp Leu Val Leu Ala Ala Asp Cys Val Tyr Leu Glu Glu				
	165	170	175	
gct tll cca tta cta gaa aaa acc cta ctt gat ctg act cac tgc ata				576
Ala Phe Pro Leu Leu Glu Lys Thr Leu Leu Asp Leu Thr His Cys Ile				
	180	185	190	
aac cca cct gta atc lly atg gcl tuc aag aag aga aga aaa gct gat				624
Asn Pro Pro Val Ile Leu Met Ala Tyr Lys Lys Arg Arg Lys Ala Asp				
	195	200	205	
aaa cat ttt ctg aac aag att auu aga aat ttt gac gtt ctt gaa att				672
Lys His Phe Phe Asn Lys Ile Lys Arg Asn Phe Asp Val Leu Glu Ile				
	210	215	220	
aca gat ttt agt aaa ttt gan cat tat ctt aag gaa aga acc cac ttg				720
Thr Asp Phe Ser Lys Phe Glu His Tyr Leu Lys Glu Arg Thr His Leu				
	225	230	235	240

ttt caq ctt atc agg aag taa

741

Phe Gln Leu Ile Arg Lys

245

<210> 156

<211> 246

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 156

Met Glu Ser Ile Phe Gly Gly Phe Gly Asp Leu Val Val Pro Arg Pro

1

5

10

15

Lys Glu Val Leu Gly Gln Thr Asp Leu Ser Phe Gly Gly Lys Leu Leu

20

25

30

Pro Ala Leu Lys Ile Cys Glu Asp Gly Gly Glu Ser Gly Cys Gly Gly

35

40

45

Lys Val Trp Ile Ala Gly Glu Leu Leu Cys Glu Tyr Ile Leu Glu Lys

50

55

60

Ser Val Asp His Leu Leu Ser Lys Thr Val Asn Gly Thr Lys Gln Phe

65

70

75

80

Lys Lys Val Leu Glu Leu Gly Ser Gly Thr Gly Leu Val Gly Leu Cys

85

90

95

Val Gly Leu Leu Glu Tyr Asn Thr Phe His Asp Gly Thr Lys Val Tyr

100

105

110

Val Thr Asp Ile Asp Lys Leu Ile Pro Leu Leu Tyr Arg Asn Ile Glu

115

120

125

Leu Asp Glu Val Gln Tyr Gln Val Leu Ala Arg Glu Leu Trp Trp Gly
130 135 140

Glu Pro Leu Ser Ala Asp Phe Ser Pro Gln Gln Gly Ala Met Gln Ala
145 150 155 160

Asn Asn Val Asp Leu Val Leu Ala Ala Asp Cys Val Tyr Leu Glu Glu
165 170 175

Ala Phe Pro Leu Leu Glu Lys Thr Leu Leu Asp Leu Thr His Cys Ile
180 185 190

Asn Pro Pro Val Ile Leu Met Ala Tyr Lys Lys Arg Arg Lys Ala Asp
195 200 205

Lys His Phe Phe Asn Lys Thr Lys Arg Asn Phe Asp Val Leu Glu Ile
210 215 220

Thr Asp Phe Ser Lys Phe Glu His Tyr Leu Lys Glu Arg Thr His Leu
225 230 235 240

Phe Gln Leu Ile Arg Lys
245

<210> 167

<211> 2022

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2022)

<400> 167

atg tca acg cac tca aac gac cac ttt tct gct tct tcc gga atg gtc 48

Met Ser Thr His Ser Asn Asp Tyr Phe Ser Ala Ser Ser Gly Met Val

1 5 10 15

tct gag aca tcc tcc gag gtt tct tcc ata aac tct tca cag cct gta 96

Ser Glu Thr Ser Ser Glu Val Ser Ser Ile Asn Ser Ser Gln Pro Val

20 25 30

tca ttc tct aag gct tct att gct gct ccg gtt cca tgc tct gat cta 144

Ser Phe Ser Lys Ala Ser Ile Ala Ala Pro Val Pro Cys Ser Asp Leu

35 40 45

cac agc acc aag tcc aac gat gca tcc aga aaa ttg tct att cgt agg 192

His Ser Thr Lys Ser Asn Asp Ala Ser Arg Lys Leu Ser Ile Ser Arg

50 55 60

acg tta act aat cgg ctc aac gac att aaa aag gct gtc gat gac gac 240

Thr Leu Thr Asn Arg Leu Asn Asp Ile Lys Lys Ala Val Asp Asp Asp

65 70 75 80

aac tcc cag acg gaa gaa aat tcc gca gac gcc aal aaa ata tta gaa 288

Asn Leu Gln Thr Glu Glu Asn Ser Ala Asp Val Asn Lys Thr Leu Glu

85 90 95

tct aga ttt gac gtc gcc gat gcc att agg cta cag cac aat gag tca 336

Ser Arg Phe Asp Val Ala Asp Ala Ile Arg Leu Gln His Asn Glu Ser

100 105 110

gtc cag tca aag tta aac atc cca gtc aca cac acc acg act gca gcc 384

Val Gln Ser Lys Leu Asn Ile Pro Val Thr His Thr Thr Thr Ala Gly

115 120 125

gcc tcc tcc tcc gca cca tct tcc tct gcc ttc tct gct tct tct att 432

Ala Ser Leu Ser Ala Pro Ser Ser Ser Ala Phe Ser Ala Ser Ser Ile

130 135 140

caa aat gat act aca gaa cat aac gct tcc atg gac tcc aaa ctg atg 480

Gln Asn Asp Thr Thr Glu His Lys Ala Ser Met Asp Ser Lys Leu Met

145 150 155 160

egg aat aga cta tat cag get too aag aax uac too ggt aag gat ctt	528
Arg Asn Arg Leu Tyr Pro Ala Ser Thr Lys His Ser Gly Lys Asp Leu	
185 170 175	
gag gcc caa gga ata acc gaa ttc gag cct gat gaa cag act gta aaa	576
Glu Ala Gln Gly Ile Thr Glu Phe Glu Pro Asp Glu Pro Thr Val Lys	
180 185 190	
aaa gta ttc acc aac aag tct acc ggg cag ctg gaa ctg ccc ccc gac	624
Lys Val Phe Thr Asn Lys Ser Thr Gly Gln Leu Glu Leu Pro Pro Asp	
195 200 205	
ggt ggt tat ggc tgg gtc gtg aca ttc tgt gtg ttc ttg acc atg ttt	672
Gly Gly Tyr Gly Trp Val Val Thr Phe Cys Val Phe Leu Thr Met Phe	
210 215 220	
too aag tgg ggc tgc aac gca too ttc ggt gtc gac ctt gcc tac tac	720
Ser Thr Trp Gly Cys Asn Ala Ser Phe Gly Val Asp Leu Ala Tyr Tyr	
225 230 235 240	
ala aac caa gat act tac cct ggt get cag aag tac gat tat gcc tta	768
Leu Asn His Asp Thr Tyr Pro Gly Ala Ser Lys Tyr Asp Tyr Ala Leu	
245 250 255	
att get ggc cca aat gtc ttt ctc ggt caa ctc tta too ccc ctt gtg	816
Ile Ala Gly Leu Thr Val Phe Leu Gly Gln Leu Leu Ser Pro Leu Val	
260 265 270	
atg gaa ctg atg aga ata att ggt ctg cgg acc acc atg ctt ttt ggt	864
Met Ala Leu Met Arg Ile Ile Gly Leu Arg Thr Thr Met Leu Phe Gly	
275 280 285	
gat gcc gta atg ctt gcc gca tat ctc ttg gcc too ttt act acc aag	912
Asp Ala Val Met Leu Ala Ala Tyr Leu Leu Ala Ser Phe Thr Thr Lys	
290 295 300	
tta tgg caa tly lal glu acc caa ggt ttt atg gtc ggt tgt tca ata	960
Leu Trp Gln Leu Tyr Val Thr Gln Gly Phe Met Val Gly Cys Ser Ile	
305 310 315 320	
tca ctg att ttc gtt caa gca aca acc gtc tta caa gga tgg ttc ttg	1008

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Ser Leu Ile Phe Val Pro Ala Thr Thr Val Leu Pro Gly Trp Phe Leu	
225 330 335	
aaa aaa aga gcl gcc gca alg ggt gtc tca tta ttg ggt acc gct gct	1056
Lys Lys Arg Ala Val Ala Met Gly Val Ser Leu Leu Gly Thr Gly Ala	
340 345 350	
ggt ggt gtc gct tac ggt ttg gct aca aac aaa atg ctt tct gac ttt	1104
Gly Gly Val Val Tyr Gly Leu Ala Thr Asn Lys Met Leu Ser Asp Phe	
355 360 365	
gga aat acc cgg cgg tgc ctt cgt atc ata ggc ata tgg cgt agc ata	1152
Gly Asn Thr Arg Trp Cys Leu Arg Ile Ile Gly Ile Ser Cys Ser Ile	
370 375 380	
agt gtt cta gtt gct att gag ctc tta aaa gag aga aac cct aca cct	1200
Ser Val Leu Val Ala Ile Ala Leu Leu Lys Glu Arg Asn Pro Thr Pro	
385 390 395 400	
gac ata gga ttg aaa tgg cct cgg gcc atg ttt gaa cag ctc aaa gcc	1248
Ala Ile Gly Leu Lys Ser Pro Arg Ala Met Phe Glu Gln Leu Lys Ala	
405 410 415	
atg tct tca tta aag gtt ata acc aag cca ttt gtg gta ctt att gcc	1296
Met Phe Ser Leu Lys Val Ile Thr Lys Pro Phe Val Val Leu Ile Ala	
420 425 430	
tta cgg ttc atg ttc gcc tta ttt gcc tac aat atg atg gtt ttt act	1344
Leu Trp Phe Met Phe Ala Leu Phe Ala Tyr Asn Met Met Val Phe Thr	
435 440 445	
tta tct tca tac gcc atc tgg aac gga tta tca tgg cac gac gct tcc	1392
Leu Ser Ser Tyr Ala Ile Ser Lys Gly Leu Ser Ser His Asp Ala Ser	
450 455 460	
aca ttg act gcc att ttg aac ggc tgg caa tcc atc gga aga cct ctg	1440
Thr Leu Thr Ala Ile Leu Asn Gly Ser Gln Ser Ile Gly Arg Pro Leu	
465 470 475 480	
atg ggt tta gag gga gat aag ttt ggt agg gca aac gla aag atc gta	1488
Met Gly Leu Ala Gly Asp Lys Phe Gly Arg Ala Asn Val Thr Ile Val	
485 490 495	

tta acc act ttg tta aca ata tat atg ttt gcg ttc tgg atc ccc gct	1536
Leu Thr Thr Leu Leu Thr Ile Tyr Met Phe Ala Phe Trp Ile Pro Ala	
500 505 510	
cat acg ttc gtt caa ttc atc ttt ttt tca att cta gtt ggc tca tga	1584
His Thr Phe Val Gln Leu Ile Phe Phe Ser Ile Leu Val Gly Ser Cys	
515 520 525	
gtt ggt gtc gcc aac gtc atg aat acc gtt ctg att gcc gat atg gtt	1632
Val Gly val Ala Asn Val Met Asn Thr Val Leu Ile Ala Asp Met Val	
530 535 540	
aaa cca gaa gag ttt ttg ccc gct tgg gcc ttc gtc aac tac tgt ggt	1680
Lys Pro Glu Glu Phe Leu Pro Ala Trp Ala Phe Val Asn Tyr Cys Gly	
545 550 555 560	
gcg cct ttc tta ttg gtt tgc gag gtg att gcc caq gca ttg acg gtg	1728
Ala Pro Phe Leu Leu Val Cys Glu Val Ile Ala Gln Ala Leu Thr Val	
565 570 575	
gag aaa gat aag agc aat cct tac tta cat gca caa att ttt tgc ggt	1776
Glu Lys Asp Lys Ser Asn Pro Tyr Leu His Ala Gln Ile Phe Cys Gly	
580 585 590	
tgc tgc ttt att gcc gca cta att tta att tct atc ctt cgt gaa tac	1824
Cys Cys Phe Ile Ala Ala Leu Ile Leu Ile Ser Ile Leu Arg Glu Tyr	
595 600 605	
tct atc agg atg aaa tta acg gaa aga caa gct atg aca aac gag aag	1872
Ser Ile Arg Met Lys Leu Thr Glu Arg Gln Ala Met Thr Asn Glu Lys	
610 615 620	
tta aaa gaa tgg aag gca agc gaa tac gat acc gat tct gcc gat gaa	1920
Leu Lys Glu Trp Lys Ala Ser Glu Tyr Asp Thr Asp Ser Ala Asp Glu	
625 630 635 640	
gat tgg ggt aaa tta aaa gaa aga aag act aaa tat gac ctt ctt cta	1968
Asp Trp Gly Lys Leu Lys Glu Arg Lys Thr Lys Tyr Asp Leu Leu Leu	
645 650 655	
ggt ccg ggc att aaa uua tuc ttc cta aga atg gta tat cca atg aag	2016

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Gly Pro Gly Ile Lys Lys Tyr Phe Leu Arg Met Val Tyr Pro Met Lys
 560 665 670

gto tag 2022
 Val

<213> 166

<211> 673

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 166

Met Ser Thr His Ser Asn Asp Tyr Phe Ser Ala Ser Ser Gly Met Val
 1 5 10 15

Ser Glu Tyr Ser Ser Glu Val Ser Ser Ile Asn Ser Ser Gln Pro Val
 20 25 30

Ser Phe Ser Lys Ala Ser Ile Ala Ala Pro Val Pro Cys Ser Asp Leu
 35 40 45

His Ser Thr Lys Ser Asn Asp Ala Ser Arg Lys Leu Ser Ile Ser Arg
 50 55 60

Thr Leu Thr Asn Arg Leu Asn Asp Ile Lys Lys Ala Val Asp Asp Asp
 65 70 75 80

Asn Leu Gln Thr Glu Glu Asn Ser Ala Asp Val Asn Lys Ile Leu Glu
 85 90 95

Ser Arg Phe Asp Val Ala Asp Ala Ile Arg Leu Gln His Asn Glu Ser
 100 105 110

Val Gln Ser Lys Leu Asn Ile Pro Val Thr His Thr Thr Thr Ala Gly
115 120 125

Ala Ser Leu Ser Ala Pro Ser Ser Ser Ala Phe Ser Ala Ser Ser Ile
130 135 140

Gln Asn Asp Thr Thr Glu His Lys Ala Ser Met Asp Ser Lys Leu Met
145 150 155 160

Arg Asn Arg Leu Tyr Pro Ala Ser Thr Lys His Ser Gly Lys Asp Leu
165 170 175

Glu Ala Gln Gly Ile Thr Gln Phe Glu Pro Asp Glu Pro Thr Val Lys
180 185 190

Lys Val Phe Thr Asn Lys Ser Thr Gly Gln Leu Glu Leu Pro Pro Asp
195 200 205

Gly Gly Tyr Gly Trp Val Val Thr Phe Cys Val Phe Leu Thr Met Phe
210 215 220

Ser Thr Trp Gly Cys Asn Ala Ser Phe Gly Val Asp Leu Ala Tyr Tyr
225 230 235 240

Leu Asn His Asp Thr Tyr Pro Gly Ala Ser Lys Tyr Asp Tyr Ala Leu
245 250 255

Ile Ala Gly Leu Thr Val Phe Leu Gly Gln Leu Leu Ser Pro Leu Val
260 265 270

Met Ala Leu Met Arg Ile Ile Gly Leu Arg Thr Thr Met Leu Phe Gly

275	280	285
Asp Ala Val Met Leu Ala Ala Tyr Leu Leu Ala Ser Phe Thr Thr Lys		
290	295	300
Leu Trp Gln Leu Tyr Val Thr Gln Gly Phe Met Val Gly Cys Ser Ile		
305	310	315
		320
Ser Leu Ile Phe Val Pro Ala Thr Thr Val Leu Pro Gly Trp Phe Leu		
	325	330
		335
Lys Lys Arg Ala Val Ala Met Gly Val Ser Leu Leu Gly Thr Gly Ala		
	340	345
		350
Gly Gly Val Val Tyr Gly Leu Ala Thr Asn Lys Met Leu Ser Arg Phe		
355	360	365
Gly Asn Thr Arg Trp Cys Leu Arg Ile Ile Gly Ile Ser Cys Ser Ile		
370	375	380
Ser Val Leu Val Ala Ile Ala Leu Leu Lys Gln Arg Asn Pro Thr Pro		
385	390	395
		400
Ala Ile Gly Leu Lys Ser Pro Arg Ala Met Phe Gln Gln Leu Lys Ala		
	405	410
		415
Met Phe Ser Leu Lys Val Ile Thr Lys Pro Phe Val Val Leu Ile Ala		
	420	425
		430
Leu Trp Phe Met Phe Ala Leu Phe Ala Tyr Asn Met Met Val Phe Thr		
435	440	445

Leu Ser Ser Tyr Ala Ile Ser Lys Gly Leu Ser Ser His Asp Ala Ser
450 455 460

Thr Leu Thr Ala Ile Leu Asn Gly Ser Gln Ser Ile Gly Arg Pro Leu
465 470 475 480

Met Gly Leu Ala Gly Asp Lys Phe Gly Arg Ala Asn Val Thr Ile Val
485 490 495

Leu Thr Thr Leu Leu Thr Ile Tyr Met Phe Ala Phe Trp His Pro Ala
500 505 510

His Thr Phe Val Gln Leu Ile Phe Phe Ser Ile Leu Val Gly Ser Cys
515 520 525

Val Gly Val Ala Asn Val Met Asn Thr Val Leu Ile Ala Asn Met Val
530 535 540

Lys Pro Glu Glu Phe Leu Pro Ala Trp Ala Phe Val Asn Tyr Cys Gly
545 550 555 560

Ala Pro Phe Leu Leu Val Cys Glu Val Ile Ala Gln Ala Leu Thr Val
565 570 575

Glu Lys Asp Lys Ser Asn Pro Tyr Leu His Ala Gln Ile Phe Cys Gly
580 585 590

Cys Cys Phe Ile Ala Ala Leu Ile Leu Ile Ser Ile Leu Arg Glu Tyr
595 600 605

Ser Ile Arg Met Lys Leu Thr Glu Arg Gln Ala Met Thr Asn Glu Lys
610

510	615	620
Leu Lys Glu Trp Lys Ala Ser Glu Tyr Asp Thr Asp Ser Ala Asp Glu		
625	630	635
Asp Trp Gly Lys Leu Lys Glu Arg Lys Thr Lys Tyr Asp Leu Leu Leu		
645	650	655
Gly Pro Gly Ile Lys Lys Tyr Phe Leu Arg Met Val Tyr Pro Met Lys		
660	665	670

Val

<210> 169
 <211> 1569
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1569)

<400> 169
 atg tgg cta ala aga aag aag ata aat gaa ttt ctg gga tgt atc cat 48
 Met Leu Leu Ile Arg Arg Thr Ile Asn Ala Phe Leu Gly Cys Ile His
 1 5 10 15
 tgc aat ctt acg gag aag tgc atc ctg att gaa ttc gtc ata acc atg 95
 Cys Asn Leu Thr Ala Thr Cys Ile Leu Ile Ala Phe Val Ile Thr Met
 20 25 30
 tat gtg gta att gta tct gag cct gca tcc gta gaa gga aat atg gga 144
 Tyr Val Val Leu Val Ser Glu Pro Ala Ser Val Asp Gly Thr Met Gly
 35 40 45

aat ttt ctt cgg ttt tcc aag atg gat ctt ggg acg aag ayy gac aga	192
Asn Phe Leu Pro Phe Ser Lys Met Asp Leu Ala Thr Lys Arg Asp Arg	
50 35 60	
ccc ttt tat tgg aat tgt gtg aat act cag gac tat ttg ttg aat cca	240
Pro Phe Tyr Ser Asn Cys Val Asn Thr Gln Asp Tyr Leu Leu Asn Pro	
65 70 75 80	
tgg tac atc aag cag aat gcc tgg ctt gtc atg cta aca agg aac ggg	288
Ser Tyr Ile Lys Gln Asn Ala Ser Phe Val Met Leu Thr Arg Asn Gly	
85 90 95	
gag cta gaa gat gtt atc aag act atc aac aqt ata gaa gag cat ttc	336
Glu Leu Glu Asp Val Ile Lys Thr Ile Asn Ser Ile Glu Glu His Phe	
100 105 110	
aat cag tgg ttc cac tat cca tat gtg ttc tta aat gac cag ccg ttt	384
Asn Gln Trp Phe His Tyr Pro Tyr Val Phe Leu Asn Asp Glu Pro Phe	
115 120 125	
gaa gag gac ttc aaa gca aac gta cgt gat gtt aca gtg ggc ggc ctg	432
Glu Glu Asp Phe Lys Ala Lys Val Arg Asp Val Thr Val Gly Ala Leu	
130 135 140	
gtg gaa ttt ggc act atc gat gag ata tct tgg aat ttt ccc agt gac	480
Val Glu Phe Gly Thr Ile Asp Glu Ile Ser Trp Asn Phe Pro Ser Asp	
145 150 155 160	
gta aag gat acg ttc gag tcc tac aac gca att gag gat caa ggt gat	528
Val Lys Asp Thr Phe Glu Phe Tyr Asn Ala Ile Glu Asp Gln Gly Asp	
165 170 175	
aga agc ata ctt tac gga aac tta gaa tca tat cai aag atg tgc cgg	576
Arg Ser Ile Leu Tyr Gly Asn Leu Glu Ser Tyr His Lys Met Cys Arg	
180 185 190	
ttt tat cca gga tta ttt tac aag cac cgg ata gta cag aag tac gaa	624
Phe Tyr Ser Gly Leu Phe Tyr Lys His Pro Leu Val Gln Lys Tyr Glu	
195 200 205	
tgg tat tgg aga ttg gaa ccc gat gtt gag ttt ttc tgt gat att acc	672
Trp Tyr Trp Arg Leu Glu Pro Asp Val Glu Phe Phe Cys Asp Ile Thr	

210		215	220	
tac gat ccc ttt ttg gag atg ctc cga act aat aag aaa tat gga ttt				720
Tyr Asp Pro Phe Leu Glu Met Leu Arg Thr Asn Lys Lys Tyr Gly Phe				
225		230	235	240
aag atc atc atc ccc gaa ttg tat tgg aca gtc cca aat ttg ttt aga				768
Thr Ile Ile Ile Pro Gln Leu Tyr Trp Thr Val Pro Asn Leu Phe Arg				
	245		250	255
cac act aaa agc ttt atc agt caa aaa ggc gtt aag ctt ggg tca tta				816
His Thr Lys Ser Phe Ile Ser Gln Lys Gly Val Thr Leu Gly Ser Leu				
	260	265		270
lyg aaa cta ttt aca aag gat tac gac att ttt gaa tcc gat gat ccc				864
Trp Lys Leu Phe Thr Lys Asp Tyr Asp Ile Phe Glu Ser Asp Asy Pro				
	275	280		285
gag tta cgg gac lgg abc sac tat gat ttt cag gcc aag gct aag aia				912
Glu Leu Arg Asp Trp Ile Asn Tyr Asp Phe Gln Ala Lys Ala Lys Ile				
	290	295		300
tcc gaa aag ata gcc atc gag cag ctt ttg aaa aag ggt gat gat ttc				960
Ser Glu Lys Ile Ala Ile Glu Gln Leu Leu Lys Lys Gly Asp Asp Phe				
305		310	315	320
caa cag ata aat gat gac aca gag gga ata atg aat ttg ata cat aag				1008
Gln Gln Ile Asn Asp Asp Lys Glu Gly Ile Met Asn Leu Ile His Lys				
	325	330		335
gat cgc tct agg aag cat atc gta gaa gac aaa ttt ttc aat qaa qaq				1056
Ala Arg Ser Arg Lys His Ile Val Glu Asp Lys Phe Phe Asn Glu Glu				
	340	345		350
tac aat cta tgc cat ttc tgg agt aat ttt gag att ggc cgg cca agc				1104
Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Gln Ile Ala Arg Leu Ser				
	355	360		365
gtg ttc gac aat gac att tac aac agt ttt ttt caa tat ttg gag aaa				1152
Val Phe Asp Asn Asp Ile Tyr Asn Ser Phe Phe Gln Tyr Leu Glu Lys				
	370	375		380

agt ggt gga ttt tgg aag gaa aga tgg ggg gac gct cct gtt cac tat 1200
 Ser Gly Gly Phe Trp Lys Glu Arg Trp Gly Asp Ala Pro Val His Ser
 385 390 395 400

att gga ttg tag cta act atg gat ttg gac gat gta cac tat ttt aga 1245
 Ile Gly Leu Ser Leu Thr Leu Asp Leu Asp Asp Val His Tyr Phe Arg
 405 410 415

gac atc gga tat aga cac tcc aca ata cag cat tgt cca cat aat gcc 1290
 Asp Ile Gly Tyr Arg His Ser Thr Ile Gln His Cys Pro His Asn Ala
 420 425 430

atc ggg aat gag gaa ttc tcc tac tta gcc agt gac tca aaa ttc aaa 1335
 Met Gly Asn Glu Glu Phe Ser Tyr Leu Ala Ser Asp Ser Lys Phe Lys
 435 440 445

cgt aaa aac gcg gcc tcc gac gag gga agg gaa ttt ggg tgt ggc tgc 1380
 Arg Lys Asn Ala Ala Tyr Asp Glu Gly Arg Gln Phe Gly Cys Gly Cys
 450 455 460

agg tgc aga tgc ccc aag aaa aag cgt gaa att gag gat tcc atg ggt 1425
 Arg Cys Arg Cys Pro Lys Lys Lys Arg Gln Ile Glu Asp Ser Met Gly
 465 470 475 480

tcc tgc gta aat att tgg gta aat ctg att aac caa cag agg gga cac 1470
 Phe Cys Val Asn Ile Trp Val Asn Leu Leu Asn Gln Gln Arg Gly His
 485 490 495

gaa cgc cac gtc gaa gca ctc aac gcc aat gaa atg gag gag cac ata 1515
 Glu Arg His Val Glu Ala Leu Asn Gly Asn Gln Met Gln Glu His Ile
 500 505 510

agg gaa gac tat cta aga cag ttc gga aac tag 1560
 Arg Glu Asp Tyr Leu Arg Gln Phe Gly Asn
 515 520

<210> 170

<211> 522

<212> PRT

<213> Saccharomyces cerevisiae

<400> 170

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Cys Asn Leu Thr Ala Thr Cys Ile Leu Ala Ala Phe Val Ile Thr Met
20 25 30

Tyr Val Val Leu Val Ser Glu Pro Ala Ser Val Asp Gly Thr Met Gly
35 40 45

Asn Phe Leu Pro Phe Ser Lys Met Asp Leu Ala Thr Lys Arg Asp Arg
50 55 60

Pro Phe Tyr Ser Asn Cys Val Asn Thr Gln Asp Tyr Leu Leu Asn Pro
65 70 75 80

Ser Tyr Ile Lys Gln Asn Ala Ser Phe Val Met Leu Thr Arg Asn Gly
85 90 95

Glu Leu Glu Asp Val Ile Lys Thr Ile Asn Ser Ile Glu Glu His Phe
100 105 110

Asn Gln Trp Phe His Tyr Pro Tyr Val Phe Leu Asn Asp Gln Pro Phe
115 120 125

Glu Glu Asp Phe Lys Ala Lys Val Arg Asp Val Thr Val Gly Ala Leu
130 135 140

Val Glu Phe Gly Thr Ile Asp Glu Ile Ser Trp Asn Phe Pro Ser Asp
145 150 155 160

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Val Lys Asp Thr Phe Glu Phe Tyr Asn Ala Ile Glu Asp Gln Gly Asp
165 170 175

Arg Ser Ile Leu Tyr Gly Asn Leu Glu Ser Tyr His Lys Met Cys Arg
180 185 190

Phe Tyr Ser Gly Leu Phe Tyr Lys His Pro Leu Val Gln Lys Tyr Glu
195 200 205

Trp Tyr Trp Arg Leu Glu Pro Asp Val Glu Phe Phe Cys Asp Ile Thr
210 215 220

Tyr Asp Pro Phe Leu Glu Met Leu Arg Thr Asn Lys Lys Tyr Gly Phe
225 230 235 240

Thr Ile Ile Ile Pro Glu Leu Tyr Trp Thr Val Pro Asn Leu Phe Arg
245 250 255

His Thr Lys Ser Phe Ile Ser Gln Lys Gly Val Thr Leu Gly Ser Leu
260 265 270

Trp Lys Leu Phe Thr Lys Asp Tyr Asp Ile Phe Glu Ser Asp Asp Pro
275 280 285

Glu Leu Arg Asp Trp Ile Asn Tyr Asp Phe Gln Ala Lys Ala Lys Ile
290 295 300

Ser Gln Lys Ile Ala Ile Glu Gln Leu Leu Lys Lys Gly Asp Asp Phe
305 310 315 320

Gln Gln Ile Asn Asp Asp Lys Glu Gly Ile Met Asn Leu Ile His Lys
325 330 335

Ala Arg Ser Arg Lys His Ile Val Glu Asp Lys Phe Phe Asn Glu Glu
340 345 350

Tyr Asn Leu Cys His Phe Trp Ser Asn Phe Glu Ile Ala Arg Leu Ser
355 360 365

Val Phe Asp Asn Asp Ile Tyr Asn Ser Phe Phe Gln Tyr Leu Glu Lys
370 375 380

Ser Gly Gly Phe Trp Lys Glu Arg Trp Gly Asp Ala Pro Val His Ser
385 390 395 400

Ile Gly Leu Ser Leu Thr Leu Asp Leu Asp Asp Val His Tyr Phe Arg
405 410 415

Asp Ile Gly Tyr Arg His Ser Thr Ile Gln His Cys Pro His Asn Ala
420 425 430

Met Gly Asn Glu Glu Phe Ser Tyr Leu Ala Ser Asp Ser Lys Phe Lys
435 440 445

Arg Lys Asn Ala Ala Tyr Asp Glu Gly Arg Glu Phe Gly Cys Gly Cys
450 455 460

Arg Cys Arg Cys Pro Lys Lys Lys Arg Glu Ile Glu Asp Ser Met Gly
465 470 475 480

Phe Cys Val Asn Ile Trp Val Asn Leu Leu Asn Gln Gln Arg Gly His
485 490 495

399/762

Glu Arg His Val Glu Ala Leu Asn Gly Asn Glu Met Glu Glu His Ile
 500 505 510

Arg Glu Asp Tyr Leu Arg Gln Phe Gly Asn
 515 520

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 1 5 10 15
 cta ttt get tcc aag att ttc aag tgg act acc aau cct got cat ata 96
 Leu Phe Ala Ser Lys Ile Leu Thr Trp Thr Thr Asn Pro Ala His Ile
 20 25 30
 cgc cac cta cat gat ata agg ccg cct gca tca aac ttc aat acc caa 144
 Arg His Leu His Asp Ile Arg Pro Pro Ala Ser Asn Phe Asn Thr Gln
 35 40 45
 gaa tgg guc ccc ata ccg gag tct cca gca aac tca cca act cga cca 192
 Glu Ser Ala Pro Ile Pro Glu Ser Pro Ala Asn Ser Pro Thr Arg Pro
 50 55 60
 cag atg gca cct uua ccc aat ttg aac aaa aaa aat agt agt tta atg 240
 Gln Met Ala Pro Lys Pro Asn Leu Lys Lys Lys Asn Arg Ser Leu Met
 65 70 75 80
 tat tct att att ggg gtt tcc ata gta agt tta tat ttt tgg ttt aaa 288
 Tyr Ser Ile Ile Gly Val Ser Ile Val Gly Leu Tyr Phe Trp Phe Lys
 85 90 95

agt aac tcc agg aaa caa aaa cta cct ctt tgg gcg caa aaa gtc tgg	336
Ser Asn Ser Arg Lys Gln Lys Leu Pro Leu Ser Ala Gln Tyr Val Trp	
100 105 110	
aag gaa gcc ata tgg caa gaa agt gac aaa atg gat ttt aat tac aaa	384
Lys Glu Ala Ile Trp Gln Glu Ser Asp Lys Met Asp Phe Asn Tyr Lys	
115 120 125	
gaa gcg cta agg cgg tat att gag gcg ttg gat gaa tgc gat cgc tct	432
Glu Ala Leu Arg Arg Tyr Ile Glu Ala Leu Asp Glu Cys Asp Arg Ser	
130 135 140	
cat gtc gat tta ttg tca gat gat tat aac aga ata gag ctg aaa atc	480
His Val Asp Leu Leu Ser Asp Asp Tyr Thr Arg Ile Glu Leu Lys Ile	
145 150 155 160	
gct gaa atg tat gaa aag ctc aat atg ctt gaa gaa gcc caa aat ttg	528
Ala Glu Met Tyr Glu Lys Leu Asn Met Leu Glu Glu Ala Gln Asn Leu	
165 170 175	
tac caa gaa tta tta agt cgg ttt ttc gaa gcg ctg aat gtc cct ggc	576
Tyr Gln Glu Leu Leu Ser Arg Phe Phe Glu Ala Leu Asn Val Pro Gly	
180 185 190	
aaa gtc gat gag agt gaa aga gcc gag gtt tta aga aaa gac ttg aga	624
Lys Val Asp Glu Ser Glu Arg Gly Glu Val Leu Arg Lys Asp Leu Arg	
195 200 205	
atc ttg att aaa ccg tta gaa atc aat aag gac ata gaa agt gcc aag	672
Ile Leu Ile Tyr Ser Leu Glu Ile Asn Lys Asp Ile Glu Ser Gly Lys	
210 215 220	
aga aaa ttg cta caa cat tta ctt tta gct caa gag gaa att tta agc	720
Arg Lys Leu Leu Gln His Leu Leu Leu Ala Gln Glu Glu Ile Leu Ser	
225 230 235 240	
aaa tgg cca gag ttg aag gaa ttt ttc gaa aac aga aaa aag aag ctc	768
Lys Ser Pro Gln Leu Lys Glu Phe Phe Glu Asn Arg Lys Lys Lys Leu	
245 250 255	
tgg atg gta aua gac atc aat aga gac cct aat gat gat ttt aaa aca	816

Ser Met Val Lys Asp Ile Asn Arg Asp Pro Asn Asp Asp Phe Lys Thr			
260	265	270	
ttt gtt agt gag gaa aat att aag ttt qat qaa caa ggc tat atg att	864		
Phe Val Ser Glu Glu Asn Ile Lys Phe Asp Glu Gln Gly Tyr Met Ile			
275	280	285	
ttg gat ctg gaa aag aat agc agc gct tgg gaa ccc ttt aag gaa gaa	912		
Leu Asp Leu Glu Lys Asn Ser Ser Ala Trp Glu Pro Phe Lys Glu Glu			
290	295	300	
ttt ttt act gag aga gat tta tat aca gct tat tgt cag tca tca aaa	960		
Phe Phe Thr Ala Arg Asp Leu Tyr Thr Ala Tyr Cys Leu Ser Ser Lys			
305	310	315	320
gac ata gct gca gct cta agt tgc aag ata act agt gtg gaa tgg atg	1008		
Asp Ile Ala Ala Ala Leu Ser Cys Lys Ile Thr Ser Val Glu Trp Met			
325	330	335	
gtt atg gca gac atg cca cca gga cag ata ttg cta tca cag gca aat	1056		
Val Met Ala Asp Met Pro Pro Gly Gln Ile Leu Leu Ser Gln Ala Asn			
340	345	350	
ttg ggg tca ttg ttc tat ctt caa gca gaa aag cta gaa gct gac tta	1104		
Leu Gly Ser Leu Phe Tyr Leu Gln Ala Glu Lys Leu Glu Ala Asp Leu			
355	360	365	
aat caa tta gag caa aag aaa agt aaa gag tcc aac caa gag tta gat	1152		
Asn Gln Leu Glu Gln Lys Lys Ser Lys Glu Ser Asn Gln Glu Leu Asp			
370	375	380	
atg gga aca tac ata aaa gcc gtt aga ttc gta cgc aaa aat cgt gac	1200		
Met Gly Thr Tyr Ile Lys Ala Val Arg Phe Val Arg Lys Asn Arg Asp			
385	390	395	400
tta tgc ctg gaa aga gca caa aaa tgt tac gac agc gtt att gcg ttt	1248		
Leu Cys Leu Glu Arg Ala Gln Lys Cys Tyr Asp Ser Val Ile Ala Phe			
405	410	415	
gcc aaa aga aac aga aaa att agg ttt cat gly aag gal caa ctg gat	1296		
Ala Lys Arg Asn Arg Lys Ile Arg Phe His Val Tyr Asp Gln Leu Asp			
420	425	430	

cct tca att gca cag tca att gct cta tct acc tat gga atg ggg gtt 1344
 Pro Ser Ile Ala Gln Ser Ile Ala Leu Ser Thr Tyr Gly Met Gly Val
 435 440 445

tta agc att cat gaa ggt gtt ttg gct aaa gct gaa aaa cta ttc aaa 1392
 Leu Ser Leu His Glu Gly Val Leu Ala Lys Ala Gln Lys Leu Phe Lys
 450 455 460

gat tgg atc act atg gcc aag gag act gaa ttt aat gaa ctc att gca 1440
 Asp Ser Ile Thr Met Ala Lys Glu Thr Glu Phe Asn Glu Leu Leu Ala
 465 470 475 480

gaa gct gaa aag gaa cta gaa cag acg acc gtc tlg aat gag gcc aat 1488
 Glu Ala Glu Lys Glu Leu Glu Lys Thr Thr Val Leu Lys Ala Ala Lys
 485 490 495

aaa gag ggt tta aac taa 1506
 Lys Glu Gly Leu Asn
 500

<210> 172
 <211> 501
 <212> FRT
 <213> *Saccharomyces cerevisiae*

<400> 172

Met Leu Leu Gln Gly Met Arg Leu Ser Gln Arg Leu His Lys Arg His
 1 5 10 15

Leu Phe Ala Ser Lys Ile Leu Thr Trp Thr Thr Asn Pro Ala His Ile
 20 25 30

Arg His Leu His Asp Ile Arg Pro Pro Ala Ser Asn Phe Asn Thr Gln
 35 40 45

Glu Ser Ala Pro Ile Pro Glu Ser Pro Ala Asn Ser Pro Thr Arg Pro

"Seq.1"

50	55	60
Gln Met Ala Pro Lys Pro Asn Leu Lys Lys Lys Asn Arg Ser Leu Met		
65	70	75
		80
Tyr Ser Phe Ile Gly Val Ser Ile Val Gly Leu Tyr Phe Trp Phe Lys		
85	90	95
Ser Asn Ser Arg Lys Gln Lys Leu Pro Leu Ser Ala Gln Lys Val Trp		
100	105	110
Lys Glu Ala Phe Trp Gln Glu Ser Asp Lys Met Asp Phe Asn Tyr Lys		
115	120	125
Glu Ala Leu Arg Arg Tyr Ile Glu Ala Leu Asp Glu Cys Asp Arg Ser		
130	135	140
His Val Asp Leu Leu Ser Asp Asp Tyr Thr Arg Ile Glu Leu Lys Phe		
145	150	155
		160
Ala Glu Met Tyr Glu Lys Leu Asn Met Leu Glu Glu Ala Gln Asn Leu		
165	170	175
Tyr Gln Glu Leu Leu Ser Arg Phe Phe Glu Ala Leu Asn Val Pro Gly		
180	185	190
Lys Val Asp Glu Ser Glu Arg Gly Glu Val Leu Arg Lys Asp Leu Arg		
195	200	205
Ile Leu Ile Lys Ser Leu Glu Ile Asn Lys Asp Ile Glu Ser Gly Lys		
210	215	220

Arg Lys Leu Leu Gln His Leu Leu Leu Ala Gln Gln Glu Ile Leu Ser
225 230 235 240

Lys Ser Pro Gln Leu Lys Glu Phe Phe Glu Asn Arg Lys Lys Lys Leu
245 250 255

Ser Met Val Lys Asp Ile Asn Arg Asp Pro Asn Asp Asp Phe Lys Thr
260 265 270

Phe Val Ser Glu Glu Asn Ile Lys Phe Asp Glu Gln Gly Tyr Met Ile
275 280 285

Leu Asp Leu Glu Lys Asn Ser Ser Ala Trp Glu Pro Phe Lys Glu Glu
290 295 300

Phe Phe Thr Ala Arg Asp Leu Tyr Thr Ala Tyr Cys Leu Ser Ser Lys
305 310 315 320

Asp Ile Ala Ala Ala Leu Ser Cys Lys Ile Thr Ser Val Glu Trp Met
325 330 335

Val Met Ala Asp Met Pro Pro Gly Gln Ile Leu Leu Ser Gln Ala Asn
340 345 350

Leu Gly Ser Leu Phe Tyr Leu Gln Ala Glu Lys Leu Glu Ala Asp Leu
355 360 365

Asn Gln Leu Glu Gln Lys Lys Ser Lys Glu Ser Asn Gln Glu Leu Asp
370 375 380

Met Gly Thr Tyr Ile Lys Ala Val Arg Phe Val Arg Lys Asn Arg Asp

<100> 173

Seq. ID NO: 1

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Met	Ser	Ile	Glu	Asn	Leu	Lys	Ser	Phe	Asp	Pro	Phe	Ala	Asp	Thr	Gly	
1				5					10					15		

gac	gac	gaa	acc	gcc	act	cca	aac	tat	att	cat	att	cgt	atc	caa	cag	96
Asp	Asp	Glu	Thr	Ala	Thr	Ser	Asn	Tyr	Ile	His	Ile	Arg	Ile	Gln	Gln	
			20					25					30			

aga	aat	ggg	aga	aaa	act	tta	act	acg	gtg	caa	ggg	gtc	cca	gag	gaa	144
Arg	Asn	Gly	Arg	Lys	Thr	Leu	Thr	Thr	Val	Gln	Gly	Val	Pro	Glu	Glu	
		35					40					45				

tat	gat	tta	aag	aga	att	cct	aag	gtc	cta	aag	aag	gac	ttt	gca	tgt	192
Tyr	Asp	Leu	Lys	Arg	Ile	Leu	Lys	Val	Leu	Lys	Lys	Asp	Phe	Ala	Cys	
		50				55					60					

aat	ggg	aac	att	gtc	aag	gat	cca	gaa	atg	ggg	gag	att	att	cag	ttg	240
Asn	Gly	Asn	Ile	Val	Lys	Asp	Pro	Glu	Met	Gly	Glu	Ile	Ile	Gln	Leu	
65					70					75				80		

cag	ggg	gac	caa	aga	gca	aag	gtt	tgc	gaa	ttt	atg	atc	ccc	caa	ctg	288
Gln	Gly	Asp	Gln	Arg	Ala	Lys	Val	Cys	Glu	Phe	Met	Ile	Ser	Gln	Leu	
				85					90					95		

gga	ttg	cca	aag	aag	aac	att	aaa	att	cat	ggg	ttt	taa				327
Gly	Leu	Gln	Lys	Lys	Asn	Ile	Lys	Ile	His	Gly	Phe					
			100				105									

<210> 174

<211> 106

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 174

Met	Ser	Ile	Glu	Asn	Leu	Lys	Ser	Phe	Asp	Pro	Phe	Ala	Asp	Thr	Gly
1				5					10					15	

Asp	Asp	Glu	Thr	Ala	Thr	Ser	Asn	Tyr	Ile	His	Ile	Arg	Ile	Gln	Gln
			20					25						30	

Arg Asn Gly Arg Lys Thr Leu Thr Thr Val Gln Gly Val Pro Glu Gln
 35 40 45

Tyr Asp Leu Lys Arg Ile Leu Lys Val Leu Lys Lys Asp Phe Ala Cys
 50 55 60

Asn Gly Asn Ile Val Lys Asp Pro Glu Met Gly Glu Ile Ile Gln Leu
 65 70 75 80

Gln Gly Asp Gln Arg Ala Lys Val Cys Glu Phe Met Ile Ser Gln Leu
 85 90 95

Gly Leu Gln Lys Lys Asn Ile Lys Ile His Gly Phe
 100 105

<210> 175

<211> 669

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (669)

<400> 175

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Met Thr Val Val Ile Gly Val Leu Ala Leu Gln Gly Ala Phe Ile Glu

1 5 10 15

cat gtg cga cac gta gaa aaa tgc atc gtc gaa aac agg gat ttc tat 96

His Val Arg His Val Glu Lys Cys Ile Val Glu Asn Arg Asp Phe Tyr

20 25 30

gaa aaa aaa cta tct gtg atg acc gtg aag gat aaa aat caa cta gct 144

Seq. ID No. 102 (1000 bp)

Glu Lys Lys Leu Ser Val Met Thr Val Lys Asp Lys Asn Gln Leu Ala	
35 40 45	
caa tgt gat gca ttg atc ata cct qqq qqa gaa tgg act gca atg tcc	192
Gln Cys Asp Ala Leu Ile Ile Pro Gly Gly Glu Ser Thr Ala Met Ser	
50 55 60	
cct att gca gaa aga cca gga ttt tac gac gat ctc tac gca ttc gta	240
Leu Ile Ala Glu Arg Thr Gly Phe Tyr Asp Asp Leu Tyr Ala Phe Val	
65 70 75 80	
cac aac cca agc aag gta acc tgg ggt act tgt gca ggt atg att tat	288
His Asn Pro Ser Lys Val Thr Asp Gly Thr Cys Ala Gly Met Ile Tyr	
85 90 95	
att tca cca cca tta tct aac gaa gaa aaa ctg gtc aag acg ctg aat	336
Ile Ser Gln Gln Leu Ser Asn Glu Glu Lys Leu Val Lys Thr Leu Asn	
100 105 110	
tca cca aag gtt aaa gta aaa aga aat gca ttt ggg aga caa got cag	384
Leu Leu Lys Val Lys Val Lys Arg Asn Ala Phe Gly Arg Gln Ala Gln	
115 120 125	
tct cct acc cgg att Lys gac ttt tca aac ttt att cct cac tgc aat	432
Ser Ser Thr Arg Ile Cys Asp Phe Ser Asn Phe Ile Pro His Cys Asn	
130 135 140	
gat ttt cct gct act ttt ata aga gcc cca gta ata gaa gag ctg ctg	480
Asp Phe Pro Ala Thr Phe Ile Arg Ala Pro Val Ile Glu Glu Val Leu	
145 150 155 160	
gat cct gaa cat gtg cag gtc ctg tac aaa tta gat ggg aag gat aat	528
Asp Pro Glu His Val Gln Val Leu Tyr Lys Leu Asp Gly Lys Asp Asn	
165 170 175	
ggc ggt caa gaa cta att gtt gcc gct aag caa aaa aac aat att att	576
Gly Gly Gln Gln Leu Ile Val Ala Ala Lys Gln Lys Asn Asn Ile Leu	
180 185 190	
ggg aca tca ttt cat ccc gaa ttg gca gaa aac gat ata cgg ttt cac	624
Ala Thr Ser Phe His Pro Glu Leu Ala Glu Asn Asp Ile Arg Thr His	
195 200 205	

gaa tgg ttc atc aga gaa ttt gtt ctt aac aac tac agt aaa taa 669
 Asp Trp Phe Ile Arg Glu Phe Val Leu Lys Asn Tyr Ser Lys
 210 215 220

<210> 176
 <211> 222
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 176

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 1 5 10 15

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 20 25 30

Glu Lys Lys Leu Ser Val Met Thr Val Lys Asp Lys Asn Gln Leu Ala
 35 40 45

Gln Cys Asp Ala Leu Ile Ile Pro Gly Gly Glu Ser Thr Ala Met Ser
 50 55 60

Leu Ile Ala Gln Arg Thr Gly Phe Tyr Asp Asp Leu Tyr Ala Phe Val
 65 70 75 80

His Asn Pro Ser Lys Val Thr Trp Gly Thr Cys Ala Gly Met Ile Tyr
 85 90 95

Ile Ser Gln Gln Leu Ser Asn Glu Gln Lys Leu Val Lys Thr Leu Asn
 100 105 110

Leu Leu Lys Val Lys Val Lys Arg Asn Ala Phe Gly Arg Gln Ala Gln

FIG. 1. Amino acid sequence of the protein.

115	120	125
Ser Ser Thr Arg Ile Cys Asp Phe Ser Asn Phe Ile Pro His Cys Asn		
130	135	140
Asp Phe Pro Ala Thr Phe Ile Arg Ala Pro Val Ile Glu Glu Val Leu		
145	150	155
Asp Pro Glu His Val Gln Val Leu Tyr Lys Leu Asp Gly Lys Asp Asn		
165	170	175
Gly Gly Gln Gln Leu Ile Val Ala Ala Lys Gln Lys Asn Asn Ile Leu		
180	185	190
Ala Thr Ser Phe His Pro Gln Leu Ala Glu Asn Asp Ile Arg Phe His		
195	200	205
Asp Trp Phe Ile Arg Glu Phe Val Leu Lys Asn Tyr Ser Lys		
210	215	220

<210> 177
 <211> 675
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(675)

<400> 177
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 Met Lys Ile Leu Thr Gln Asp Glu Ile Glu Ala His Arg Ser His Thr
 1 5 10 15

SEQUENCE LISTING

cta aag ggt ggt att gaa ggt gcc att gcc gga ttt gca atc tat gct	96
Leu Lys Gly Gly Ile Glu Gly Ala Leu Ala Gly Phe Ala Ile Ser Ala	
20 25 30	
ata att ttc aaa gtc cta cca aga agg tac cca aaa ttc aag cct tcc	144
Ile Ile Phe Lys Val Leu Pro Arg Arg Tyr Pro Lys Phe Lys Pro Ser	
35 40 45	
act cta aca tgg tcc ata aaa acc gcc att tgg atc acc cct ccc aag	192
Thr Leu Thr Trp Ser Ile Lys Thr Ala Leu Trp Ile Thr Pro Pro Thr	
50 55 60	
gtc ttg act gct ata tct gag gag gag gcc tcc aac aat ttc gac gct	240
Val Leu Thr Ala Ile Cys Ala Glu Glu Ala Ser Asn Asn Phe Asp Ala	
65 70 75 80	
aca atg tac gga tcc ggt tcc tcc tcc gaa gac gca cta gat gag cac	288
Thr Met Tyr Gly Ser Gly Ser Ser Ser Glu Asp Ala Leu Asp Glu His	
85 90 95	
aga aga tgg aag agt ttg agt aca aag gac aag ttt gtc gaa ggt cta	336
Arg Arg Trp Lys Ser Leu Ser Thr Lys Asp Lys Phe Val Gln Gly Leu	
100 105 110	
tct aat aac aag tat aag atc atc acc ggt gcc tgg gcc gct tcc atg	384
Ser Asn Asn Lys Tyr Lys Ile Ile Thr Gly Ala Trp Ala Ala Ser Leu	
115 120 125	
tat ggg tcc tgg gta atc gtg aac aaa gac ccc atc atg acc aaa gct	432
Tyr Gly Ser Trp Val Ile Val Asn Lys Asp Pro Ile Met Thr Lys Ala	
130 135 140	
cag aag atc gtg cag gcc aga atg tac gct cca ttc att acc gtc ggg	480
Gln Lys Ile Val Gln Ala Arg Met Tyr Ala Gln Phe Ile Thr Val Gly	
145 150 155 160	
ctg ctg ctg gcc tcc gtt ggt ttg agc atg tac gag aat aag tta cct	528
Leu Leu Leu Ala Ser Val Gly Leu Ser Met Tyr Glu Asn Lys Leu His	
165 170 175	
cct aat aaa caa aag gtc aac gaa atg cgc cgc tgg gaa aac gca ctg	576
Pro Asn Lys Gln Lys Val Asn Glu Met Arg Arg Trp Glu Asn Ala Leu	

	180	185	190	
	agg gtc ggc gaa gag gaa gag aga ctc gag aac gag gga aga agg acc			624
	Arg Val Ala Glu Glu Glu Glu Arg Leu Glu Lys Glu Gly Arg Arg Thr			
	195	200	205	
	ggc cac ggt tct aac gaa gaa aga ata aac tcc aag atc ttc aag tcc			672
	Gly Tyr Val Ser Asn Glu Glu Arg Ile Asn Ser Lys Ile Phe Lys Ser			
	210	215	220	
	taa			675

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<210> 178
<211> 224
<212> PRT
<213> Saccharomyces cerevisiae
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<400> 178

Met Lys Ile Leu Thr Gln Asp Glu Ile Gly Ala His Arg Ser His Thr
1 5 10 15

Leu Lys Gly Gly Ile Glu Gly Ala Leu Ala Gly Phe Ala Ile Ser Ala
20 25 30

Ile Ile Phe Lys Val Leu Pro Arg Arg Tyr Pro Lys Phe Lys Pro Ser
35 40 45

Thr Leu Thr Trp Ser Ile Lys Thr Ala Leu Trp Ile Thr Pro Pro Thr
50 55 60

Val	Leu	Thr	Ala	Ile	Cys	Ala	Glu	Glu	Ala	Ser	Asn	Asn	Phe	Asp	Ala
65					70					75					80

Thr Met Tyr Gly Ser Gly Ser Ser Ser Glu Arg Ala Val Asp Glu His
85 90 95

FIG. 2. Amino acid sequence of the protein.

Arg Arg Trp Lys Ser Leu Ser Thr Lys Asp Lys Phe Val Glu Gly Leu
100 105 110

Ser Asn Asn Lys Tyr Lys Ile Ile Thr Gly Ala Trp Ala Ala Ser Leu
115 120 125

Tyr Gly Ser Trp Val Ile Val Asn Lys Asp Pro Ile Met Thr Lys Ala
130 135 140

Gln Lys Ile Val Gln Ala Arg Met Tyr Ala Gln Phe Ile Thr Val Gly
145 150 155 160

Leu Leu Leu Ala Ser Val Gly Leu Ser Met Tyr Glu Asn Lys Leu His
165 170 175

Pro Asn Lys Gln Lys Val Asn Glu Met Arg Arg Trp Glu Asn Ala Leu
180 185 190

Arg Val Ala Glu Glu Glu Glu Arg Leu Glu Lys Glu Gly Arg Arg Thr
195 200 205

Gly Tyr Val Ser Asn Glu Glu Arg Ile Asn Ser Tyr Ile Phe Lys Ser
210 215 220

<210> 179

<211> 1461

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

FIG. 14. Amino acid sequence.

<222> (1) .. (1461)

<400> 179

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Met	Ser	His	Thr	Leu	Lys	Ser	Lys	Thr	Ileu	Gln	Glu	Leu	Asp	Ile	Glu	
1				5					10					15		

gag	atc	aag	gaa	act	aac	cca	tgg	ctc	aaa	cta	ggt	caa	ggg	cag	agg	96
Glu	Ile	Lys	Glu	Thr	Asn	Pro	Leu	Leu	Lys	Leu	Val	Gln	Gly	Gln	Arg	
			20					25					30			

att	gtc	caa	gtt	cgg	gaa	cta	gtg	ctt	gag	tct	ggc	gtg	gtc	ata	aac	144
Ile	Val	Gln	Val	Pro	Glu	Leu	Val	Leu	Glu	Ser	Gly	Val	Val	Ile	Asn	
			25				40						45			

aac	ttc	ccc	att	gct	tat	aag	acg	tgg	ggc	aca	ctg	aat	gaa	gct	ggc	192
Asn	Phe	Pro	Ile	Ala	Tyr	Lys	Thr	Trp	Gly	Thr	Leu	Asn	Glu	Ala	Gly	
			50				55					60				

cat	aac	gtc	ctg	gta	att	tgt	cat	gac	tgg	act	ggg	tcc	gca	gat	gtt	240
Asp	Asn	Val	Leu	Val	Ile	Cys	His	Ala	Leu	Thr	Gly	Ser	Ala	Asp	Val	
65					70					75				80		

gct	gac	cgg	tgg	ggc	ccc	ctt	ctg	ggc	aac	gac	tta	gca	ttc	gac	cca	288
Ala	Asp	Trp	Trp	Gly	Pro	Leu	Leu	Gly	Asn	Asp	Leu	Ala	Phe	Asp	Pro	
				95				90					95			

tcc	agg	ttt	ttt	atc	ata	tgt	tta	aac	tct	atg	ggc	tct	cca	tat	ggg	336
Ser	Arg	Phe	Phe	Ile	Ile	Cys	Leu	Asn	Ser	Met	Gly	Ser	Pro	Tyr	Gly	
			100					105					110			

tct	ttt	tgg	cca	tta	acg	ata	aat	gag	gag	acg	ggc	gtt	aga	tat	gga	384
Ser	Phe	Ser	Pro	Leu	Thr	Ile	Asn	Glu	Glu	Thr	Gly	Val	Arg	Tyr	Gly	
			115					120					125			

ccc	gaa	ttc	cca	tta	tgt	act	ctg	cgc	gat	gac	gtt	aga	gct	cac	aga	432
Pro	Glu	Phe	Pro	Leu	Cys	Thr	Val	Arg	Asp	Asp	Val	Arg	Ala	His	Arg	
			130				135					140				

att	gtt	ctg	gat	tct	ctg	gga	gta	aag	tca	ata	gcc	tgt	gtt	att	ggt	480
Ile	Val	Leu	Asp	Ser	Leu	Gly	Val	Lys	Ser	Ile	Ala	Cys	Val	Pro	Gly	
145					150					155				160		

ggc tct atg gag ggg atg ctg agt ttg gaa tgg gct gcc atg tat ggt Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly 165 170 175	528
aag gaa tat gtg aag aat atg ggt gct utg gcg aca taa gca aga cat Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His 180 185 190	576
tct gcc tgg tgc ata tgg tgg tct gag gct caa aga caa tgg att cac Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr 195 200 205	624
tca gat ccc aac tac ttg gac ggg tac tat ccg gta gag gag caa cct Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Gln Glu Gln Pro 210 215 220	672
gag gcc gga cta tgg gcl gca agt atg tct gca ttg tlg acg tac agg Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg 225 230 235 240	720
aca aga aac agt ttc gag aac aca ttc tcc aga aga tct cct tca ata Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile 245 250 255	768
gca caa caa caa aca gct caa agg gag gag aca cgc aca cca tct acg Ala Gln Gln Gln Lys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr 260 265 270	816
gtc agc qaa cao tcc cta caa atc cao aat gat ggg tat aca ace aaa Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys 275 280 285	864
ggc agc act gcc atc gct ggc att tct ggg caa aaa ggt caa agc gtg Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Gln Lys Gly Gln Ser Val 290 295 300	912
gtg tcc acc gca tct tct tgg gat leu thg aat tct tca aca tgg atg Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met 305 310 315 320	960
act tgg gta agt tct gta acg ggt gaa gtg aag gac ata aag cct gag 1008	

FIG. 11. Amino acid sequence of the protein.

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Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala	
325 330 335	
cag aag Lal Ltt tct gca caa agt tac ttg agg tac cag ggc aca aag	1056
Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys	
340 345 350	
ttc atc aat agg ttc gac gcc aat tgt tac att gcc atc aca cgt aaa	1104
Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys	
355 360 365	
ctg gat aag cac gat ttg gca cga gac aga gta gat gac atc act gag	1152
Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu	
370 375 380	
gtc ctc tct acc atc caa caa cca tgc ctg ata atc ggt atc caa tcc	1200
Val Leu Ser Thr Ile Gln Gln Pro Ser Leu Ile Ile Gly Ile Gln Ser	
385 390 395 400	
gat gga ctg ttc aca tat tca gaa caa gaa ltt ttg gct gag cac ata	1248
Asp Gly Leu Thr Thr Tyr Ser Glu Gln Glu Phe Asn Ala Glu His Ile	
405 410 415	
cag aag tgg caa cta gaa aaa att gaa tct ccc gaa ggt cac gat gcc	1296
Pro Lys Ser Gln Leu Glu Lys Ile Gln Ser Pro Glu Gly His Asp Ala	
420 425 430	
ttc cta ttg gag ttt aag ctg ata aac aaa ctg ata gta caa ttt tta	1344
Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu	
435 440 445	
aaa acc aac tgc aag gcc att acc gat gcc gct cca aga gct tgg gga	1392
Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly	
450 455 460	
ggc gac gtl ggc aac gat gaa acg aag acg tct gtc ttt ggt gag gcc	1440
Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala	
465 470 475 480	
gaa gaa gtt acc aac tgg tag	1488
Glu Glu Val Thr Asn Trp	
485	

<210> 100
 <211> 486
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<410> 180

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Glu Ile Lys Glu Thr Asn Pro Leu Leu Cys Leu Val Gln Gly Gln Arg
 20 25 30

Ile Val Gln Val Pro Glu Leu Val Leu Glu Ser Gly Val Val Ile Asn
 35 40 45

Asn Phe Pro Ile Ala Tyr Lys Thr Trp Gly Thr Leu Asn Glu Ala Gly
 50 55 60

Asp Asn Val Leu Val Ile Cys His Ala Leu Thr Gly Ser Ala Asp Val
 65 70 75 80

Ala Asp Trp Trp Gly Pro Leu Leu Gly Asn Asp Leu Ala Phe Asp Pro
 85 90 95

Ser Arg Phe Phe Ile Ile Cys Leu Asn Ser Met Gly Ser Pro Tyr Gly
 100 105 110

Ser Phe Ser Pro Leu Thr Ile Asn Glu Glu Thr Gly Val Arg Tyr Gly
 115 120 125

Pro Glu Phe Pro Leu Cys Thr Val Arg Asp Asp Val Arg Ala His Arg

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130 135 140

Ile Val Leu Asp Ser Leu Gly Val Lys Ser Ile Ala Cys Val Ile Gly
145 150 155 160

Gly Ser Met Gly Gly Met Leu Ser Leu Glu Trp Ala Ala Met Tyr Gly
165 170 175

Lys Glu Tyr Val Lys Asn Met Val Ala Leu Ala Thr Ser Ala Arg His
180 185 190

Ser Ala Trp Cys Ile Ser Trp Ser Glu Ala Gln Arg Gln Ser Ile Tyr
195 200 205

Ser Asp Pro Asn Tyr Leu Asp Gly Tyr Tyr Pro Val Glu Glu Gln Pro
210 215 220

Val Ala Gly Leu Ser Ala Ala Arg Met Ser Ala Leu Leu Thr Tyr Arg
225 230 235 240

Thr Arg Asn Ser Phe Glu Asn Lys Phe Ser Arg Arg Ser Pro Ser Ile
245 250 255

Ala Gln Gln Gln Pys Ala Gln Arg Glu Glu Thr Arg Lys Pro Ser Thr
260 265 270

Val Ser Glu His Ser Leu Gln Ile His Asn Asp Gly Tyr Lys Thr Lys
275 280 285

Ala Ser Thr Ala Ile Ala Gly Ile Ser Gly Glu Lys Gly Gln Ser Val
290 295 300

Val Ser Thr Ala Ser Ser Ser Asp Ser Leu Asn Ser Ser Thr Ser Met
305 310 315 320

Thr Ser Val Ser Ser Val Thr Gly Glu Val Lys Asp Ile Lys Pro Ala
325 330 335

Gln Thr Tyr Phe Ser Ala Gln Ser Tyr Leu Arg Tyr Gln Gly Thr Lys
340 345 350

Phe Ile Asn Arg Phe Asp Ala Asn Cys Tyr Ile Ala Ile Thr Arg Lys
355 360 365

Leu Asp Thr His Asp Leu Ala Arg Asp Arg Val Asp Asp Ile Thr Glu
370 375 380

Val Leu Ser Thr Ala Gln Glu Pro Ser Leu Ile Ile Gly Ile Gln Ser
385 390 395 400

Asp Gly Leu Phe Thr Tyr Ser Glu Gln Glu Phe Leu Ala Glu His Ile
405 410 415

Pro Lys Ser Gln Leu Glu Lys Ile Glu Ser Pro Glu Gly His Asp Ala
420 425 430

Phe Leu Leu Glu Phe Lys Leu Ile Asn Lys Leu Ile Val Gln Phe Leu
435 440 445

Lys Thr Asn Cys Lys Ala Ile Thr Asp Ala Ala Pro Arg Ala Trp Gly
450 455 460

Gly Asp Val Gly Asn Asp Glu Thr Lys Thr Ser Val Phe Gly Glu Ala

Sequence of the nucleotide sequence of the DNA

465

470

475

480

Glu Glu Val Thr Asn Trp

485

<210> 181

<211> 309

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

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<400> 181

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Met Ser Phe Arg Lys Lys Lys Leu Lys Pro Pro Ala Gly Ser Gln Phe

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att ata aac gac tcc ata atg agc tac att gac cgc acg aaa aca cta 96

Ile Ile Asn Asp Ser Ile Met Ser Tyr Ile Asp Arg Thr Lys Thr Leu

20 25 30

ata agg atg att gga tgc aag aac cag tac ata aaa gca cgt atg aaa 144

Ile Arg Met Ile Gly Cys Lys Asn Gln Tyr Ile Lys Ala Arg Met Lys

35 40 45

gat aag aac ttc ttc tat acg aag caa ttc cgt aca gcc aaa aac aaa 192

Asp Lys Thr Phe Phe Tyr Thr Lys Gln Phe Arg Thr Ala Lys Asn Lys

50 55 60

ttt ttc ttt cat atg tac cat tgg gag gcc act cat att aac gtt gac 240

Phe Phe Phe His Leu Tyr His Trp Glu Ala Thr His Ile Asn Val Asp

65 70 75 80

cac tat ata tgt aca tgt cat ccc att tct tgg ggc tct ata ggt aag 288

His Tyr Ile Cys Thr Cys His Pro Ile Phe Trp Gly Ser Ile Gly Gln

85 90 95

FIG. 1: Amino acid sequence of the protein

421/762

aaa ctc agg aga tcc gcc tga

309

Lys Leu Arg Arg Ser Ala

100

<210> 182

<211> 102

<212> PRT

<213> Saccharomyces cerevisiae

<400> 182

Met Ser Phe Arg Lys Lys Lys Leu Lys Pro Pro Ala Gly Ser Gln Phe

1

5

10

15

Ile Ile Asn Asp Ser Ile Met Ser Tyr Ile Asp Arg Thr Lys Thr Leu

20

25

30

Ile Arg Met Ile Gly Cys Lys Asn Gln Tyr Ile Lys Ala Arg Met Lys

35

40

45

Asp Lys Thr Phe Phe Tyr Thr Lys Gln Phe Arg Thr Ala Lys Asn Lys

50

55

60

Phe Phe Phe His Leu Tyr His Trp Glu Ala Thr His Ile Asn Val Asp

65

70

75

80

His Tyr Ile Cys Thr Cys His Pro Ile Phe Trp Gly Ser Ile Gly Gln

85

90

95

Lys Leu Arg Arg Ser Ala

100

<210> 183

<211> 1605

SEQ. ID NO. 1: CDS OF THE INVENTION

422/762

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (1605)

<400> 183

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ccg acc act act gaa gaa gtc aaa aaa gaa gaa gaa caa aat aag gct	96
Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Gln Asn Lys Ala	
20 25 30	
ggc agt ggt acc tgg caa cta gat caa cta gcc gca cta caa gca tta	144
Gly Ser Gly Thr Ser Gln Leu Asp Gln Leu Ala Ala Leu Gln Ala Leu	
35 40 45	
tct tct agc tgg aac aaa cta aat aat cca aat agt aac aac act agt	192
Ser Ser Ser Leu Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser	
50 55 60	
agt aat aat agt aac cca gac aca tct tct agt aag caa gat gcc act	240
Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr	
65 70 75 80	
ggc aat gac aag gaa ggt tcc aat gaa gac act aag aat gaa aac aac	288
Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Gln Lys Lys	
85 90 95	
caa gaa agc gct aca tca gca aat gcc aat gcc aac gcc agt tct gca	336
Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn Ala Ser Ser Ala	
100 105 110	
gga cct tct gcc tta cct tgg gaa caa ctt caa caa acc atg tca caa	384
Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Gln Thr Met Ser Gln	
115 120 125	
ttc cag caa cca tct tct caa tca cca cct caa cag caa gta act caa	432

FIG. 1. Amino acid sequence of the protein.

Phe	Gln	Gln	Pro	Ser	Ser	Gln	Ser	Pro	Pro	Gln	Gln	Gln	Val	Thr	Gln		
130							135						140				
acc	aaa	gaq	gaa	cgt	log	aaa	gag	gat	tgg	tct	aaa	gaa	agt	tgc	aag	480	
Thr	Lys	Glu	Glu	Arg	Ser	Lys	Ala	Asp	Leu	Ser	Lys	Gln	Ser	Cys	Lys		
145						150					155			160			
atg	ttc	att	ggc	ggt	ctg	aat	tgg	gac	act	acg	gaa	gal	aet	ctt	cgc	528	
Met	Phe	Ile	Gly	Gly	Leu	Asn	Trp	Asp	Thr	Thr	Glu	Asp	Asn	Leu	Arg		
					165				170					175			
gaa	tat	ttt	ggc	aag	tat	ggc	acc	gtc	act	gat	tty	aaa	alc	atg	aaa	576	
Glu	Tyr	Phe	Gly	Lys	Tyr	Gly	Thr	Val	Thr	Asp	Leu	Lys	Ile	Met	Lys		
			180					185					190				
gac	cct	gca	aca	ggc	aga	tct	aga	ggg	ttc	ggc	ttc	tta	tct	ttt	gaa	624	
Asp	Pro	Ala	Thr	Gly	Arg	Ser	Arg	Gly	Phe	Gly	Phe	Leu	Ser	Phe	Gln		
			195				200						205				
aaa	cct	tct	agt	gtt	gat	gaa	gtg	gta	aag	aca	caa	cat	atc	ctc	gat	672	
Lys	Pro	Ser	Ser	Val	Asp	Gly	Val	Val	Lys	Thr	Gln	His	Ile	Leu	Asp		
	210					215					220						
ggc	aaa	gtt	atc	gac	cca	aaa	aga	gct	atc	cca	aga	gac	gag	caa	gat	720	
Gly	Lys	Val	Ile	Asp	Pro	Lys	Arg	Ala	Ile	Pro	Arg	Asp	Glu	Gln	Asp		
225					230					235			240				
aaa	acc	ggc	aaa	atc	ttt	gtc	ggc	ggc	att	ggc	cct	gat	gtg	aga	cca	768	
Lys	Thr	Gly	Lys	Ile	Phe	Val	Gly	Gly	Ile	Gly	Pro	Asp	Val	Arg	Pro		
			245					250				255					
aag	gaa	ttt	gaa	gaa	ttt	ttt	tct	cag	ggg	ggc	acg	att	atc	gat	ggc	816	
Lys	Glu	Phe	Glu	Glu	Phe	Phe	Ser	Gln	Trp	Gly	Thr	Ile	Ile	Asp	Ala		
			260					265				270					
caa	ctg	atg	tta	gat	aag	gat	acc	ggc	caa	tca	aga	ggc	tct	ggc	ttt	864	
Gln	Leu	Met	Leu	Asp	Lys	Asp	Thr	Gly	Gln	Ser	Arg	Gly	Phe	Gly	Phe		
		275					280					285					
gtg	acg	tat	gac	tcc	gct	gac	goc	gtc	gac	aga	gtt	tgt	cag	aat	aaa	912	
Val	Thr	Tyr	Asp	Ser	Ala	Asp	Ala	Val	Asp	Arg	Val	Cys	Gln	Asn	Lys		
		290					295					300					

ttc atc gat ttc aac gat cgc aag atc gaa atc aag aga ggt gag cca	960
Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Gln Pro	
305 310 315 320	
aga cat atg caa caa aac tca tca aac aat ggt ggt aac aat ggt gga	1008
Arg His Met Gln Gln Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly	
325 330 335	
aac aac atg aat cgt cgt ggc ggt aac ttc ggt aac caa ggc gat ttc	1056
Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Gln Gly Asp Phe	
340 345 350	
aac caa atg tat caa aac cct atg atg ggc ggt tac aac cca atg atg	1104
Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met	
355 360 365	
aat ccc caa gca atg aca gat tac tat caa aag atg caa gaa tat tac	1152
Asn Pro Gln Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr	
370 375 380	
caa caa atg caa aag caa act cgt atg gat tat act caa atg tac caa	1200
Gln Gln Met Gln Lys Gln Thr Gly Met Asp Tyr Thr Gln Met Tyr Gln	
385 390 395 400	
caa caa atg cag caa atg gca atg atg atg cca ggg ttt gcc atg cca	1248
Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro	
405 410 415	
cct aat gca atg act ttc aac cca cca cag caa gat tca aat gcc act	1296
Pro Asn Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr	
420 425 430	
caa ggt tcc cca gca cct tcc gat tcc gat aat aat aaa tcc aat gac	1344
Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp	
435 440 445	
gtc caa act att ggt aat aca tca aac act gac tct ggt tca ccg cca	1392
Val Gln Thr Ile Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro	
450 455 460	
ttg aat tta cct aat ggt cca aag ggc cca tca caa tac aat gat gac	1440

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Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
 465 470 475 480

 cac aat agc ggt tat ggc tac aac cgt gat cgc ggt gat cgt gat cgt 1460
 His Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asp Arg
 485 490 495

 aac gat cgt gac cgc gat tac aat cac cgt agt ggt gga aac cat aga 1536
 Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
 500 505 510

 aga aac ggc cgt ggt ggt cgc ggt gga tac aat aga cgt aat aat ggc 1564
 Arg Asn Gly Arg Gly Gly Arg Gly Gly Tyr Asn Arg Arg Asn Asn Gly
 515 520 525

 tac cat cca tat aat agg taa 1605
 Tyr His Pro Tyr Asn Arg
 530

<210> 184

<211> 534

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 184

Met Ser Ser Asp Glu Glu Asp Phe Asn Asp Ile Tyr Gly Asp Asp Lys
 1 5 10 15

Pro Thr Thr Thr Glu Glu Val Lys Lys Glu Glu Glu Gln Asn Lys Ala
 20 25 30

Gly Ser Gly Thr Ser Glu Leu Asp Gln Leu Ala Ala Leu Glu Ala Leu
 35 40 45

Ser Ser Ser Ser Asn Lys Leu Asn Asn Pro Asn Ser Asn Asn Ser Ser
 50 55 60

Ser Asn Asn Ser Asn Gln Asp Thr Ser Ser Ser Lys Gln Asp Gly Thr
 65 70 75 80

Ala Asn Asp Lys Glu Gly Ser Asn Glu Asp Thr Lys Asn Glu Lys Lys
 85 90 95

Gln Glu Ser Ala Thr Ser Ala Asn Ala Asn Ala Asn Ala Ser Ser Ala
 100 105 110

Gly Pro Ser Gly Leu Pro Trp Glu Gln Leu Gln Gln Thr Met Ser Gln
 115 120 125

Phe Gln Gln Pro Ser Ser Gln Ser Pro Pro Gln Gln Gln Val Thr Gln
 130 135 140

Thr Lys Gln Gln Arg Ser Lys Ala Asp Leu Ser Lys Gln Ser Lys Lys
 145 150 155 160

Met Phe Ile Gly Gly Leu Asn Trp Asp Thr Thr Glu Asp Asn Leu Arg
 165 170 175

Glu Tyr Phe Gly Lys Tyr Gly Thr Val Thr Asp Leu Lys Ile Met Lys
 180 185 190

Asp Pro Ala Thr Gly Arg Ser Arg Gly Phe Gly Phe Leu Ser Phe Glu
 195 200 205

Lys Pro Ser Ser Val Asp Glu Val Val Lys Thr Gln His Ile Leu Asp
 210 215 220

Gly Lys Val Ile Asp Pro Lys Arg Ala Ile Pro Arg Asp Glu Gln Asp

225	230	235	240
Lys Thr Gly Lys Ile Phe Val Gly Gly Ile Gly Pro Asp Val Arg Pro			
245	250	255	
Lys Glu Phe Glu Glu Phe Phe Ser Gln Trp Gly Thr Ile Ile Asp Ala			
260	265	270	
Gln Leu Met Leu Asp Lys Asp Thr Gly Cln Ser Arg Gly Phe Gly Phe			
275	280	285	
Val Thr Tyr Asp Ser Ala Asp Ala Val Asp Arg Val Cys Gln Asn Lys			
290	295	300	
Phe Ile Asp Phe Lys Asp Arg Lys Ile Glu Ile Lys Arg Ala Glu Pro			
305	310	315	320
Arg His Met Gln Gln Lys Ser Ser Asn Asn Gly Gly Asn Asn Gly Gly			
325	330	335	
Asn Asn Met Asn Arg Arg Gly Gly Asn Phe Gly Asn Gln Gly Asp Phe			
340	345	350	
Asn Gln Met Tyr Gln Asn Pro Met Met Gly Gly Tyr Asn Pro Met Met			
355	360	365	
Asn Pro Gln Ala Met Thr Asp Tyr Tyr Gln Lys Met Gln Glu Tyr Tyr			
370	375	380	
Gln Gln Met Gln Lys Gln Thr Gly Met Asp Tyr Thr Gln Met Tyr Gln			
385	390	395	400

Gln Gln Met Gln Gln Met Ala Met Met Met Pro Gly Phe Ala Met Pro
405 410 415

Pro Asn Ala Met Thr Leu Asn Gln Pro Gln Gln Asp Ser Asn Ala Thr
420 425 430

Gln Gly Ser Pro Ala Pro Ser Asp Ser Asp Asn Asn Lys Ser Asn Asp
435 440 445

Val Gln Thr Ile Gly Asn Thr Ser Asn Thr Asp Ser Gly Ser Pro Pro
450 455 460

Leu Asn Leu Pro Asn Gly Pro Lys Gly Pro Ser Gln Tyr Asn Asp Asp
465 470 475 480

Phe Asn Ser Gly Tyr Gly Tyr Asn Arg Asp Arg Gly Asp Arg Asp Arg
485 490 495

Asn Asp Arg Asp Arg Asp Tyr Asn His Arg Ser Gly Gly Asn His Arg
500 505 510

Arg Asn Gly Arg Gly Gly Arg Gly Gly Tyr Asn Arg Arg Asn Asn Gly
515 520 525

Tyr His Pro Tyr Asn Arg
530

<213> 185

<211> 321

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(321)

<400> 185

atg tcc acc ctc ttg aag tct gct aaa tct atc gtt cca ttg atg gac 49

Met Ser Thr Leu Leu Lys Ser Ala Lys Ser Ile Val Pro Leu Met Asp

1 5 10 15

cgt gtc ctt gtc caa aga atc aag gca caa gca aag aca gca tcc ggg 95

Arg Val Leu Val Gln Arg Ile Lys Ala Glu Ala Lys Thr Ala Ser Gly

20 25 30

ttg tat tta cct gaa aag aac gtg gag aag tta aac caa gct gaa gtt 144

Leu Tyr Leu Pro Glu Lys Asn Val Glu Lys Leu Asn Gln Ala Glu Val

35 40 45

gtt gcc gta ggc ccc ggc cta act gat gct aac ggc aat aag gtt gtt 192

Val Ala Val Gly Pro Gly Phe Thr Asp Ala Asn Gly Asn Lys Val Val

50 55 60

cct caa gtt aaa gtt ggt gac caa gtt ttg att cca cag ttt ggt ggt 240

Pro Glu Val Lys Val Gly Asp Glu Val Leu Ile Pro Gln Phe Gly Gly

65 70 75 80

tct acc att aaa ttg ggt aac gac gat gaa gtt att ctt ttc aag gac 288

Ser Thr Ile Lys Leu Gly Asn Asp Asp Glu Val Ile Leu Phe Arg Asp

85 90 95

gct gaa atc ctg gct aag att gcc aag gac taa 321

Ala Glu Ile Leu Ala Lys Ile Ala Lys Asp

100 105

<210> 186

<211> 106

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 186

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Met Ser Thr Leu Leu Tyr Ser Ala Lys Ser Ile Val Pro Leu Met Asp
 1 5 10 15

Arg Val Leu Val Gln Arg Ile Lys Ala Gln Ala Lys Thr Ala Ser Gly
 20 25 30

Leu Tyr Leu Pro Glu Lys Asn Val Glu Lys Leu Asn Gln Ala Glu Val
 35 40 45

Val Ala Val Gly Pro Gly Phe Thr Asp Ala Asn Gly Asn Lys Val Val
 50 55 60

Pro Gln Val Lys Val Gly Asp Gln Val Leu Ile Pro Gln Phe Gly Gly
 65 70 75 80

Ser Thr Ile Lys Leu Gly Asn Asp Asp Glu Val Ile Leu Phe Arg Asp
 85 90 95

Ala Gln Ile Leu Ala Lys Ile Ala Lys Asp
 100 105

<210> 187

<211> 1149

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (1149)

<400> 187

atg gcc agt aac cag cac ata gga gct tca aac cta aat gag aat gag 40
 Met Ala Ser Asn Gln His Ile Gly Ala Ser Asn Leu Asn Gln Asn Gln
 1 5 10 15

gct ata tta acc aac cgc gct gct qag ctg gaa agg cgt atg tgg atg	96
Ala Ile Leu Thr Asn Arg Val Ala Glu Leu Glu Arg Arg Met Ser Met	
20 25 30	
ttt gag ggt ata ttt cac gcg tta agt aac cgt ctg gat ctt cac ttt	144
Phe Glu Gly Ile Phe His Ala Leu Ser Asn Arg Leu Asp Leu His Phe	
35 40 45	
aaa aaa tat gat gta gtg gta aac tcc caa cag caa cca atc aac gaa	192
Lys Lys Tyr Asp Val Val Val Asn Ser Gln Gln Gln Gln Ile Asn Glu	
50 55 60	
ctg acc gcg ttt tta tca aca ttg ctg aat gac caa caa cgc cac gct	240
Leu Thr Ala Phe Leu Ser Thr Leu Leu Asn Asp Gln Gln Arg His Ala	
65 70 75 80	
gaa att ctg agt gaa aaa tta agc gga agc ttg cat ggg gtg tca gct	288
Glu Ile Leu Ser Glu Lys Leu Ser Gly Thr Leu His Gly Val Ser Ala	
85 90 95	
acg tca ata tcc tta agc caa act ctg gac caa caa ggc ttc act gat	336
Thr Ser Ile Ser Leu Ser Gln Thr Leu Asp Pro Gln Gly Thr Thr Asp	
100 105 110	
ggc act acg gga cca gga gct cct agg aat tat act leu glg cct atg	384
Gly Thr Thr Ala Pro Gly Ala Pro Arg Asn Tyr Thr Ser Val Pro Met	
115 120 125	
aat aat gat caa act gct cat ccg caa aat gaa gga gct gtt agt aat	432
Asn Asn Asp Gln Thr Ala His Pro Gln Asn Gln Gly Ala Val Ser Asn	
130 135 140	
gaa aca ctt ttt gag gac att ttg aat gga aat tca caa gaa aat gat	480
Glu Thr Leu Phe Gln Asp Ile Leu Asn Gly Asn Ser Gln Gln Asn Asp	
145 150 155 160	
aag agt caa caa caa act aac agc leu aat tct ala agc caa gaa aat	528
Lys Ser Gln Gln Gln Thr Asn Ser Ser Asn Ser Ile Ser Gln Gln Asn	
165 170 175	
aat agc acc aac cct tca gtg gac act cgg ttc aac aag ccg caa aat	576

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Asn Ser Thr Asn Pro Ser Val Asp Thr Arg Phe Asn Lys Pro Gln Asn			
180	185	190	
tat aat tcc aat tta gtc cca tcc ttg gag gag tat tca gca aat cca	624		
Tyr Asn Ser Asn Leu Val Pro Ser Leu Gln Gln Tyr Ser Ala Asn Pro			
195	200	205	
oct aac aat gat ggc ggc cca agt caa gga ctg tac ata agc agc aac	672		
Pro Asn Asn Asp Gly Gly Gln Ser Gln Gly Leu Tyr Ile Ser Ser Asn			
210	215	220	
tct tct caa tca cgg cag tct cct aat ttc cag aaa gtt tct cct aac	720		
Ser Ser Gln Ser Arg Gln Ser Pro Asn Leu Gln Lys Val Ser Pro Asn			
225	230	235	240
cat gaa aat gcg gtt gaa tca aat gca caa gag agc gtg cgg aca ttt	768		
His Glu Asn Ala Val Glu Ser Asn Ala Gln Glu Ser Val Pro Thr Phe			
245	250	255	
gag gag gaa cag tat gag act aaa aca gga ttg aaa cgg aaa cga ata	816		
Gln Gln Glu Gln Tyr Glu Thr Lys Thr Gly Leu Lys Arg Lys Arg Ile			
260	265	270	
gtc tgc aca aga ccc ttc gaa ttt atc aag tca cca cac tct gtc atg	864		
Val Cys Thr Arg Pro Phe Gln Phe Ile Lys Ser Pro His Ser Val Met			
275	280	285	
gag gtt tgg aag gag tat aca gaa ggt gtt aac ggg cag cct tct ata	912		
Glu Val Trp Lys Glu Tyr Thr Glu Gly Val Asn Gly Gln Pro Ser Ile			
290	295	300	
agg aaa atg gaa gct ctt tat caa acg gca tgg agg cga gat cca gca	960		
Arg Lys Met Glu Ala Leu Tyr Gln Thr Ala Trp Arg Arg Asp Pro Ala			
305	310	315	320
gta aat aac aga tat tcc aga aga aag gtt ctt tgg aac ggc att caa	1008		
Val Asn Lys Arg Tyr Ser Arg Arg Lys Val Leu Trp Lys Ala Ile Gln			
325	330	335	
act ggc ctt aat cgt ggg tat tca tta aac tat gtt gtt gaa ata tta	1056		
Thr Gly Leu Asn Arg Gly Tyr Ser Leu Asn Tyr Val Val Glu Ile Leu			
340	345	350	

gaa aac tca aga tat gtt aat gat aaa gag aag gtt aaa caa cct att 1104
Glu Asn Ser Arg Tyr Val Asn Asp Lys Gln Lys Val Lys Gln Pro Ile
355 360 365

ggc tgg tta tgc cac agt tct cat att cca gag acg ttg aag tga 1149
Gly Trp Leu Cys His Ser Ser His Ile Pro Glu Thr Leu Lys
370 375 380

<210> 188

<211> 382

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 185

Met Ala Ser Asn Gln His Ile Gly Ala Ser Asn Leu Asn Glu Asn Glu
1 5 10 15

Ala Ile Leu Thr Asn Arg Val Ala Glu Leu Glu Arg Arg Met Ser Met
20 25 30

Phe Glu Gly Ile Phe His Ala Leu Ser Asn Arg Leu Asp Leu His Phe
35 40 45

Lys Lys Tyr Asp Val Val Val Asn Ser Gln Gln Gln Gln Ile Asn Glu
50 55 60

Leu Thr Ala Phe Leu Ser Thr Leu Leu Asn Asp Gln Gln Arg His Ala
65 70 75 80

Glu Ile Leu Ser Glu Lys Leu Ser Gly Thr Ser His Gly Val Ser Ala
85 90 95

Thr Ser Ile Ser Leu Ser Gln Thr Leu Asp Pro Gln Gly Phe Thr Asp

	100		105		110
Gly Thr Thr Ala Pro Gly Ala Pro Arg Asn Tyr Thr Ser Val Pro Met					
	115		120		125
Asn Asn Asp Gln Thr Ala His Pro Gln Asn Glu Gly Ala Val Ser Asn					
	130		135		140
Glu Thr Leu Phe Glu Asp Ile Leu Asn Gly Asn Ser Gln Glu Asn Asp					
	145		150		155
					160
Lys Ser Gln Gln Gln Thr Asn Ser Ser Asn Ser Ile Ser Gln Glu Asn					
		165		170	175
Asn Ser Thr Asn Pro Ser Val Asp Thr Arg Phe Asn Lys Pro Gln Asn					
	180		185		190
Tyr Asn Ser Asn Leu Val Pro Ser Leu Gln Glu Tyr Ser Ala Asn Pro					
	195		200		205
Pro Asn Asn Asp Gly Gly Gln Ser Gln Gly Leu Tyr Ile Ser Ser Asn					
	210		215		220
Ser Ser Gln Ser Arg Gln Ser Pro Asn Leu Glu Lys Val Ser Pro Asn					
	225		230		235
					240
His Glu Asn Ala Val Glu Ser Asn Ala Gln Glu Ser Val Pro Thr Phe					
	245		250		255
Glu Glu Glu Gln Tyr Glu Thr Lys Thr Gly Leu Lys Arg Lys Arg Ile					
	260		265		270

Val Cys Thr Arg Pro Phe Glu Phe Ile Lys Ser Pro His Ser Val Met
 275 280 285

Glu Val Trp Lys Glu Tyr Thr Glu Gly Val Asn Gly Gln Pro Ser Ile
 290 295 300

Arg Lys Met Glu Ala Leu Tyr Gln Thr Ala Trp Arg Arg Asp Pro Ala
 305 310 315 320

Val Asn Lys Arg Tyr Ser Arg Arg Lys Val Leu Trp Lys Ala Ile Gln
 325 330 335

Thr Gly Leu Asn Arg Gly Tyr Ser Leu Asn Tyr Val Val Gln Ile Leu
 340 345 350

Glu Asn Ser Arg Tyr Val Asn Asp Lys Gln Lys Val Lys Gln Pro Ile
 355 360 365

Gly Trp Leu Cys His Ser Ser His Ile Pro Glu Thr Leu Lys
 370 375 380

<210> 189
 <211> 729
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (729)

<400> 109
 atg ata aaa aac tat ttg gga oga aga tgg ctc aat aat cct gca att
 Met Ile Lys Asn Tyr Leu Gly Arg Arg Trp Leu Asn Asn Pro Ala Ile

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1	5	10	15	
caa gca tat gtg aaa caa aat gct gct gtc gcc cat tcc acg gtg ttt				96
Gln Ala Tyr Val Lys Glu Asn Ala Ala Val Ala His Ser Thr Val Phe				
20	25	30		
caa gga aat ctt tat gaa tat acg gtg atg agg gag tta tct gag aaa				144
Gln Gly Asn Leu Tyr Glu Tyr Thr Val Met Arg Glu Leu Ser Glu Lys				
35	40	45		
cta cga atg aca aag ttg aga aaa acc ggt ggc gcc cat gat ggt ggc				192
Leu Arg Met Thr Lys Leu Arg Lys Thr Gly Gly Ala His Asp Gly Gly				
50	55	60		
gta gac ata aag gga agt tgg cca gta gat gat att tat tgg aaa att				240
Val Asp Ile Lys Gly Ser Trp Pro Val Asp Asp Ile Tyr Trp Lys Ile				
65	70	75	80	
tca tgg tta atg acc aat ttg gaa atg gct agt aac ata aaa aga acg				288
Ser Ser Leu Met Pro Asn Leu Glu Met Ala Ser Asn Ile Lys Arg Thr				
85	90	95		
aac tgg caa aat ggc tta gta ttg aac cct tta aag tat agg ata atc				336
Asn Ser Gln Asn Gly Phe Val Leu Lys Pro Leu Lys Tyr Arg Ile Ile				
100	105	110		
gac cat act ttc gaa cca tlg aaa gta cta gtc caa tgt aag gct ttc				384
Asp His Thr Phe Glu Pro Leu Lys Val Leu Val Gln Cys Lys Ala Phe				
115	120	125		
act aaa tca aaa tta tct cct aga gaa ttc cgt gag tta glu gga aca				432
Thr Lys Ser Lys Leu Ser Pro Arg Glu Phe Arg Glu Leu Val Gly Thr				
130	135	140		
tta acc tca cta gta tca cat agt caa cgc aac aza uca gta tgc att				480
Phe Thr Ser Leu Val Ser His Ser Gln Arg Asn Lys Thr Val Cys Ile				
145	150	155	160	
atg tgt tcc cct cat atg tta aca aaa gat acc tta aat ctt atc aat				528
Met Cys Ser Pro His Met Leu Thr Lys Asp Thr Leu Asn Leu Ile Asn				
165	170	175		

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aac atc aag ctt cct ctg ata tat tta cgt gtr gag atg ctg aaa gag 576
 Asn Ile Thr Leu Pro Leu Ile Tyr Leu Arg Val Glu Met Leu Lys Gln
 130 185 190

aag act gac ggg cac ttt gac tta atc aat tca gga aaa cta att aat 624
 Lys Thr Asp Gly His Phe Asp Leu Ile Asn Ser Gly Lys Leu Ile Asn
 195 200 205

tat tac gag aat tca tac gcc tct acg tta atg caa gat tgc aag att 672
 Tyr Tyr Glu Asn Ser Tyr Ala Ser Thr Leu Met Gln Asp Cys Lys Ile
 210 215 220

tct gaa tgg ctg aag ttg aag ttg tcc aaa aat agt gac ttt aat tgc 720
 Ser Glu Trp Leu Lys Leu Lys Leu Tyr Lys Asn Ser Asp Phe Asn Ser
 225 230 235 240

gaa aaa taa 723
 Glu Lys

<210> 150

<211> 242

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 150

Met Ile Lys Asn Tyr Leu Gly Arg Arg Thr Leu Asn Asn Pro Ala Ile
 1 5 10 15

Gln Ala Tyr Val Lys Gln Asn Ala Ala Val Ala His Ser Thr Val Phe
 20 25 30

Gln Gly Asn Leu Tyr Glu Tyr Thr Val Met Arg Glu Leu Ser Glu Lys
 35 40 45

Leu Arg Met Thr Lys Leu Arg Lys Thr Gly Gly Ala His Asp Gly Gly
 50 55 60

Tyr Tyr Glu Asn Ser Tyr Ala Ser Thr Leu Met Gln Asp Cys Lys Ile
210 215 220

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Ser Glu Trp Leu Lys Leu Lys Leu Tyr Lys Asn Ser Asp Phe Asn Ser
 225 230 235 240

Glu Lys

<210> 191

<211> 630

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(630)

<400> 191

atg ata tca cca tca aaa aag aga acc att tta tca agc aag aat ata 48

Met Ile Ser Pro Ser Lys Lys Arg Thr Ile Leu Ser Ser Lys Asn Ile

1 5 10 15

aac caa aaa cca cga gca gtg gta aaa ggc aat gaa att cgt tca cca 96

Asn Glu Lys Pro Arg Ala Val Val Lys Gly Asn Glu Leu Arg Ser Pro

20 25 30

tca aag aga agg tca caa ata gcc aca gac tat gca cta agg cga agt 144

Ser Lys Arg Arg Ser Gln Ile Asp Thr Asp Tyr Ala Leu Arg Arg Ser

35 40 45

cca ata aag aca atc caa att tct aac gct gca caa ttt atg ctg tac 192

Pro Ile Lys Thr Ile Gln Ile Ser Lys Ala Ala Gln Phe Met Leu Tyr

50 55 60

gag gaa acg gct gaa gaa aga aac ata gct gtc cac aga cat aat gaa 240

Glu Glu Thr Ala Glu Glu Arg Asn Ile Ala Val His Arg His Asn Glu

65 70 75 80

ata tac aat aat aac aat tct gtg agc aat gag aat aat cct tcc caa 288

Ile Tyr Asn Asn Asn Ser Val Ser Asn Glu Asn Asn Pro Ser Gln

85 90 95

gta aaa gaa aac ctt tca ccc gct aaa att tgc cct tat gaa aga gca 336
 Val Lys Glu Asn Leu Ser Pro Ala Lys Ile Cys Pro Tyr Glu Arg Ala
 130 105 110

ttt tta agg gaa gga gga aga att gca ttg aag gac tta agt gtt gac 384
 Phe Leu Arg Gln Gly Gly Arg Ile Ala Leu Lys Asp Leu Ser Val Asp
 115 120 125

gaa ttc aaa ggt tac ata cag gat cct ctc acc gat gag act ata cca 432
 Glu Phe Lys Gly Tyr Ile Gln Asp Pro Leu Thr Asp Glu Thr Ile Pro
 130 135 140

ctg acg ttg cca ctg ggt gat aaa aaa atc agc cta ccc agt ttt ata 480
 Leu Thr Leu Pro Leu Gly Asp Lys Lys Ile Ser Leu Pro Ser Phe Ile
 145 150 155 160

acg ccg cca aga aat tgg aag ata tct att ttc ttc act agt aaa cac 528
 Thr Pro Pro Arg Asn Ser Lys Ile Ser Ile Phe Phe Thr Ser Lys His
 165 170 175

caa gga cag aac cca gag acc aag ata tcc cgt tct acc gct gac gtc 576
 Gln Gly Gln Asn Pro Glu Thr Lys Ile Ser Arg Ser Thr Asp Asp Val
 180 185 190

agt gaa aaa aaa gta gta aga aaa ctg tcc ttc cac gtc tat gaa gat 624
 Ser Glu Lys Lys Val Val Arg Lys Leu Ser Phe His Val Tyr Glu Asp
 195 200 205

gag taa 630
 Glu

<210> 192

<211> 209

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 192

Ket Ile Ser Pro Ser Lys Lys Arg Thr Ile Leu Ser Ser Lys Asn Ile

1	5	10	15
Asn Glu Lys Pro Arg Ala Val Val Lys Gly Asn Glu Leu Arg Ser Pro	20	25	30
Ser Lys Arg Arg Ser Glu Ile Asp Thr Asp Tyr Ala Leu Arg Arg Ser	35	40	45
Pro Ile Lys Thr Ile Glu Ile Ser Lys Ala Ala Glu Phe Met Leu Tyr	50	55	60
Glu Glu Thr Ala Glu Glu Arg Asn Ile Ala Val His Arg His Asn Glu	65	70	75
Ile Tyr Asn Asn Asn Asn Ser Val Ser Asn Glu Asn Asn Pro Ser Glu	80	85	90
Val Lys Glu Asn Leu Ser Pro Ala Lys Ile Cys Pro Tyr Glu Arg Ala	95	100	105
Phe Leu Arg Glu Gly Gly Arg Ile Ala Leu Lys Asp Leu Ser Val Asp	110	115	120
Glu Phe Lys Gly Tyr Ile Glu Asp Pro Leu Thr Asp Glu Thr Ile Pro	125	130	135
Leu Thr Leu Pro Leu Gly Asp Lys Lys Ile Ser Leu Pro Ser Phe Ile	140	145	150
Thr Pro Pro Arg Asn Ser Lys Ile Ser Ile Phe Phe Thr Ser Lys His	155	160	165

Gln Gly Gln Asn Pro Glu Thr Lys Ile Ser Arg Ser Thr Asp Asp Val
 182 185 190

Ser Glu Lys Lys Val Val Arg Lys Leu Ser Phe His Val Tyr Glu Asp
 195 200 205

Cln

<210> 191
 <211> 621
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(621)

<400> 193
 atg atg ccc tac aac acc cct cca aat atc caa gaa cct atg aac ttc 48
 Met Met Pro Tyr Asn Thr Pro Pro Asn Ile Gln Glu Pro Met Asn Phe
 1 5 10 15
 gca agc agc aac ccc ttt ggt att att cca gat gag ctg agt ttc cag 96
 Ala Ser Ser Asn Pro Phe Gly Ile Ile Pro Asp Ala Leu Ser Phe Gln
 20 25 30
 aat ttc aaa tat gat cgt ctt cag cag cag caa cag cag cag caa cag 144
 Asn Phe Lys Tyr Asp Arg Leu Gln Gln Gln Gln Gln Gln Gln Gln
 35 40 45
 cag caa caa aat cgc act gag tca tgg tta cag cag cag caa cag caa 192
 Gln Gln Gln Asn Arg Thr Ala Ser Ser Leu Gln Gln Pro Gln Gln Gln
 50 55 60
 caa cca ata agc cag cct ttg ttt tta gta ggg gcc ggt acc agc gaa 240
 Gln Pro Ile Ser Pro Pro Leu Phe Leu Val Gly Ala Gly Thr Ser Glu

65	70	75	80	
aac tca aac ctt aac aag aat gcc aac aat agt aat atc cct cct tta				288
Asn Ser Asn Leu Asn Lys Asn Ala Asn Thr Ser Thr Ile Pro Pro Leu				
85	90	95		
ctc ttt agc aga tgg tot cag cat tat gtt gtc cca gat ata gac aac				336
Leu Phe Ser Arg Ser Ser Gln His Tyr Val Val Pro Asp Ile Asp His				
100	105	110		
tcc tcc ata ata tac aag aac aac atc cgc aaa tot ttc aaa gat gac				384
Ser Ser Ile Ile Tyr Lys Asn Asn Ile Cys Lys Ser Thr Lys Asp Asp				
115	120	125		
tta ttt ttc tgt cca aga tct tta ctg tct ctg gaa gaa caa caa gca				432
Leu Phe Phe Cys Pro Arg Ser Asn Leu Ser Leu Glu Glu Gln Gln Ala				
130	135	140		
lyc gag aaa atg gat agg ctg acc gcc gaa caa atg tca ttg tat cat				480
Cys Glu Lys Met Asp Arg Leu Thr Ala Glu Gln Met Ser Leu Tyr His				
145	150	155	160	
cag aac aag caa tcc agt tct aat cct ggt tct atg tct tct tca cct				528
Gln Asn Thr Gln Ser Ser Ser Asn Pro Gly Ser Met Ser Ser Ser Pro				
165	170	175		
cca aat tct gcc tct tct ata ttc aac tct agg cag aag ttc aat cct				576
Pro Asn Ser Ala Ser Ser Ile Phe Asn Ser Arg Pro Lys Phe Asn Pro				
180	185	190		
tat aca tct caa agt ttt aat cct ttg gaa agt gtt caa gaa tga				624
Tyr Thr Ser Gln Ser Phe Asn Pro Leu Glu Ser Val Gln Glu				
195	200	205		

<210> 194

<211> 206

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 194

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Met Met Pro Tyr Asn Thr Pro Pro Asn Ile Gln Glu Pro Met Asn Phe
 1 5 10 15

Ala Ser Ser Asn Pro Phe Gly Ile Ile Pro Asp Ala Leu Ser Phe Gln
 20 25 30

Asn Phe Lys Tyr Asp Arg Leu Gln Gln Gln Gln Gln Gln Gln Gln
 35 40 45

Gln Gln Gln Asn Arg Thr Ala Ser Ser Leu Gln Gln Pro Gln Gln Gln
 50 55 60

Gln Pro Ile Ser Pro Pro Leu Phe Leu Val Gly Ala Gly Thr Ser Glu
 65 70 75 80

Asn Ser Asn Leu Asn Lys Asn Ala Asn Thr Ser Thr Ile Pro Pro Leu
 85 90 95

Leu Phe Ser Arg Ser Ser Gln His Tyr Val Val Pro Asp Ile Asp His
 100 105 110

Ser Ser Ile Ile Tyr Lys Asn Asn Ile Cys Lys Ser Phe Lys Asp Asp
 115 120 125

Leu Phe Phe Cys Pro Arg Ser Leu Leu Ser Leu Glu Glu Gln Gln Ala
 130 135 140

Cys Gln Lys Met Asp Arg Leu Thr Ala Glu Gln Met Ser Ile Tyr His
 145 150 155 160

Gln Asn Thr Gln Ser Ser Ser Asn Pro Gly Ser Met Ser Ser Ser Pro
 165 170 175

Pro Asn Ser Ala Ser Ser Ile Phe Asn Ser Arg Pro Lys Phe Asn Pro
 180 185 190

Tyr Thr Ser Gln Ser Phe Asn Pro Leu Glu Ser Val Gln Glu
 195 200 205

<210> 195
 <211> 534
 <212> CDS
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <223> (1)..(534)

<400> 195
 atg aac atg gag aac gac atg aat gta gat gaa ata ttt ctc aac caa 45
 Met Lys Leu Ala Gln Asp Met Asn Val Asp Glu Ile Phe Leu Lys Gln
 1 5 10 15
 gag gca gaa gct ata gag gta atc tca tca agt ccc aat cat aag gaa 35
 Ala Ala Glu Ala Ile Ala Val Ile Ser Ser Ser Pro Thr His Thr Asp
 20 25 30
 ccc ata ata cga gag cta ctc caa aga att cga caa tcc agc cca ttg 111
 Pro Ile Ile Arg Glu Leu Leu His Arg Ile Arg Gln Ser Ser Pro Leu
 35 40 45
 agc gca gtt ata cca gca cca gaa aat gtt tta aag gct ggg gag cag 192
 Ser Ala Val Ile Pro Ala Pro Glu Asn Val Leu Lys Ala Gly Glu Pro
 50 55 60
 gaa aat atg gct aga ggt ctt ata agg att cca gaa aca caa aca aac 240
 Glu Asn Met Ala Arg Gly Leu Ile Arg Ile Pro Glu Thr Gln Thr Lys
 65 70 75 80
 aga aca gga ggt aac aac cat agc aag gaa ggc gca cag ctc tac agc 288

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Arg Thr Gly Gly Asn Asn His Ser Pys Glu Gly Ala Gln Leu Tyr Ser	
85 90 95	
tgt gcg aaa tgt cag ttg aaa ttc agc aga agt tct gat ctg aga aga	336
Cys Ala Lys Cys Gln Leu Lys Phe Ser Arg Ser Ser Asp Leu Arg Arg	
100 105 110	
cat gaa aag gta cac tca ctc gtg ctg ccg cat att tgc tca aac tgt	384
His Glu Lys Val His Ser Leu Val Leu Pro His Ile Cys Ser Asn Cys	
115 120 125	
ggc aaa ggg ttt gcc agg aag gat gct cta aaa aga cat tct aac acc	432
Gly Lys Gly Phe Ala Arg Lys Asp Ala Leu Lys Arg His Ser Asn Thr	
130 135 140	
ctg acc tgt cca aca aac aga aag aaa cta agt gaa ggt tca gac gtt	480
Leu Thr Cys Gln Arg Asn Arg Lys Lys Leu Ser Glu Gly Ser Asp Val	
145 150 155 160	
gat gta gat gag ctc atc aag gat ggc ata aag aat ggt acc gcc ctg	528
Asp Val Asp Glu Leu Ile Lys Asp Ala Ile Lys Asn Gly Thr Gly Leu	
165 170 175	
ttg taa	534
Leu	

<210> 196

<211> 177

<213> FRT

<214> *Saccharomyces cerevisiae*

<400> 196

Met Lys Leu Ala Gln Asp Met Asn Val Asp Glu Ile Phe Leu Lys Gln
1 5 10 15

Ala Ala Glu Ala Ile Ala Val Ile Ser Ser Ser Pro Thr His Thr Asp
20 25 30

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Pro Ile Ile Arg Glu Leu Leu His Arg Ile Arg Gln Ser Ser Pro Leu
 35 40 45

Ser Ala Val Ile Pro Ala Pro Glu Asn Val Leu Lys Ala Gly Glu Pro
 50 55 60

Gln Asn Met Ala Arg Gly Leu Ile Arg Ile Pro Glu Thr Gln Thr Lys
 65 70 75 80

Arg Thr Gly Gly Asn Asn His Ser Lys Gln Gly Ala Gln Asn Tyr Ser
 85 90 95

Cys Ala Lys Cys Gln Leu Lys Phe Ser Arg Ser Ser Asp Leu Arg Arg
 100 105 110

His Gln Lys Val His Ser Leu Val Leu Pro His Ile Cys Ser Asn Cys
 115 120 125

Gly Lys Gly Phe Ala Arg Lys Asp Ala Leu Lys Arg His Ser Asn Thr
 130 135 140

Leu Thr Cys Gln Arg Asn Arg Lys Lys Leu Ser Gln Gly Ser Asp Val
 145 150 155 160

Asp Val Asp Glu Leu Ile Lys Asp Ala Ile Lys Asn Gly Thr Gly Leu
 165 170 175

Leu

<210> 197

<211> 1425

<212> DNA

<213> Saccharomyces cerevisiae

<220>

<221> CDS

<222> (1) .. (1425)

<400> 197

atg gag gta act tca atg ttc ctc aat aga atg atg aag acc egg act	48
Met Glu Val Thr Ser Met Phe Leu Asn Arg Met Met Lys Thr Arg Thr	
1 5 10 15	

ggc ctt tat cgc tta tat tca acc ctt aaa gtt cca cat gta gaa atc	96
Gly Leu Tyr Arg Leu Tyr Ser Thr Leu Lys Val Pro His Val Glu Ile	
20 25 30	

aat ggc ata aaa tgc aag acc gac cca cag act acc aat gtt aca gat	144
Asn Gly Ile Lys Tyr Lys Thr Asp Pro Gln Thr Thr Asn Val Thr Asp	
35 40 45	

tca ata ata aag ctt acc gac aga tca tta cat ttg aac gaa tca cat	192
Ser Ile Ile Lys Leu Thr Asp Arg Ser Leu His Leu Lys Glu Ser His	
50 55 60	

cca gta ggc ctt ctt cgc gat cta att gaa aag aaa tta aac tca gtc	240
Pro Val Gly Ile Leu Arg Asp Leu Ile Glu Lys Lys Leu Asn Ser Val	
65 70 75 80	

gac aac aca ttt aag atc ttt aat aat ttc aag ccc gtg gta acc aca	288
Asp Asn Thr Phe Lys Ile Phe Asn Asn Phe Lys Pro Val Val Thr Thr	
85 90 95	

atg gaa aac ttc gat tct tta ggg ttt cct aag gat cat cct gga aga	336
Met Glu Asn Phe Asp Ser Leu Gly Phe Pro Lys Asp His Pro Gly Arg	
100 105 110	

tca aaa tct gac aca tat tat ata aat gag acc cac cta ctg aga aca	384
Ser Lys Ser Asp Thr Tyr Tyr Ile Asn Glu Thr His Leu Leu Arg Thr	
115 120 125	

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cat act tca gcc cac gaa tta gag tgc ttt caa aaa ata aga aac gat	432
His Thr Ser Ala His Glu Leu Glu Cys Phe Gln Lys Ile Arg Asn Asp	
130 135 140	
tca gat aat att aaa agt gga ttt tta ata tct gca gat gtg tac aga	480
Ser Asp Asn Ile Lys Ser Gly Phe Leu Ile Ser Ala Asp Val Tyr Arg	
145 150 155 160	
aga gat gaa att gac aaa act cac tat ccg gta ttc cac caa atg gaa	528
Arg Asp Glu Ile Asp Lys Thr His Tyr Pro Val Phe His Gln Met Glu	
165 170 175	
gga gcc aca att tgg aaa cga acg aag gct gat gtg ggc gta aag gag	576
Gly Ala Thr Ile Trp Lys Arg Thr Lys Ala Asp Val Gly Val Lys Glu	
180 185 190	
aca atg tat atc gag aaa atc cgt gaa gat atc aga cag gta gag aac	624
Pro Met Tyr Ile Glu Lys Ile Arg Glu Asp Ile Arg Glu Val Glu Asn	
195 200 205	
att tta aat aaa gaa aat gta aag att acg gtt gcc gat gat act ata	672
Leu Leu Asn Iys Glu Asn Val Lys Ile Thr Val Asp Asp Asp Thr Ile	
210 215 220	
ccg ttg aac gaa aat aat cct aaa caa gag tat atg tcc gat ctg gag	720
Pro Leu Lys Glu Asn Asn Pro Lys Gln Glu Tyr Met Ser Asp Leu Glu	
225 230 235 240	
att gat ttg tgc tct caa cat ttg aag agg tcc att gaa ctg ata gtt	768
Val Asp Leu Cys Ser Gln His Leu Lys Arg Ser Ile Glu Leu Ile Val	
245 250 255	
tct gaa gtt ttt aac aaa aaa ata tct agc atg atc aag aac aaa gcc	816
Ser Glu Val Phe Asn Lys Lys Ile Ser Ser Met Ile Lys Asn Lys Ala	
260 265 270	
aat aat aca ccc aaa gag cta aca gtc cgt tgg att aac gct tac ttc	864
Asn Asn Thr Pro Lys Glu Leu Lys Val Arg Trp Ile Asn Ala Tyr Phe	
275 280 285	
ccc tgg acc gcc ccc tca tgg gaa ata gag gtt tgg tgg cag gcc gaa	912
Pro Trp Thr Ala Pro Ser Trp Glu Ile Glu Val Trp Trp Gln Gly Glu	

280	290	300	
tgg ctc gaa ctc tgc gga tgc gga ttg att cgt caa gat gtg cta ctc			960
Trp Leu Glu Leu Cys Gly Cys Gly Leu Ile Arg Gln Asp Val Leu Leu			
305	310	315	320
aga gcc gga tat aaa cct tct gaa aca att ggg tgg gct ttt ggc ttg			1008
Arg Ala Gly Tyr Lys Pro Ser Glu Thr Ile Gly Trp Ala Phe Gly Leu			
	325	330	335
ggt ttg gac cgc att gct atg ctt ctt ttt gaa att cca gat att aga			1056
Gly Leu Asp Arg Ile Ala Met Leu Leu Phe Glu Ile Pro Asp Ile Arg			
	340	345	350
ctg ctt tgg agt cgt gat gaa aga ttt tca aga aca ttc tcc aag gga			1104
Leu Leu Trp Ser Arg Asp Glu Arg Phe Ser Arg Gln Phe Ser Tyr Gly			
	355	360	365
cta att act tcc ttc aaa cct tat tca aaa cac ccg gga tca ttt agg			1152
Leu Ile Thr Ser Phe Lys Pro Tyr Ser Lys His Pro Gly Ser Phe Arg			
	370	375	380
gat gtt gcg ttt tgg tta cca gaa gat aaa cca gat att cat caa gtt			1200
Asp Val Ala Phe Trp Leu Pro Glu Asp Lys Pro Asp Ile His Gln Val			
385	390	395	400
cac gaa aat gat ttg atg gaa att atc aga aat ata gct ggc gat ttg			1248
His Gln Asn Asp Leu Met Glu Ile Ile Arg Asn Ile Ala Gly Asp Leu			
	405	410	415
gta gag agt gtc aag cta gtc gat agc ttt aac cat ccg aua act ggg			1296
Val Glu Ser Val Lys Leu Val Asp Ser Phe Thr His Pro Lys Thr Gly			
	420	425	430
aga aaa tct atg tgc tac agg atc aac tat caa tca atg gac aga aat			1344
Arg Lys Ser Met Cys Tyr Arg Ile Asn Tyr Gln Ser Met Asp Arg Asn			
	435	440	445
ttg aca aac gcc gaa gtt aac act ttg caa gac atg gtg tgt tct aaa			1392
Leu Thr Asn Ala Glu Val Asn Thr Leu Gln Asp Met Val Cys Ser Lys			
450	455	460	

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ttg gta aac gac tac agc gta gaa ctg aga tag 1425
 Leu Val Lys Glu Tyr Ser Val Glu Leu Arg
 465 470

<210> 198
 <211> 474
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 198

Met Glu Val Thr Ser Met Phe Leu Asn Arg Met Met Lys Thr Arg Thr
 5 10 15

Gly Leu Tyr Arg Leu Tyr Ser Thr Leu Lys Val Pro His Val Glu Ile
 20 25 30

Asn Gly Ile Lys Tyr Lys Thr Asp Pro Gln Thr Thr Asn Val Thr Asp
 35 40 45

Ser Ile Ile Lys Leu Thr Asp Arg Ser Leu His Leu Lys Glu Ser His
 50 55 60

Pro Val Gly Ile Leu Arg Asp Leu Ile Glu Lys Lys Leu Asn Ser Val
 65 70 75 80

Asp Asn Thr Phe Lys Ile Phe Asn Asn Phe Lys Pro Val Val Thr Thr
 85 90 95

Met Glu Asn Phe Asp Ser Leu Gly Phe Pro Lys Asp His Pro Gly Arg
 100 105 110

Ser Lys Ser Asp Thr Tyr Tyr Ile Asn Glu Thr His Leu Leu Arg Thr
 115 120 125

His Thr Ser Ala His Glu Leu Glu Cys Phe Gln Lys Ile Arg Asn Asp
130 135 140

Ser Asp Asn Ile Lys Ser Gly Phe Leu Ile Ser Ala Asp Val Tyr Arg
145 150 155 160

Arg Asp Glu Ile Asp Lys Thr His Tyr Pro Val Phe His Gln Met Glu
165 170 175

Gly Ala Thr Ile Trp Lys Arg Thr Lys Ala Asp Val Gly Val Lys Glu
180 185 190

Pro Met Tyr Ile Glu Lys Ile Arg Glu Asp Ile Arg Gln Val Glu Asn
195 200 205

Leu Ser Asn Lys Glu Asn Val Lys Ile Thr Val Asp Asp Asp Thr Ile
210 215 220

Pro Leu Lys Glu Asn Asn Pro Lys Gln Glu Tyr Met Ser Asp Leu Glu
225 230 235 240

Val Asp Leu Cys Ser Gln His Leu Lys Arg Ser Ile Glu Leu Ile Val
245 250 255

Ser Glu Val Phe Asn Lys Lys Ile Ser Ser Met Ile Lys Asn Lys Ala
260 265 270

Asn Asn Thr Pro Lys Glu Ser Lys Val Arg Trp Ile Asn Ala Tyr Phe
275 280 285

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Pro Trp Thr Ala Pro Ser Trp Glu Ile Glu Val Trp Trp Gln Gly Glu
290 295 300

Trp Leu Glu Leu Cys Gly Cys Gly Leu Ile Arg Gln Asp Val Leu Leu
305 310 315 320

Arg Ala Gly Tyr Lys Pro Ser Glu Thr Ile Gly Trp Ala Phe Gly Leu
325 330 335

Gly Leu Asp Arg Ile Ala Met Leu Leu Phe Glu Ile Pro Asp Ile Arg
340 345 350

Leu Leu Trp Ser Arg Asp Glu Arg Phe Ser Arg Gln Phe Ser Lys Gly
355 360 365

Leu Ile Thr Ser Phe Lys Pro Tyr Ser Lys His Pro Gly Ser Phe Arg
370 375 380

Asp Val Ala Phe Trp Leu Pro Glu Asp Lys Pro Asp Ile His Gln Val
385 390 395 400

His Glu Asn Asp Leu Met Glu Ile Ile Arg Asn Ile Ala Gly Asp Leu
405 410 415

Val Glu Ser Val Lys Leu Val Asp Ser Phe Thr His Pro Lys Thr Gly
420 425 430

Arg Lys Ser Met Cys Tyr Arg Ile Asn Tyr Gln Ser Met Asp Arg Asn
435 440 445

Leu Thr Asn Ala Glu Val Asn Thr Leu Gln Asp Met Val Cys Ser Lys
450 455 460

Leu Val Lys Glu Tyr Ser Val Glu Leu Arg

465

470

<210> 199

<211> 1062

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1062)

<400> 199

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Met Thr Thr Asn Asn Asp Phe Tyr Phe Ala Leu Leu Arg Ile Ser Ile

1 5 10 15

ctc caa cta ttg aag gca caa gga lll gac agg gca agg ccc agt ctg 96

Leu Gln Leu Leu Lys Ala Gln Gly Phe Asp Arg Ala Arg Pro Ser Leu

20 25 30

gtg gat gtc atg acc gat ctc tat gca aaa ttc ttg agt ttg tta gca 144

Val Asp Val Met Thr Asn Leu Tyr Ala Lys Phe Leu Ser Leu Leu Ala

35 40 45

tca gag gtc agt tct atc gct cag gca aga tgt gat cag gac gat aca 192

Ser Gln Val Ser Ser Ile Ala Gln Ala Arg Cys Asp Gln Asp Asp Thr

50 55 60

att gct tta caa gat ala acc ctg gct ctg gaa aat cta ggt att gtt 240

Ile Ala Leu Gln Asp Ile Thr Leu Ala Leu Glu Asn Leu Gly Ile Val

65 70 75 80

aag cct acg aac gtt ctg gat gtc tat gal gaa aac tcc gaa tta tca 288

Lys Pro Thr Asn Val Leu Asp Val Tyr Asp Glu Asn Ser Glu Leu Ser

85 90 95

agt tca cga gga atg gaa aag ttc aag gac tgg tgt att tat agt act 336

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Ser Ser Arg Gly Met Glu Lys Phe Lys Asp Trp Cys Ile Tyr Ser Thr	
100 105 110	
caa ttg acc gac gag cga ata act gcc tta acc aca gla gaa tca cta	384
Gln Leu Thr Asp Ala Arg Ile Thr Ala Leu Pro Thr Val Gln Leu Leu	
115 120 125	
caa agt gag gaa aaa gaa tct gat cct ttg tca gca ata cct gac tat	432
Gln Ser Glu Glu Lys Glu Ser Asp Pro Leu Ser Ala Ile Pro Asp Tyr	
130 135 140	
ctc aat caa tta ctg caa aac aag ggc ggg aaa cag aaa tta gaa aca	480
Leu Asn Gln Leu Leu Gln Asn Lys Gly Ala Lys Gln Lys Leu Glu Thr	
145 150 155 160	
aag aat aga aaa acc gag ttg ata gaa gat cta ata aat aat cct gga	528
Lys Asn Arg Lys Thr Glu Leu Ile Glu Asp Ser Ile Asn Asn Asn Gly	
165 170 175	
tta gat gat tgg atc aaa tta gtc att gct aga caa cgt ata aac ttg	576
Leu Asp Asp Trp Ile Lys Leu Val Ile Ala Arg Gln Arg Ile Asn Met	
180 185 190	
att gaa aga gct tcc aac aac gaa tct caa aat gta cag gct tta cca	624
Ile Glu Arg Ala Ser Lys Lys Glu Ser Gln Asn Val Pro Ala Leu Pro	
195 200 205	
cac att gca ggc tat aaa tct tcc att cta agc cgc cat cac cac act	672
His Ile Ala Gly Tyr Lys Ser Ser Ile Leu Ser Arg His His His Thr	
210 215 220	
acc ata aca aac gaa gat agg atg cct tcg gag atg acc cca aga gat	720
Thr Ile Thr Asn Glu Asp Arg Met Pro Ser Ala Met Thr Pro Arg Asp	
225 230 235 240	
gag gat gcc cta acc gag atc caa gaa aat cca ttt gta act agc aac	768
Glu Asp Ala Leu Thr Glu Ile Gln Glu Asn Pro Phe Val Thr Ser Lys	
245 250 255	
ctg ccg ata atg aga aaa gaa aat agg tta gaa aat ata act cct tca	816
Leu Pro Ile Met Arg Lys Gln Asn Arg Leu Glu Asn Ile Thr Leu Ser	
260 265 270	

ttt gag gat gag gag ctt gaa tca ctt ggc gaa gtg gaa ggc cct aac 854
 Phe Glu Asp Glu Glu Leu Glu Ser Leu Gly Glu Val Glu Gly Pro Asn
 275 280 285

 caa aag tct caa gaa aat aac aat gag gaa agt ttt aaa gag aac aat 912
 Gln Lys Ser Gln Glu Asn Asn Asn Gln Glu Ser Phe Lys Glu Asn Asn
 290 295 300

 aaa agt tta aaa gag tct cct cat ggt gat gac cgt gac ata tca atg 960
 Lys Ser Leu Thr Glu Ser Pro His Gly Asp Asp Arg Asp Ile Ser Met
 305 310 315 320

 ttt caa ttc gac tca aat gtt gat act aaa tgg gca gag cag gaa gat 1008
 Phe Gln Phe Asp Ser Asn Val Asp Thr Lys Trp Ala Glu Gln Glu Asp
 325 330 335

 atg gac agc aca ttt caa cgt cga acc tca cta gat tat ggg ggt tac 1056
 Met Asp Ser Thr Phe Gln Arg Arg Thr Ser Leu Asp Tyr Gly Gly Tyr
 340 345 350

 ttt taa 1062
 Phe

<210> 200

<211> 353

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 200

Met Thr Thr Asn Asn Asp Phe Tyr Phe Ala Leu Leu Arg Ile Ser Ile
 1 5 10 15

Leu Gln Leu Leu Lys Ala Gln Gly Phe Asp Arg Ala Arg Pro Ser Leu
 20 25 30

Val Asp Val Met Thr Asp Leu Tyr Ala Lys Phe Leu Ser Leu Leu Ala

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35	40	45
Ser Glu Val Ser Ser Ile Ala Gln Ala Arg Cys Asp Gln Asp Asp Thr		
50	55	60
Ile Ala Leu Gln Asp Ile Thr Ser Ala Leu Glu Asn Leu Gly Ile Val		
65	70	75
		80
Lys Pro Thr Asn Val Leu Asp Val Tyr Asp Glu Asn Ser Glu Leu Ser		
	85	90
		95
Ser Ser Arg Gly Met Glu Lys Phe Lys Asp Trp Cys Ile Tyr Ser Thr		
	100	105
		110
Gln Leu Thr Asp Ala Arg Ile Thr Ala Leu Pro Thr Val Glu Leu Leu		
	115	120
		125
Gln Ser Glu Glu Lys Glu Ser Asp Pro Leu Ser Ala Ile Pro Asp Tyr		
	130	135
		140
Leu Asn Gln Leu Leu Gln Asn Tyr Gly Ala Lys Gln Lys Leu Glu Thr		
145	150	155
		160
Lys Asn Arg Lys Thr Glu Leu Ile Glu Asp Leu Ile Asn Asn Asn Gly		
	165	170
		175
Leu Asp Asp Trp Ile Lys Leu Val Ile Ala Arg Gln Arg Ile Asn Met		
	180	185
		190
Ile Glu Arg Ala Ser Lys Lys Glu Ser Gln Asn Val Pro Ala Leu Pro		
	195	200
		205

His Ile Ala Gly Tyr Lys Ser Ser Ile Leu Ser Arg His His His Thr
210 215 220

Thr Ile Thr Asn Glu Asp Arg Met Pro Ser Ala Met Thr Pro Arg Asp
225 230 235 240

Glu Asp Ala Leu Thr Glu Ile Gln Glu Asn Pro Phe Val Thr Ser Lys
245 250 255

Leu Pro Ile Met Arg Lys Glu Asn Arg Leu Glu Asn Ile Thr Leu Ser
260 265 270

Phe Glu Asp Glu Glu Leu Glu Ser Leu Gly Glu Val Glu Gly Pro Asn
275 280 285

Glu Lys Ser Gln Glu Asn Asn Asn Glu Glu Ser Phe Lys Glu Asn Asn
290 295 300

Lys Ser Leu Thr Glu Ser Pro His Gly Asp Asp Arg Asp Ile Ser Met
305 310 315 320

Phe Gln Phe Asp Ser Asn Val Asp Thr Lys Trp Ala Glu Gln Glu Asp
325 330 335

Met Asp Ser Thr Phe Gln Arg Arg Thr Ser Leu Asp Tyr Gly Gly Tyr
340 345 350

Phe

<210> 201

<211> 1308

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1308)

<400> 201

atg	tct	ggt	tat	tct	tcg	ggg	ttt	tct	cta	aac	aag	atc	acc	gat	tca	48
Met	Ser	Gly	Tyr	Phe	Ser	Gly	Phe	Ser	Leu	Asn	Lys	Ile	Thr	Asp	Ser	
1			5					10					15			

att	gac	acc	gct	gct	cac	nag	acc	caa	gac	act	ctg	aac	aat	gca	ttc	96
Ile	Ala	Thr	Ala	Ala	His	Lys	Thr	Gln	Asp	Thr	Leu	Asn	Asn	Ala	Leu	
			20					25					30			

gca	aat	gca	aat	gta	aac	tta	aat	gac	cct	caa	aca	aga	cta	tca	atc	144
Ala	Asn	Ala	Asn	Val	Asn	Leu	Asn	Asp	Pro	Gln	Thr	Arg	Leu	Ser	Ile	
		35					40					45				

aaa	tcg	cga	act	aga	ttt	ggt	cag	gaa	tca	ttg	ggt	act	gta	tca	gat	192
Lys	Ser	Arg	Thr	Arg	Phe	Val	Gln	Glu	Ser	Leu	Gly	Thr	Val	Ser	Asp	
	50					55					60					

ata	agt	aaa	tta	cca	cca	cag	tac	caa	ttc	ttg	gag	aaa	aaa	agt	gat	240
Ile	Ser	Lys	Leu	Pro	Pro	Gln	Tyr	Gln	Phe	Leu	Glu	Lys	Lys	Ser	Asp	
65				70					75					80		

tcc	tta	gag	aag	gta	tgt	aaa	agg	att	cta	ctg	gtg	tca	aaa	acg	ttc	288
Ser	Leu	Glu	Lys	Val	Cys	Lys	Arg	Ile	Leu	Leu	Val	Ser	Lys	Thr	Phe	
			85					90					95			

gaa	gta	gag	ggc	tac	gac	tat	cca	cca	aat	tta	acg	gag	agt	att	tcg	346
Glu	Val	Glu	Gly	Tyr	Asp	Tyr	Pro	Pro	Asn	Leu	Thr	Gln	Ser	Ile	Ser	
			100					105					110			

gat	tgg	tgg	tct	ctc	aat	aaa	gat	ggc	tgg	ttt	ggc	tct	aaa	aaa	tcc	394
Asp	Trp	Trp	Ser	Leu	Asn	Lys	Asp	Gly	Trp	Phe	Gly	Ser	Lys	Lys	Ser	
			115					120					125			

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gaa agt tuc act aaa aaa aag gga tuc aac cat gac gat gct ttt ttg	432
Glu Ser Ser Thr Lys Lys Lys Gly Ser Asn His Asp Asp Ala Phe Leu	
130 135 140	
con agg tct ttt gct caa guc acu tca aaa gcc ggt gtt gac tgc gaa	480
Pro Arg Ser Phe Ala Gln Ala Ile Ser Lys Ala Ala Val Asp Cys Glu	
145 150 155 160	
tgt gaa ttt caa aat tta gaa cac aac gaa aag gca gan cta aag aag	528
Cys Glu Phe Gln Asn Leu Glu His Asn Glu Lys Ala Glu Leu Lys Lys	
165 170 175	
aaa aag gag tct atc aaa act gca cag aca aag gaa gct cag ggt gcc	576
Lys Lys Gln Ser Ile Lys Thr Ala Gln Thr Thr Glu Ala Gln Gly Ala	
180 185 190	
gac cat aat gaa gca gat gag gaa gat gaa gaa gai gaa gaa gat gat	624
Asp His Asn Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Asp Asp	
195 200 205	
gaa gat tly tct aat ttg atc aaa gtc ttc gal lcg tgg tgg aca tgc	672
Glu Asp Leu Ser Asn Leu Ile Lys Val Phe Asp Ser Trp Ser Thr Cys	
210 215 220	
tat aca aat atc gat gaa ggg aag gca gag atg gat tct atg atg gtc	720
Tyr Lys Asn Ile Asp Gln Gly Lys Ala Glu Met Asp Ser Met Met Val	
225 230 235 240	
aag gaa tcc aac aaa aaa tta gaa aca tta ata aac caa gac ttc aag	768
Lys Glu Phe Asn Lys Lys Leu Glu Thr Asn Ile Asn Gln Asp Phe Lys	
245 250 255	
aag gtc cat gac ctg cgc aaa aaa gtc gaa gaa tca aga ctg aca ttc	816
Lys Val His Asp Leu Arg Lys Lys Val Glu Glu Ser Arg Leu Lys Phe	
260 265 270	
gat aca atg cgt tat gaa gtc aac gca aaa gaa gca gag tta gag gog	864
Asp Thr Met Arg Tyr Gln Val Lys Ala Lys Glu Ala Glu Leu Glu Ala	
275 280 285	
aaa aaa gct gaa guc aca gga gaa gca cat acc aag gat gtt ayc gca	912
Lys Lys Ala Glu Ala Thr Gly Glu Ala His Ser Lys Asp Val Ser Ala	

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290	295	300	
aag gac att ago gaa aac act acc acc tct ttt gac gaa aag cca tcc			960
Lys Asp Ile Ser Ala Asn Thr Thr Thr Ser Phe Asp Glu Thr Pro Ser			
305	310	315	320
acc gag gat gaa aag cca aaa tca gag ggt gcc gaa gag gaa tca aag			1008
Thr Glu Asp Glu Lys Pro Lys Ser Glu Gly Ala Glu Glu Glu Ser Lys			
	325	330	335
aaa gaa gag aat gag cct act gtt gat gac gtt gct gat aga aaa gaa			1056
Lys Glu Ala Asn Glu Pro Thr Val Asp Asp Val Ala Asp Arg Lys Glu			
	340	345	350
gat tta aag agt aac aaa gta aat gat gag cca cag att gaa gaa tct			1104
Asp Leu Lys Ser Asn Lys Val Asn Asp Glu Pro Pro Ile Glu Glu Ser			
	355	360	365
gag gat aat aca tta ctg gac aaa ctg gag gat gaa ttt gtc tcc aat			1152
Glu Asp Asn Lys Leu Leu Glu Lys Leu Glu Asp Glu Phe Val Ser Asn			
	370	375	380
act aca gca gaa glg gaa aca atg gaa gaa atc act gac agt tct gaa			1200
Thr Thr Ala Ala Val Glu Thr Met Glu Glu Ile Thr Asp Ser Ser Glu			
385	390	395	400
att ctg ggc ttg ata aaa ctg ttc cag aat ttc cag ttg gtt tac ttt			1248
Ile Leu Gly Leu Ile Lys Leu Phe Gln Asn Phe Gln Leu Val Tyr Phe			
	405	410	415
aga caa tgt gtc caa gaa gtg gag gca aac ctt aaa gtt cta act ggt			1296
Arg Gln Cys Val Gln Glu Val Glu Ala Asn Leu Lys Val Leu Asn Gly			
	420	425	430
ctg gaa att tag			1308
Leu Glu Ile			
	435		
<210>	202		
<211>	435		
<212>	BBB		

<213> Saccharomyces cerevisiae

<400> 202

Met Ser Gly Tyr Phe Ser Gly Phe Ser Leu Asn Lys Ile Thr Asp Ser
1 5 10 15

Ile Ala Thr Ala Ala His Lys Thr Gln Asp Thr Leu Asn Asn Ala Leu
20 25 30

Ala Asn Ala Asn Val Asn Leu Asn Asp Pro Gln Thr Arg Leu Ser Ile
35 40 45

Lys Ser Arg Thr Arg Phe Val Gln Glu Ser Leu Gly Thr Val Ser Asp
50 55 60

Ile Ser Lys Leu Pro Pro Gln Tyr Gln Phe Leu Glu Lys Lys Ser Asp
65 70 75 80

Ser Leu Glu Lys Val Cys Lys Arg Ile Asn Asn Val Ser Lys Thr Phe
85 90 95

Glu Val Glu Gly Tyr Asp Tyr Pro Pro Asn Leu Thr Glu Ser Ile Ser
100 105 110

Asp Trp Trp Ser Leu Asn Lys Asp Gly Trp Phe Gly Ser Lys Lys Ser
115 120 125

Glu Ser Ser Thr Lys Lys Lys Gly Ser Asn His Asp Asp Ala Phe Leu
130 135 140

Pro Arg Ser Phe Ala Gln Ala Ile Ser Lys Ala Ala Val Asp Cys Glu
145 150 155 160

Cys Glu Phe Gln Asn Leu Glu His Asp Glu Lys Ala Glu Leu Iys Lys
165 170 175

Lys Lys Glu Ser Ile Lys Thr Ala Gln Thr Thr Glu Ala Gln Gly Ala
180 185 190

Asp His Asn Glu Glu Asp Glu Glu Asp Glu Glu Asp Glu Glu Asp Asp
195 200 205

Glu Asp Leu Ser Asn Leu Ile Lys Val Phe Asp Ser Trp Ser Thr Cys
210 215 220

Tyr Lys Asn Ile Asp Glu Gly Lys Ala Glu Met Asp Ser Met Met Val
225 230 235 240

Lys Glu Phe Asn Lys Lys Leu Glu Thr Leu Ile Asn Glu Asp Phe Lys
245 250 255

Lys Val His Asp Leu Arg Lys Lys Val Glu Glu Ser Arg Leu Lys Phe
260 265 270

Asp Thr Met Arg Tyr Glu Val Lys Ala Lys Glu Ala Glu Leu Glu Ala
275 280 285

Lys Lys Ala Glu Ala Thr Gly Glu Ala His Ser Lys Asp Val Ser Ala
290 295 300

Lys Asp Ile Ser Ala Asn Thr Thr Thr Ser Phe Asp Glu Thr Pro Ser
305 310 315 320

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Thr Glu Asp Glu Lys Pro Lys Ser Glu Gly Ala Glu Glu Glu Ser Lys
325 330 335

Lys Glu Ala Asn Glu Pro Thr Val Asp Asp Val Ala Asp Arg Lys Glu
340 345 350

Asp Leu Lys Ser Asn Lys Val Asn Asp Glu Pro Pro Ile Glu Glu Ser
355 360 365

Glu Asp Asn Lys Leu Leu Glu Lys Leu Glu Asp Glu Phe Val Ser Asn
370 375 380

Thr Thr Ala Ala Val Glu Thr Met Glu Glu Ile Thr Asp Ser Ser Glu
385 390 395 400

Ile Leu Gly Leu Ile Lys Leu Phe Gln Asn Phe Glu Leu Val Tyr Phe
405 410 415

Arg Gln Cys Val Gln Glu Val Glu Ala Asn Leu Lys Val Leu Asn Gly
420 425 430

Leu Glu Ile
435

<210> 203
<211> 1839
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(1839)

<400> 203

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Met	Ala	Glu	Met	Lys	Asn	Ser	Thr	Ala	Ala	Ser	Ser	Arg	Tyr	Thr	Lys	
1			5					10				15				

agt	cgt	ctc	tcc	cat	tcc	ttt	ccc	tcc	tac	act	aat	agc	agt	ggc	atg	95
Ser	Arg	Leu	Ser	His	Phe	Phe	Pro	Ser	Tyr	Thr	Asn	Ser	Ser	Gly	Met	
		20					25					30				

ggg	gcc	gac	tca	act	gat	caa	tct	tct	acg	cag	gga	gaa	gaa	ctg	cac	114
Gly	Ala	Ala	Ser	Thr	Asp	Gln	Ser	Ser	Thr	Gln	Gly	Glu	Glu	Leu	His	
	35					40					45					

cat	agg	aag	cac	tgt	gaa	gaa	gac	aat	gat	ggc	caa	aaa	cgc	aaa	aag	132
His	Arg	Lys	His	Cys	Glu	Glu	Asp	Asn	Asp	Gly	Gln	Lys	Pro	Lys	Lys	
	50					55				60						

tct	ccc	gta	tcc	acc	tct	aca	atg	caa	ata	aaa	tct	aga	cag	gat	gag	240
Ser	Pro	Val	Ser	Thr	Ser	Thr	Met	Gln	Ile	Lys	Ser	Arg	Gln	Asp	Glu	
65			70				75					80				

gac	gag	gat	gac	ggc	cga	att	gtc	att	aaa	ccc	gtt	aac	gat	gaa	gat	288
Asp	Gln	Asp	Asp	Gly	Arg	Ile	Val	Ile	Lys	Pro	Val	Asn	Asp	Glu	Asp	
		85				90					95					

gat	aca	tca	gtg	att	ata	act	ttc	aat	cag	tca	ala	tcc	ccc	ttt	att	336
Asp	Thr	Ser	Val	Ile	Ile	Thr	Phe	Asn	Gln	Ser	Ile	Ser	Pro	Phe	Ile	
		100				105					110					

att	aca	tcc	aca	ttc	gtt	ggc	tcc	att	tct	ggc	ttc	atg	ttt	ggc	tat	384
Ile	Thr	Leu	Thr	Phe	Val	Ala	Ser	Ile	Ser	Gly	Phe	Met	Phe	Gly	Tyr	
	115			120				125								

gat	act	ggc	tac	ata	tcc	agt	ggc	cta	att	tct	atc	aat	aga	gat	tta	432
Asp	Thr	Gly	Tyr	Ile	Ser	Ser	Ala	Leu	Ile	Ser	Ile	Asn	Arg	Asp	Leu	
	130			135			140									

gac	aac	aaa	ggt	tta	act	tat	gga	gaa	aaa	gaa	tta	att	acg	gac	gac	480
Asp	Asn	Lys	Val	Leu	Thr	Tyr	Gly	Glu	Lys	Glu	Leu	Ile	Thr	Ala	Ala	
145			150				155				160					

aca	caa	tcc	ggc	gct	tcc	att	aca	agt	gtg	ggc	gct	ggt	act	gct	gct	528
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

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Thr Ser Leu Gly Ala Leu Ile Thr Ser Val Gly Ala Gly Thr Ala Ala	
165	175
gat gtc ttt gga aga aga cca tgt tta atg ctc ccc aat cty atg ttt	576
Asp Val Phe Gly Arg Arg Pro Cys Leu Met Phe Ser Asn Leu Met Phe	
180	195
ttg acc gga gca att tta caa att acc ggc cac aag ttt tgg cca atg	634
Leu Ile Gly Ala Ile Leu Gln Ile Thr Ala His Lys Phe Trp Gln Met	
195	200
ggc gcc ggt aga ctg att atg ggt ttc ggt gtc ggt att ggc tct ttg	672
Ala Ala Gly Arg Leu Ile Met Gly Phe Gly Val Gly Ile Gly Ser Leu	
210	220
att tct cct ctt ttt att agt gaa att gct cct aag atg atc agg ggt	720
Ile Ser Pro Leu Phe Ile Ser Glu Ile Ala Pro Lys Met Ile Arg Gly	
225	235
agg tta acc gtt ata aat tcc cta tgg ctg acc ggt ggt caa ttg att	758
Arg Leu Thr Val Ile Asn Ser Leu Trp Leu Thr Gly Gly Gln Leu Ile	
245	255
gct tac ggt tgt ggt ggc ggc ctg aac cac gtc aaa aac ggt tgg aga	816
Ala Tyr Gly Cys Gly Ala Gly Leu Asn His Val Lys Asn Gly Trp Arg	
260	270
alc tta gtt ggt ttg ccc ttg ata cct act gtt ttg cag ttt tct ttt	864
Ile Leu Val Gly Leu Ser Leu Ile Pro Thr Val Leu Gln Phe Ser Phe	
275	285
ttc tgt ttt ttg ccg gat acc cca aga tac tac gta atg aaa ggc gat	912
Phe Cys Phe Leu Pro Asp Thr Pro Arg Tyr Tyr Val Met Lys Gly Asp	
290	300
tta aag aga gca aaa atg gtt ctc aaa cga agt tac gta aac act gaa	960
Leu Lys Arg Ala Lys Met Val Leu Lys Arg Ser Tyr Val Asn Thr Glu	
305	320
gat gaa ata att gat caa aaa gtt gaa gaa tta tct agc tta aat caa	1008
Asp Glu Ile Ile Asp Gln Lys Val Glu Glu Leu Ser Ser Leu Asn Gln	
325	335

tcg ata cca gga aaa aat cca ata aca aaa ttc tgg aat atg ctc aag	1055
Ser Ile Pro Gly Tyr Asn Pro Ile Thr Lys Phe Trp Asn Met Val Lys	
340 345 350	
gaa ttg cac act gtg cct tca aat ttc aga ggc ttg att att ggt tgt	1104
Glu Leu His Thr Val Pro Ser Asn Phe Arg Ala Leu Ile Ile Gly Cys	
355 360 365	
ggc cta caa gcc att caa caa ttc tca ggt tgg aat tcc tta atg tac	1153
Gly Ieu Gln Ala Ile Gln Gln Phe Thr Gly Trp Asn Ser Leu Met Tyr	
370 375 380	
ttc tcc ggt aca ata ttt gaa act gtt gga ttc aaa aat tct tct gcc	1200
Phe Ser Gly Thr Ile Phe Glu Thr Val Gly Phe Lys Asn Ser Ser Ala	
385 390 395 400	
ggt tct att att gtc tca ggt act aat ttt gtg ttc aca tta ata gca	1248
Val Ser Ile Ile Val Ser Gly Thr Asn Phe Val Phe Thr Leu Ile Ala	
405 410 415	
ttt ttc tgg att gat aaa aac ggc cgt agg tac att tta ctg att gga	1296
Phe Phe Cys Ile Asp Lys Ile Gly Arg Arg Tyr Ile Leu Leu Ile Gly	
420 425 430	
cta cct ggt atg act gtg ggc ctg gtt ata tgt gct ata ggc ttc cat	1344
Leu Pro Gly Met Thr Val Ala Leu Val Ile Cys Ala Ile Ala Phe His	
435 440 445	
ttc cta ggt abb aag ttt aac ggt gct gat gca gta gtg gca tct gat	1392
Phe Leu Gly Ile Lys Phe Asn Gly Ala Asp Ala Val Val Ala Ser Asp	
450 455 460	
gga ttt tca tct tgg gcc att gtc att atc gta ttt act att gtg tat	1440
Gly Phe Ser Ser Trp Gly Ile Val Ile Ile Val Phe Ile Ile Val Tyr	
465 470 475 480	
gca gcc ttt tat gcc ctg ggt atc ggc act gtt cca tgg caa caa tgg	1488
Ala Ala Phe Tyr Ala Leu Gly Ile Gly Thr Val Pro Trp Gln Gln Ser	
485 490 495	
gaa tta ttt cca caa aac gtc aga ggt gta ggg aca tcc tac gct act	1536

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Glu	Leu	Phe	Pro	Gln	Asn	Val	Arg	Gly	Val	Gly	Thr	Ser	Tyr	Ala	Thr		
			500					505					510				
gcc	acc	aat	tgg	gca	ggc	tct	tta	gac	att	gag	tct	acg	ttc	tty	act	1534	
Ala	Thr	Asn	Trp	Ala	Gly	Ser	Leu	Val	Ile	Ala	Ser	Thr	Phe	Leu	Thr		
		515				520					525						
atg	tta	caa	aat	att	aca	cca	acg	ggc	aca	ttt	tca	ctc	ttt	gcc	ggc	1632	
Met	Leu	Gln	Asn	Ile	Thr	Pro	Thr	Gly	Thr	Phe	Ser	Phe	Phe	Ala	Gly		
		530				535					540						
gta	gca	tgt	tta	tca	acc	att	ttt	tgt	tac	ttt	tgt	tat	cca	gaa	cta	1680	
Val	Ala	Cys	Leu	Ser	Thr	Ile	Phe	Cys	Tyr	Phe	Cys	Tyr	Pro	Glu	Leu		
545					550					555				560			
tca	gga	tty	gag	tta	gag	gaa	gtt	caa	cca	att	tta	aag	gac	gga	ttc	1728	
Ser	Gly	Leu	Glu	Leu	Gln	Gln	Val	Gln	Thr	Ile	Leu	Lys	Asp	Gly	Phe		
			565					570					575				
aat	atc	aaa	gcc	tct	aaa	gct	cta	gct	aaa	aag	agg	aaa	caa	cag	gtg	1776	
Asn	Ile	Lys	Ala	Ser	Lys	Ala	Leu	Ala	Lys	Lys	Arg	Lys	Gln	Gln	Val		
		580						585					590				
gcc	gaa	ggc	gct	gcc	cat	cat	aaa	atc	aaa	ttc	gaa	cct	aca	cag	gaa	1824	
Ala	Glu	Gly	Ala	Ala	His	His	Lys	Leu	Lys	Phe	Glu	Pro	Thr	Gln	Glu		
		595				600						605					
att	gta	gaa	agt	tag												1872	
Ile	Val	Glu	Ser														
		610															
<210>	204																
<211>	612																
<212>	FRT																
<213>	Shocharomyces cerevisiae																
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Met	Ala	Glu	Met	Lys	Asn	Ser	Thr	Ala	Ala	Ser	Ser	Arg	Trp	Thr	Lys		
1				5						10					15		

Ser Arg Leu Ser His Phe Phe Pro Ser Tyr Thr Asn Ser Ser Gly Met
20 25 30

Gly Ala Ala Ser Thr Asp Gln Ser Ser Thr Gln Gly Glu Glu Leu His
35 40 45

His Arg Lys His Cys Glu Glu Asp Asn Asp Gly Gln Lys Pro Lys Lys
50 55 60

Ser Pro Val Ser Thr Ser Thr Met Gln Ile Lys Ser Arg Gln Asp Glu
65 70 75 80

Asp Glu Asp Asp Gly Arg Ile Val Ile Lys Pro Val Asn Asp Glu Asp
85 90 95

Asp Thr Ser Val Ile Ile Thr Phe Asn Gln Ser Ile Ser Pro Phe Ile
100 105 110

Ile Thr Leu Thr Phe Val Ala Ser Ile Ser Gly Phe Met Phe Gly Tyr
115 120 125

Asp Thr Gly Tyr Ile Ser Ser Ala Leu Ile Ser Ile Asn Arg Asp Leu
130 135 140

Asp Asn Lys Val Leu Thr Tyr Gly Glu Lys Glu Leu Ile Thr Ala Ala
145 150 155 160

Thr Ser Leu Gly Ala Leu Ile Thr Ser Val Gly Ala Gly Thr Ala Ala
165 170 175

Asp Val Phe Gly Arg Arg Pro Cys Leu Met Phe Ser Asn Leu Met Phe

130	185	190
Leu Ile Gly Ala Ile Leu Gln Ile Thr Ala His Lys Phe Trp Gln Met		
195	200	205
Ala Ala Gly Arg Leu Ile Met Gly Phe Gly Val Gly Ile Gly Ser Leu		
210	215	220
Ile Ser Pro Leu Phe Ile Ser Glu Ile Ala Pro Lys Met Ile Arg Gly		
225	230	235
Arg Leu Thr Val Ile Asn Ser Leu Trp Leu Thr Gly Gly Gln Leu Ile		
245	250	255
Ala Tyr Gly Cys Gly Ala Gly Leu Asn His Val Lys Asn Gly Trp Arg		
260	265	270
Ile Leu Val Gly Leu Ser Leu Ile Pro Thr Val Leu Gln Phe Ser Phe		
275	280	285
Phe Cys Phe Leu Pro Asp Thr Pro Arg Tyr Tyr Val Met Lys Gly Asp		
290	295	300
Leu Lys Arg Ala Lys Met Val Leu Lys Arg Ser Tyr Val Asn Thr Glu		
305	310	315
Asp Glu Ile Ile Asp Gln Lys Val Glu Glu Leu Ser Ser Leu Asn Gln		
325	330	335
Ser Ile Pro Gly Lys Asn Pro Ile Thr Lys Phe Trp Asn Met Val Lys		
340	345	350

Glu Leu His Thr Val Pro Ser Asn Phe Arg Ala Leu Ile Ile Gly Cys
355 360 365

Gly Leu Gln Ala Ile Gln Gln Phe Thr Gly Trp Asn Ser Leu Met Tyr
370 375 380

Phe Ser Gly Thr Ile Phe Glu Thr Val Gly Phe Lys Asn Ser Ser Ala
385 390 395 400

Val Ser Ile Ile Val Ser Gly Thr Asn Phe Val Phe Thr Leu Ile Ala
405 410 415

Phe Phe Cys Ile Asp Lys Ile Gly Arg Arg Tyr Ile Leu Leu Ile Gly
420 425 430

Leu Pro Gly Met Thr Val Ala Leu Val Ile Cys Ala Ile Ala Phe His
435 440 445

Phe Leu Gly Ile Lys Phe Ser Gly Ala Asp Ala Val Val Ala Ser Asp
450 455 460

Gly Phe Ser Ser Trp Gly Ile Val Ile Ile Val Phe Ile Ile Val Tyr
465 470 475 480

Ala Ala Phe Tyr Ala Leu Gly Ile Gly Thr Val Pro Trp Gln Gln Ser
485 490 495

Glu Leu Phe Pro Gln Asn Val Arg Gly Val Gly Thr Ser Tyr Ala Thr
500 505 510

Ala Thr Asn Trp Ala Gly Ser Leu Val Ile Ala Ser Thr Phe Leu Thr

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515

520

525

Met Leu Gln Asn Ile Thr Pro Thr Gly Thr Phe Ser Phe Phe Ala Gly
 530 535 540

Val Ala Cys Leu Ser Thr Ile Phe Cys Tyr Phe Cys Tyr Pro Glu Leu
 545 550 555 560

Ser Gly Leu Glu Leu Glu Glu Val Glu Thr Ile Leu Lys Asp Gly Phe
 565 570 575

Asn Ile Lys Ala Ser Lys Ala Leu Ala Lys Lys Arg Lys Gln Gln Val
 580 585 590

Ala Gly Gly Ala Ala His His Lys Leu Lys Phe Glu Pro Thr Gln Glu
 595 600 605

Ile Val Glu Ser
 610

<210> 205
 <211> 624
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (624)

<400> 205
 atg cgc gtt ttt act ttg att ggc att ttg ttt agt tca tct ttg tta
 Met Arg Val Phe Thr Leu Ile Ala Ile Leu Phe Ser Ser Ser Leu Leu
 1 5 10 15

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aca cat gca ttc tcc tct aat tat gct cct gta ggc ata tca tta cct	96
Thr His Ala Phe Ser Ser Asn Tyr Ala Pro Val Gly Ile Ser Leu Pro	
20 25 30	
ggt ttt acc aaa gaa tgt ctt tac tat gat tta tcc tct gat aaa gat	144
Ala Phe Thr Lys Glu Cys Leu Tyr Tyr Asp Leu Ser Ser Asp Lys Asp	
35 40 45	
gtc ctt gtg gtc agt tac caa gtt ctg aca ggt ggg aat ttc gag ata	192
Val Leu Val Val Ser Tyr Gln Val Leu Thr Gly Gly Asn Phe Gln Ile	
50 55 60	
gac ttc gat act acc ggc cct gat ggc tct gtt acg glu act gaa aga	240
Asp Phe Asp Ile Thr Ala Pro Asp Gly Ser Val Ile Val Thr Glu Arg	
65 70 75 80	
caa aag aag cat tct gat ttt cta ctg aag tct ttt ggt ata ggt aag	288
Gln Lys Lys His Ser Asp Phe Leu Leu Lys Ser Phe Gly Ile Gly Lys	
85 90 95	
tac act ttc tgc ttg agt aat aac tac ggc act tcc cca aag aaa gtt	336
Tyr Thr Phe Cys Leu Ser Asn Asn Tyr Gly Thr Ser Pro Lys Lys Val	
100 105 110	
gaa atc acc ctc gaa aag gaa aag gaa att gtt tct tcc cat gaa agc	384
Glu Ile Thr Leu Glu Lys Glu Lys Glu Ile Val Ser Ser His Glu Ser	
115 120 125	
aaa gag gac ata atc gca aac aac ggc atc gag gaa att gat agg aac	432
Lys Glu Asp Ile Ile Ala Asn Leu Ala Ile Glu Gln Ile Asp Arg Asn	
130 135 140	
ctg aat aag atc acc aaa aca atg gat tat tta agg gct aga gaa tgg	480
Leu Asn Lys Ile Thr Lys Thr Met Asp Tyr Leu Arg Ala Arg Gln Trp	
145 150 155 160	
aga aac atg tat act gtg agt tct act gag tca aga tta aca tgg ctc	528
Arg Asn Met Tyr Thr Val Ser Ser Thr Glu Ser Arg Leu Thr Trp Leu	
165 170 175	
tca tta cta att atg ggg gta atg gtc ggt atc aat ata gta caa gca	576
Ser Leu Leu Ile Met Gly Val Met Val Gly Ile Ser Ile Val Gln Ala	

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180	185	190	
tta att att cag ttc ttt ttt acc agt cgc gaa asa aac tac gta tag			624
Leu Ile Ile Gln Phe Phe Phe Thr Ser Arg Gln Lys Asn Tyr Val			
195	200	205	
<210>	206		
<211>	207		
<212>	PRT		
<213>	<i>Saccharomyces cerevisiae</i>		
<400>	206		
Met Arg Val Phe Thr Leu Ile Ala Ile Leu Phe Ser Ser Ser Leu Leu			
1	5	10	15
Thr His Ala Phe Ser Ser Asn Tyr Ala Pro Val Gly Ile Ser Leu Pro			
20	25	30	
Ala Phe Thr Lys Glu Cys Leu Tyr Tyr Asp Leu Ser Ser Asp Lys Asp			
35	40	45	
Val Leu Val Val Ser Tyr Gln Val Leu Thr Gly Gly Asn Phe Glu Ile			
50	55	60	
Asp Phe Asp Ile Thr Ala Pro Asp Gly Ser Val Ile Val Thr Glu Arg			
65	70	75	80
Gln Lys Lys His Ser Asp Phe Leu Leu Lys Ser Phe Gly Ile Gly Lys			
85	90	95	
Tyr Thr Phe Cys Leu Ser Asn Asn Tyr Gly Thr Ser Pro Lys Lys Val			
100	105	110	

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Glu Ile Thr Leu Glu Lys Glu Lys Glu Ile Val Ser Ser His Glu Ser
 115 120 125

Lys Glu Asp Ile Ile Ala Asn Asn Ala Ile Glu Glu Ile Asp Arg Asn
 130 135 140

Leu Asn Lys Ile Thr Lys Thr Met Asp Tyr Leu Arg Ala Arg Glu Trp
 145 150 155 160

Arg Asn Met Tyr Thr Val Ser Ser Thr Glu Ser Arg Leu Thr Trp Leu
 165 170 175

Ser Leu Leu Ile Met Gly Val Met Val Gly Ile Ser Ile Val Gln Ala
 180 185 190

Leu Ile Ile Gln Phe Phe Phe Thr Ser Arg Gln Lys Asn Tyr Val
 195 200 205

<210> 207
 <211> 483
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (483)

<400> 207
 atg ggt aaa tca cat ggt tac aga tct cgt aca cgt tac atg ttc caa 48
 Met Gly Lys Ser His Gly Tyr Arg Ser Arg Thr Arg Tyr Met Phe Gln
 1 5 10 15

cgt gac ttc aga aag cat ggt gac gtt cac atg tcc acc tac ttg aag 96
 Arg Asp Phe Arg Lys His Gly Ala Val His Met Ser Thr Tyr Leu Lys
 20 25 30

atc tac aag gtt ggt gac att gtc gac atc aaa gcc aat ggt tct aic	144
Ile Tyr Lys Val Gly Asp Ile Val Asp Ile Lys Ala Asn Gly Ser Ile	
35 40 45	
caa aag ggt atg cca cac aag ttc tac caa ggt aag acc ggt gtc gtc	192
Gln Lys Gly Met Pro His Lys Phe Tyr Gln Gly Lys Thr Gly Val Val	
50 55 60	
tac aac gtt acc aag tcc tct gtt ggt gtt atc atc aac aag atg gtc	240
Tyr Asn Val Thr Lys Ser Ser Val Gly Val Ile Ile Asn Lys Met Val	
65 70 75 80	
ggt aac aga tac ttg gaa aag aga ttg aac ttg aga gtt gaa cac aic	288
Gly Asn Arg Tyr Leu Glu Lys Arg Leu Asn Leu Arg Val Glu His Ile	
85 90 95	
aag cac tct aaa tgt aga caa gaa ttt ttg gaa aga gtt aag gcc aat	336
Lys His Ser Lys Cys Arg Gln Glu Phe Iou Glu Arg Val Lys Ala Asn	
100 105 110	
gct gct aag tgt gct gaa gcc aag gcc caa ggt gtt gct gtc caa ttg	384
Ala Ala Lys Arg Ala Glu Ala Lys Ala Glu Gly Val Ala Val Glu Leu	
115 120 125	
aag aga caa cca gct cca cca aga gaa tcc cgt att gtc tct act gaa	432
Lys Arg Gln Pro Ala Glu Pro Arg Glu Ser Arg Ile Val Ser Thr Glu	
130 135 140	
ggt aac gtt acc caa act tta gct cca gtt cca tac gaa acc ttc att	480
Gly Asn Val Pro Gln Thr Leu Ala Pro Val Pro Tyr Glu Thr Phe Ile	
145 150 155 160	
taa	483

<210> 208

<211> 160

<212> PRT

<213> Saccharomyces cerevisiae

<400> 208

Met Gly Lys Ser His Gly Tyr Arg Ser Arg Thr Arg Tyr Met Phe Gln
 1 5 10 15

Arg Asp Phe Arg Lys His Gly Ala Val His Met Ser Thr Tyr Leu Lys
 20 25 30

Ile Tyr Lys Val Gly Asp Ile Val Asp Ile Lys Ala Asn Gly Ser Ile
 35 40 45

Gln Lys Gly Met Pro His Lys Phe Tyr Gln Gly Lys Thr Gly Val Val
 50 55 60

Tyr Asn Val Thr Lys Ser Ser Val Gly Val Ile Ile Asn Lys Met Val
 65 70 75 80

Gly Asn Arg Tyr Leu Glu Lys Arg Leu Asn Leu Arg Val Glu His Ile
 85 90 95

Lys His Ser Lys Cys Arg Gln Glu Phe Leu Glu Arg Val Lys Ala Asn
 100 105 110

Ala Ala Lys Arg Ala Glu Ala Lys Ala Gln Gly Val Ala Val Gln Leu
 115 120 125

Lys Arg Glu Pro Ala Gln Pro Arg Glu Ser Arg Ile Val Ser Thr Glu
 130 135 140

Gly Asn Val Pro Gln Thr Leu Ala Pro Val Pro Tyr Glu Thr Phe Ile
 145 150 155 160

<210> 209

<211> 1737

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1737)

<400> 209

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Met	Ser	Ile	Gln	Ala	Phe	Val	Phe	Cys	Gly	Lys	Gly	Ser	Asn	Leu	Ala	
1			5					10				15				

ccc	ttc	acc	cag	cca	gat	ttt	cca	ttc	caa	acg	cag	aac	aaa	gac	agt	96
Pro	Phe	Thr	Gln	Pro	Asp	Phe	Pro	Phe	Gln	Thr	Gln	Asn	Lys	Asp	Ser	
			20				25					30				

aca	gct	gcc	acg	agg	ggg	gac	aaa	ctt	aat	gag	ttg	gtc	act	agc	gcc	144
Thr	Ala	Ala	Thr	Ser	Gly	Asp	Lys	Leu	Asn	Glu	Leu	Val	Asn	Ser	Ala	
			35				40					45				

ctc	gat	tca	act	gtc	ata	aat	gag	ttc	atg	caa	cat	tca	acg	cgc	tgg	192
Ile	Asp	Ser	Thr	Val	Ile	Asn	Glu	Phe	Met	Gln	His	Ser	Thr	Arg	Leu	
			50				55					60				

ccc	aag	ggt	gtt	tgg	ccc	atc	ggg	aat	aga	cct	atg	att	gaa	tac	gtc	240
Pro	Lys	Ala	Leu	Leu	Pro	Ile	Gly	Asn	Arg	Pro	Met	Ile	Glu	Tyr	Val	
65				70				75				80				

ttg	gat	tgg	tgt	gat	cag	gca	gat	ttc	aaa	gaa	atc	agt	gtg	gtc	gca	288
Leu	Asp	Trp	Cys	Asp	Gln	Ala	Asp	Phe	Lys	Glu	Ile	Ser	Val	Val	Ala	
			85					90				95				

ccc	gtt	gac	gaa	atc	gaa	tta	att	gaa	agt	ggg	ctg	act	tgg	ttt	ttg	336
Pro	Val	Asp	Glu	Ile	Glu	Leu	Ile	Glu	Ser	Gly	Leu	Thr	Ser	Phe	Leu	
			100					105				110				

tcc	cta	aga	aag	caa	caa	ttt	gaa	cta	ata	tac	aag	gct	ttg	tca	aat	384
Ser	Leu	Arg	Lys	Gln	Gln	Phe	Glu	Leu	Ile	Tyr	Lys	Ala	Leu	Ser	Asn	
			115					120				125				

tcc aac cac agt cat cac ttg cca gat cct aag aaa att aat ttc atc	432
Ser Asn His Ser His His Leu Gln Asp Pro Lys Lys Ile Asn Phe Ile	
130 135 140	
cct tgg aag gca aat tct acc ggt gag tcc ttg caa aaa gag ctt ttg	480
Pro Ser Lys Ala Asn Ser Thr Gly Gln Ser Leu Gln Lys Glu Leu Leu	
145 150 155 160	
cct aga atc aat ggc gat ttt gta ata ttg ccc tgt gat ttt gtc aca	528
Pro Arg Ile Asn Gly Asp Phe Val Ile Leu Pro Cys Asp Phe Val Thr	
165 170 175	
gat ata cct cca caa gtc ttg gtc gat caa ttt agg aat agg gat gat	576
Asp Ile Pro Pro Gln Val Leu Val Asp Gln Phe Arg Asn Arg Asp Asp	
180 185 190	
aat aac cta gca atg aat atc tac tat aag aac tct tta gat agt agt	624
Asn Asn Leu Ala Met Thr Ile Tyr Tyr Lys Asn Ser Ser Asp Ser Ser	
195 200 205	
atc gat aaa aag caa cag caa aag caa aaa caa cag caa ttt ttc act	672
Ile Asp Lys Lys Gln Gln Gln Lys Gln Lys Gln Gln Cln Phe Phe Thr	
210 215 220	
att tat tca gaa aac gaa gac tca gag agg cag cca ata ctt ttg gac	720
Val Tyr Ser Glu Asn Glu Asp Ser Glu Arg Gln Pro Ile Leu Leu Asp	
225 230 235 240	
gtt tat tct caa agg gac gtc acc aag acc aaa tat cta cag atc aga	768
Val Tyr Ser Gln Arg Asp Val Thr Lys Thr Lys Tyr Leu Gln Ile Arg	
245 250 255	
tct cat tta tta tgg aac tcc acc aat tta acc gta tcc act aag tta	816
Ser His Leu Leu Trp Asn Tyr Pro Asn Leu Thr Val Ser Thr Lys Leu	
260 265 270	
ctg aac tca ttc atc cac ccc tgt tcc ttt gaa ctt tgc cag ttg tta	864
Leu Asn Ser Phe Ile Tyr Phe Cys Ser Phe Gln Leu Cys Gln Leu Leu	
275 280 285	
aaa tta gga cct caa tca atg tca aga caa gct tca ttc aaa gat cca	912
Lys Leu Gly Pro Gln Ser Met Ser Arg Gln Ala Ser Phe Lys Asp Pro	

280	295	300	
ttt act gga aac caa caa cag caa aac cct cct act act gat gat gat			960
Phe Thr Gly Asn Gln Gln Gln Gln Asn Pro Pro Thr Thr Asp Asp Asp			
305	310	315	320
gaa gat cgc aat cat gat gat gac gat gat tac aaa cct tcg ggt acc			1008
Glu Asp Arg Asn His Asp Asp Asp Asp Asp Tyr Lys Pro Ser Ala Thr			
	325	330	335
tct atc cag cct acc tac ttc aaa aaa aag aat gat ctc atc ttg gac			1056
Ser Ile Gln Pro Thr Tyr Phe Lys Lys Lys Asn Asp Leu Ile Leu Asp			
	340	345	350
cca ata aac tgt aat aaa tca ttg agt aag gtt ttt aga gat tta cct			1104
Pro Ile Asn Cys Asn Lys Ser Leu Ser Lys Val Phe Arg Asp Leu Ser			
	355	360	365
cgt cgt tcg tgg caa cat tcg aca ccg agg gaa cca ata ggt att ttt			1152
Arg Arg Ser Trp Gln His Ser Lys Pro Arg Glu Pro Ile Gly Ile Phe			
	370	375	380
att tta cca aac gaa acc ttg ttc atc aga gcc aat aac ttg aat gct			1200
Ile Leu Pro Asn Glu Thr Leu Phe Ile Arg Ala Asn Asn Leu Asn Ala			
	385	390	395
tac atg gac gct aat aga ttt gta cta aag ata aaa tca caa acg atg			1248
Tyr Met Asp Ala Asn Arg Phe Val Leu Lys Ile Lys Ser Gln Thr Met			
	405	410	415
ttc acg aaa aat ata cag att caa tct gcc gct atc ggt gct gat gcc			1296
Phe Thr Lys Asn Ile Gln Ile Gln Ser Ala Ala Ile Gly Ala Asp Ala			
	420	425	430
ata gta gat ccc aaa tgc caa acc tct ggt cat agt aat gtc aag atg			1344
Ile Val Asp Pro Lys Cys Gln Ile Ser Ala His Ser Asn Val Lys Met			
	435	440	445
tct gtt ctc ggt act cag gcc aat att ggt tcc aga tgt cgt gtt gcc			1392
Ser Val Leu Gly Thr Gln Ala Asn Ile Gly Ser Arg Cys Arg Val Ala			
	450	455	460

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ggg tct ctc tta ttt cct gga gtc cat ctt ggt gac gaa gta atc ctg 1440
 Gly Ser Leu Leu Phe Pro Gly Val His Leu Gly Asp Gln Val Ile Leu
 465 470 475 480

gaa aat tgt att att gga cct atg gca aaa atc ggt tca aag tgt aaa 1488
 Glu Asn Cys Ile Ile Gly Pro Met Ala Lys Ile Gly Ser Lys Cys Lys
 485 490 495

ctc agc aat tgt tat atc gaa ggc aat tat gtt gtg gag cct aaa aat 1536
 Leu Ser Asn Cys Tyr Ile Glu Gly His Tyr Val Val Glu Pro Lys Asn
 500 505 510

aac cct aaa ggc gaa aca ctc gcc aac gtt tat ttc gat gaa gat gag 1584
 Asn Phe Lys Gly Glu Thr Leu Ala Asn Val Tyr Leu Asp Glu Asp Glu
 515 520 525

gag gac gag tta ata tat gat gat agt gtt att gct gga gaa agt gaa 1632
 Glu Asp Glu Leu Ile Tyr Asp Asp Ser Val Ile Ala Gly Glu Ser Glu
 530 535 540

atc gcc gaa gaa act gac agt gat gat aga agc gat gaa gat tct gat 1680
 Ile Ala Glu Glu Thr Asp Ser Asp Asp Arg Ser Asp Glu Asp Ser Asp
 545 550 555 560

gat agt gaa tat acc gac gag tac gag tac gaa gat gac gga tta tct 1728
 Asp Ser Glu Tyr Thr Asp Glu Tyr Glu Tyr Glu Asp Asp Gly Leu Phe
 565 570 575

gag agt taa 1737
 Glu Arg

<210> 210

<211> 578

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 210

Met Ser Ile Gln Ala Phe Val Phe Cys Gly Lys Gly Ser Asp Leu Ala
 1 5 10 15

Pro Phe Thr Gln Pro Asp Phe Pro Phe Gln Thr Gln Asn Lys Asp Ser
20 25 30

Thr Ala Ala Thr Ser Gly Asp Lys Leu Asn Gln Leu Val Asn Ser Ala
35 40 45

Leu Asp Ser Thr Val Ile Asn Glu Phe Met Gln His Ser Thr Arg Leu
50 55 60

Pro Lys Ala Leu Leu Pro Ile Gly Asn Arg Pro Met Ile Glu Tyr Val
65 70 75 80

Leu Asp Thr Cys Asp Gln Ala Asp Phe Lys Glu Ile Ser Val Val Ala
85 90 95

Pro Val Asp Glu Ile Glu Leu Ile Glu Ser Gly Leu Thr Ser Phe Leu
100 105 110

Ser Leu Arg Lys Gln Gln Phe Glu Leu Ile Tyr Lys Ala Leu Ser Asn
115 120 125

Ser Asn His Ser His His Leu Gln Asp Pro Lys Lys Ile Asn Phe Ile
130 135 140

Pro Ser Lys Ala Asn Ser Thr Gly Gln Ser Leu Gln Lys Glu Leu Leu
145 150 155 160

Pro Arg Ile Asn Gly Asp Phe Val Ile Leu Pro Cys Asp Phe Val Thr
165 170 175

Asp Ile Pro Pro Gln Val Leu Val Asp Gln Phe Arg Asn Arg Asp Asp
180 185 190

Asn Asn Leu Ala Met Thr Ile Tyr Tyr Lys Asn Ser Leu Asp Ser Ser
195 200 205

Ile Asp Lys Lys Gln Gln Gln Lys Gln Lys Gln Gln Gln Phe Phe Thr
210 215 220

Val Tyr Ser Glu Asn Glu Asp Ser Glu Arg Gln Pro Ile Leu Leu Asp
225 230 235 240

Val Tyr Ser Gln Arg Asp Val Thr Lys Thr Lys Tyr Leu Gln Ile Arg
245 250 255

Ser His Asn Leu Trp Asn Tyr Pro Asn Leu Thr Val Ser Thr Lys Leu
260 265 270

Leu Asn Ser Phe Ile Tyr Phe Cys Ser Phe Gln Leu Cys Gln Leu Leu
275 280 285

Lys Leu Gly Pro Gln Ser Met Ser Arg Gln Ala Ser Phe Lys Asp Pro
290 295 300

Phe Thr Gly Asn Gln Gln Gln Gln Asn Pro Pro Thr Thr Asp Asp Asp
305 310 315 320

Glu Asp Arg Asn His Asp Asp Asp Asp Asp Tyr Lys Pro Ser Ala Thr
325 330 335

Ser Ile Gln Pro Thr Tyr Phe Lys Lys Lys Asn Asp Leu Ile Leu Asp
340 345 350

Pro Ile Asn Cys Asn Lys Ser Leu Ser Lys Val Phe Arg Asp Leu Ser
355 360 365

Arg Arg Ser Trp Gln His Ser Lys Pro Arg Glu Pro Ile Gly Ile Phe
370 375 380

Ile Leu Pro Asn Glu Thr Leu Phe Ile Arg Ala Asn Asn Leu Asn Ala
385 390 395 400

Tyr Met Asp Ala Asn Arg Phe Val Leu Lys Ile Lys Ser Gln Thr Met
405 410 415

Phe Thr Lys Asn Ile Gln Ile Gln Ser Ala Ala Ile Gly Ala Asp Ala
420 425 430

Ile Val Asp Pro Lys Cys Gln Ile Ser Ala His Ser Asn Val Lys Met
435 440 445

Ser Val Leu Gly Thr Gln Ala Asn Ile Gly Ser Arg Cys Arg Val Ala
450 455 460

Gly Ser Leu Leu Phe Pro Gly Val His Leu Gly Asp Glu Val Ile Leu
465 470 475 480

Glu Asn Cys Ile Ile Gly Pro Met Ala Lys Ile Gly Ser Lys Cys Lys
485 490 495

Leu Ser Asn Cys Tyr Ile Glu Gly His Tyr Val Val Glu Pro Lys Asn
500 505 510

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Asn Phe Lys Gly Glu Thr Leu Ala Asn Val Tyr Leu Asp Glu Asp Glu .
 515 520 525

Glu Asp Glu Leu Ile Tyr Asp Asp Ser Val Ile Ala Gly Glu Ser Glu
 530 535 540

Ile Ala Glu Glu Thr Asp Ser Asp Asp Arg Ser Asp Glu Asp Ser Asp
 545 550 555 560

Asp Ser Glu Tyr Thr Asp Glu Tyr Glu Tyr Glu Asp Asp Gly Leu Phe
 565 570 575

Glu Arg

<210> 211
 <211> 1581
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1581)

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 Met Ser Thr Leu Phe Leu Ile Gly Ile His Glu Ile Glu Lys Ser Gln
 1 5 10 15
 aca att gta cag aat gaa cac tat ttt gat aga gtg att gag ctt caa 96
 Thr Ile Val Gln Asn Gln His Tyr Phe Asp Arg Val Ile Glu Leu Gln
 20 25 30
 gat ttg gat tct ctg atg gta gca ttg tat aag gac aga gtt tgg cct 144
 Asp Leu Asp Ser Leu Met Val Ala Leu Tyr Lys Asp Arg Val Ser Pro
 35 40 45

ttt cca aac gtc sat aac ttt qaa acg qgc gta tct ata gct ott tat	193
Phe Pro Asn Val His Asn Phe Glu Thr Gly Val Ser Ile Val Leu Tyr	
50 55 60	
gac cct tca aaa ttt caa tta tct gtg cga caa ttg gal ggt cta ttc	240
Asp Pro Ser Lys Phe Gln Leu Ser Val Arg Gln Leu Asp Val Leu Phe	
65 70 75 80	
aag cga ttt ttc cca tct ttc aat att tct ggc ata gat caa aca cga	288
Lys Arg Phe Phe Pro Ser Phe Asn Ile Ser Ala Ile Asp His Thr Arg	
85 90 95	
gag gaa aac atg caa cgt ctt gaa tgt gtt gag cgt gaa aat agc atc	326
Glu Gln Asn Leu Gln Arg Leu Glu Cys Val Glu Arg Glu Asn Ser Ile	
100 105 110	
tgt cgt aat aga ata acg aga att aac caa tgg atg tat caa cat caa	384
Cys Arg Asn Arg Ile Thr Arg Ile Asn His Trp Met Tyr His His His	
115 120 125	
gal gat aat caa gaa ggt att aac aca aac agc tat ggt act gta aat	432
Asp Asp Thr Pro Asp Gly Ile Asn Lys Asn Ser Tyr Gly Thr Val Asn	
130 135 140	
ggg aat tct gtc ccc act caa gca tgt gaa gca aac att taa act tta	480
Gly Asn Ser Val Pro Thr Gln Ala Cys Glu Ala Asn Ile Tyr Thr Leu	
145 150 155 160	
tta ttg cat ttg aat gat tcc aag gca caa cat tta cga aag gca tca	528
Leu Leu His Ser Asn Asp Ser Lys Ala Gln His Leu Arg Lys Ala Ser	
165 170 175	
ctg cca agg cta att cgc aac atc gag ttt atg tct tat ttg tca gat	576
Val Pro Arg Leu Ile Arg Asn Ile Glu Phe Met Ser Phe Leu Ser Asp	
180 185 190	
cca ata gaa aaa att tct caa gag gga taa caa tat tgg aac att cta	624
Pro Ile Glu Lys Ile Ser Gln Glu Gly Ser His Tyr Trp Asn Ile Leu	
195 200 205	
tca act tgg gac ttt tgt gct tta tca tta agc act caa gaa ttg att	672

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Ser Thr Trp Asp Phe Cys Ala Leu Ser Leu Ser Thr Gln Glu Asn Ile	
210	220
tgg tgc ggg ttc acg ctc atc aaa aag lta tcl aag cat gca aaa gta	720
Trp Cys Gly Phe Thr Leu Ile Lys Lys Leu Ser Tyr Asp Ala Lys Val	
225	230 235 240
ctc att gca gat aat aag lta ctg cta cta cta ttt act tta gaa tca	768
Leu Ile Ala Asp Asn Lys Leu Leu Leu Leu Leu Phe Thr Leu Glu Ser	
	245 250 255
tcc tat cat caa gtt aac aaa ttt cac aat ttt agg cat gcc atc gat	816
Ser Tyr His Gln Val Asn Lys Phe His Asn Phe Arg His Ala Ile Asp	
	260 265 270
gtc atg caa gcc aca tgg cga ttg tgt aca tat ctt ctt aaa gat aat	864
Val Met Gln Ala Thr Trp Arg Leu Cys Thr Tyr Leu Leu Lys Asp Asn	
	275 280 285
acc gta caa aca cta ctg ttg tgt atg gct gcc ata ggt cat gat gtc	912
Pro Val Gln Thr Leu Leu Leu Cys Met Ala Ala Ile Gly His Asp Val	
	290 295 300
ggc cat cct ggg act aac aat caa cta ttg tgc aac tgt gaa tca gag	960
Gly His Pro Gly Thr Asn Asn Gln Leu Leu Cys Asn Cys Glu Ser Gln	
305	310 315 320
gtc gct caa aat lta aaa aat gtc tct atc ttg gag aat ttt cac agg	1008
Val Ala Gln Asn Phe Lys Asn Val Ser Leu Leu Glu Asn Phe His Arg	
	325 330 335
gaa tta tll caa caa ttg cta tca gag cat tgg cct caa ttg cta tct	1056
Glu Leu Phe Gln Gln Leu Leu Ser Glu His Trp Pro Gln Leu Leu Ser	
	340 345 350
atc tcc aac aaa aac ttt gat ttt att tcc gag gct att ctg gcc aca	1104
Ile Ser Lys Lys Lys Phe Asp Phe Ile Ser Glu Ala Ile Leu Ala Thr	
	355 360 365
gat atg gca ttg cat tct cag tat gag gat aga tta atg cat gaa aac	1152
Asp Met Ala Leu His Ser Gln Tyr Glu Asp Arg Leu Met His Glu Asn	
	370 375 380

cca atg aaa caa atc act ttg ata tct cta att att aaa gct gca gac 1200
 Pro Met Lys Gln Ile Thr Leu Ile Ser Leu Ile Ile Lys Ala Ala Asp
 385 390 395 400

atc tct aat gtg acg aga add ttg tca ata tca gca cgt tgg gca tac 1248
 Ile Ser Asn Val Thr Arg Thr Leu Ser Ile Ser Ala Arg Trp Ala Tyr
 405 410 415

ctc att act ctc gaa ttt aat gat tgc gct cct ttg gaa aca ttt cct 1296
 Leu Ile Thr Leu Glu Phe Asn Asp Cys Ala Leu Leu Glu Thr Phe His
 420 425 430

aaa gct cac cgc cca gaa caa gac tgt ttt ggc gat tca tac aag aat 1344
 Lys Ala His Arg Pro Glu Gln Asp Cys Phe Gly Asp Ser Tyr Lys Asn
 435 440 445

gtt gat tct cgg aaa gaa gat ttg gaa tca att caa aat att ttg gtg 1392
 Val Asp Ser Pro Lys Glu Asp Leu Glu Ser Ile Gln Asn Ile Leu Val
 450 455 460

aac gta aca gac cct gat gat att atc aac gac cat cgg cat att caa 1440
 Asn Val Thr Asp Pro Asp Asp Ile Ile Lys Asp His Pro His Ile Pro
 465 470 475 480

aac ggt caa ata ttt ttc att aat acg ttt gct gaa gta ttt ttc aac 1488
 Asn Gly Gln Ile Phe Phe Ile Asn Thr Phe Ala Glu Val Phe Phe Asn
 485 490 495

gaa tta agt caa aaa ttc tca gga tta aaa ttc tta agc gat aat gtc 1536
 Ala Leu Ser Gln Lys Phe Ser Gly Leu Lys Phe Leu Ser Asp Asn Val
 500 505 510

aaa atc aat aaa gaa tac tgg atg aaa cac aag aaa cca caa tag 1581
 Lys Ile Asn Lys Glu Tyr Trp Met Lys His Lys Lys Pro Gln
 515 520 525

<210> 212

<211> 526

<212> PRT

<213> Saccharomyces cerevisiae

<400> 212

Met Ser Thr Leu Phe Leu Ile Gly Ile His Glu Ile Glu Lys Ser Glu
 1 5 10 15

Thr Ile Val Gln Asn Glu His Tyr Phe Asp Arg Val Ile Glu Leu Glu
 20 25 30

Asp Leu Asp Ser Leu Met Val Ala Leu Tyr Lys Asp Arg Val Ser Pro
 35 40 45

Phe Pro Asn Val His Asn Phe Glu Thr Gly Val Ser Ile Val Leu Tyr
 50 55 60

Asp Pro Ser Lys Phe Gln Leu Ser Val Arg Glu Leu Asp Val Leu Phe
 65 70 75 80

Lys Arg Phe Phe Pro Ser Phe Asn Ile Ser Ala Ile Asp His Thr Arg
 85 90 95

Glu Glu Asn Leu Gln Arg Leu Glu Cys Val Glu Arg Glu Asn Ser Ile
 100 105 110

Cys Arg Asn Arg Ile Thr Arg Ile Asn His Trp Met Tyr His His His
 115 120 125

Asp Asp Thr Pro Asp Gly Ile Asn Lys Asn Ser Tyr Gly Thr Val Asn
 130 135 140

Gly Asn Ser Val Pro Thr Gln Ala Cys Glu Ala Asn Ile Tyr Thr Leu
 145 150 155 160

Leu Leu His Leu Asn Asp Ser Lys Ala Gln His Leu Arg Lys Ala Ser
165 170 175

Val Pro Arg Leu Ile Arg Asn Ile Glu Phe Met Ser Phe Leu Ser Asp
180 185 190

Pro Ile Glu Lys Ile Ser Gln Glu Gly Ser His Tyr Trp Asn Ile Leu
195 200 205

Ser Thr Trp Asp Phe Cys Ala Leu Ser Leu Ser Thr Gln Gln Leu Ile
210 215 220

Trp Cys Gly Phe Thr Leu Ile Lys Lys Leu Ser Lys Asp Ala Lys Val
225 230 235 240

Leu Ile Ala Asp Asn Lys Leu Leu Leu Leu Leu Phe Thr Leu Glu Ser
245 250 255

Ser Tyr His Gln Val Asn Lys Phe His Asn Phe Arg His Ala Ile Asp
260 265 270

Val Met Gln Ala Thr Trp Arg Leu Cys Thr Tyr Leu Leu Lys Asp Asn
275 280 285

Pro Val Gln Thr Leu Leu Leu Cys Met Ala Ala Ile Gly His Asp Val
290 295 300

Gly His Pro Gly Thr Asn Asn Gln Leu Leu Cys Asn Cys Glu Ser Glu
305 310 315 320

Val Ala Gln Asn Phe Lys Asn Val Ser Ile Leu Glu Asn Phe His Arg

325 330 335
Glu Leu Phe Gln Gln Leu Leu Ser Gln His Trp Pro Gln Leu Leu Ser
340 345 350
Ile Ser Lys Lys Lys Phe Asp Phe Ile Ser Glu Ala Ile Leu Ala Thr
355 360 365
Asp Met Ala Leu His Ser Gln Tyr Glu Asp Arg Leu Met His Glu Asn
370 375 380
Pro Met Lys Gln Ile Thr Leu Ile Ser Leu Ile Ile Lys Ala Ala Asp
385 390 395 400
Ile Ser Asn Val Thr Arg Thr Leu Ser Ile Ser Ala Arg Trp Ala Tyr
405 410 415
Leu Ile Thr Leu Glu Phe Asn Asp Cys Ala Leu Leu Glu Thr Phe His
420 425 430
Lys Ala His Arg Pro Glu Gln Asp Cys Phe Gly Asp Ser Tyr Lys Asn
435 440 445
Val Asp Ser Pro Lys Glu Asp Leu Glu Ser Ile Gln Asn Ile Leu Val
450 455 460
Asn Val Thr Asp Pro Asp Asp Ile Ile Lys Asp His Pro His Ile Pro
465 470 475 480
Asn Gly Gln Ile Phe Phe Ile Asn Thr Phe Ala Glu Val Phe Phe Asn
485 490 495

Ala Leu Ser Gln Lys Phe Ser Gly Leu Lys Phe Leu Ser Asp Asn Val
 500 505 510

Lys Ile Asn Lys Glu Tyr Trp Met Lys His Lys Lys Pro Gln
 515 520 525

<210> 213
 <211> 2367
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(2367)

<400> 213
 atg gca ggt cat tca cac agg tca tca tta aaa aac cga cac aaa tct 48
 Met Ala Gly His Ser His Arg Ser Ser Leu Lys Asn Gly His Lys Ser
 1 5 10 15
 tac aac tcc aaa cat gct tct aaa ggt gct ttg aaa aga tra tcc aag 96
 Tyr Lys Ser Lys His Ala Ser Lys Gly Ala Leu Lys Arg Leu Tyr Lys
 20 25 30
 ggg aaa gtg gaa aaa gaa ccc gtg ggc act ggc aaa ccc gac aaa cna 144
 Gly Lys Val Glu Lys Glu Pro Val Gly Thr Gly Lys Pro Asp Lys Gln
 35 40 45
 gct tca aaa ttg caa cgt aaa aac aag gca aaa caa tta agg gcc caa 192
 Val Ser Lys Leu Gln Arg Lys Asn Lys Ala Lys Gln Leu Arg Ala Gln
 50 55 60
 agg atc ttg gat tcc att gaa aac agg aaa tta ttc gaa gga aaa aat 240
 Arg Ile Leu Asp Ser Ile Glu Asn Arg Lys Leu Phe Glu Gly Lys Asn
 65 70 75 80
 ggc gct gcc aaa atc att act att gtc ccg tta qtg aat gat tta gac 288
 Gly Ala Ala Lys Ile Ile Thr Ile Val Pro Leu Val Asn Asp Leu Asp

	85	90	95	
	cca ttg gac ata att tac aag cta tta aag tgg gca gat gat gaa gga			336
	Pro Leu Asp Ile Leu Tyr Lys Leu Leu Lys Cys Ala Asp Asp Glu Gly			
	130	105	110	
	acc atg gtg cag gaa gta gac tca aaa cgt ata ttt aat gtt cat ata			384
	Ile Met Val Gln Glu Val Asp Ser Lys Arg Ile Phe Asn Val His Ile			
	115	120	125	
	aag aag ttt aaa agc aat ctt aaa atc ata att cca gac atg acc aat			432
	Lys Lys Phe Lys Ser Asn Leu Lys Ile Ile Ile Pro Asp Met Thr Asn			
	130	135	140	
	ttt ttg aac att cta gat tgc gct aaa gta gca gac ttt gtt gtg ttt			480
	Phe Leu Asn Ile Leu Asp Cys Ala Lys Val Ala Asp Phe Val Val Phe			
	145	150	155	160
	ggg ctc agt ggt gtc caa gaa gtc gat gaa gaa ttt ggt gag cag acc			528
	Gly Leu Ser Gly Val Gln Glu Val Asp Glu Glu Phe Gly Glu Gln Ile			
	165	170	175	
	atc cgt gcg tca gaa cta caa ggt att gct tca tat atc ggt gtc tta			576
	Ile Arg Ala Leu Glu Leu Gln Gly Ile Ala Ser Tyr Ile Gly Val Ile			
	180	185	190	
	agc aac ctc tca gca gtc cat gaa aag gag aaa ctc caa ttg gat gtc			624
	Ser Asn Leu Ser Ala Val His Glu Lys Glu Lys Phe Gln Leu Asp Val			
	195	200	205	
	aag caa tcc tta gaa agt tat ttc aag cac ttt ttc cca agt gaa gaa			672
	Lys Gln Ser Leu Glu Ser Tyr Phe Lys His Phe Phe Pro Ser Glu Glu			
	210	215	220	
	cgt gtt tat aat ttg gaa aaa aac tca gac gct tta aac gtc ttg aga			720
	Arg Val Tyr Asn Leu Gln Lys Asn Ser Asp Ala Leu Asn Val Leu Arg			
	225	230	235	240
	aca ttg tgg cag agg cta cca aga tca atc aat tgg aga gac aat aga			768
	Thr Leu Cys Gln Arg Leu Pro Arg Ser Ile Asn Trp Arg Asp Asn Arg			
	245	250	255	

ggc tac gta glu gct gac ttt gtt gat ttc gtt gaa acc tct ccc gat	815
Gly Tyr Val Val Ala Asp Phe Val Asp Phe Val Glu Thr Ser Pro Asp	
260 265 270	
tct ggt gac ctg gta att gag ggg acc gtc cgt ggt att ggc ttc aac	864
Ser Gly Asp Leu Val Ile Glu Gly Thr Val Arg Gly Ile Gly Phe Asn	
275 280 285	
gcc aat aga ctg gtc cat att cct gat ttt ggt gac ttc caa ctc aat	912
Ala Asn Arg Leu Val His Ile Pro Asp Phe Gly Asp Phe Gln Leu Asn	
290 295 300	
aag ata gaa aaa atc agt gaa tct tcc cag aaa agg aaa ala ala aag	960
Lys Ile Glu Lys Ile Ser Glu Ser Ser Gln Lys Arg Lys Ile Ile Lys	
305 310 315 320	
gaa aaa gct aca gat agt ctg agc tta gag ctg gat tta caa aca gct	1008
Glu Lys Ala Thr Asp Ser Leu Ser Leu Glu Leu Asp Leu Gln Thr Val	
325 330 335	
ttc gaa agt aat atg aat aga gat aat ctg gac gaa tat gcc cca gaa	1056
Phe Glu Ser Asn Met Asn Arg Asp Thr Leu Asp Glu Tyr Ala Pro Glu	
340 345 350	
ggc acc gaa gat tgg tca gat tat gac gag gat ttt gag tac gac ggt	1104
Gly Thr Glu Asp Trp Ser Asp Tyr Asp Glu Asp Phe Glu Tyr Asp Gly	
355 360 365	
ttg aca acc gcy aga tac gac gac cat ggc ttc tly cca ggg agg gaa	1152
Leu Thr Thr Ala Arg Tyr Asp Asp His Gly Phe Leu Pro Gly Arg Glu	
370 375 380	
caa aca tca aaa aag gcg gcc gtc cct aag gga act tct gac tat caa	1200
Gln Thr Ser Lys Lys Ala Ala Val Pro Lys Gly Thr Ser Asp Tyr Gln	
385 390 395 400	
gcg aag tgg tac ttg gat gac gtc att gac gca aat gag gaa gaa gag	1248
Ala Lys Trp Tyr Leu Asp Asp Val Ile Asp Ala Asn Glu Glu Glu Glu	
405 410 415	
gca gaa cag acc aat gga aag gat cag aca atg atg gaa att gat gat	1296
Ala Glu Gln Thr Asn Gly Lys Asp Glu Thr Met Met Glu Ile Asp Asp	

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420	425	430	
gaa atg atg gtg gag caa gac aat gaa gag gta gca ggc gac gaa gaa			1344
Glu Met Met Val Glu Glu Asp Asn Glu Glu Val Ala Gly Asp Glu Glu			
435	440	445	
tat gac ata gag gat aat gaa gga ttt gaa gag ctt tca ccc gaa gaa			1392
Tyr Asp Ile Glu Asp Asn Glu Gly Phe Glu Glu Leu Ser Pro Glu Glu			
450	455	460	
gaa gaa cgt caa ctg agg gaa ttt aga gat atg gaa aag gag gac aga			1440
Glu Glu Arg Gln Leu Arg Glu Phe Arg Asp Met Glu Lys Glu Asp Arg			
465	470	475	480
gag ttc ccc gat gag atc gaa cta gag ccc agt gaa tct gcc atc gaa			1488
Glu Phe Pro Asp Glu Ile Glu Leu Glu Pro Ser Glu Ser Ala Ile Glu			
485	490	495	
cgt ttg aaa agg tat aga ggt ttg aaa aac tta tcc aac tgt gat tgg			1536
Arg Leu Lys Arg Tyr Arg Gly Leu Lys Asn Leu Tyr Asn Cys Asp Trp			
500	505	510	
caa gtt gat gaa aag gac caa tca tca caa gag gaa tgg aac cgt cta			1584
Gln Val Asp Glu Lys Asp Pro Ser Ser Pro Ala Glu Trp Lys Arg Leu			
515	520	525	
tta agg att ggc aat tcc aaa aac act aaa aac aga atc ata aag gaa			1632
Leu Arg Ile Gly Asn Tyr Lys Asn Thr Lys Asn Arg Ile His Lys Glu			
530	535	540	
acc aag aat gaa gca cag gcc att gca ggt gat cgt att agg atg ttc			1680
Thr Lys Asn Glu Ala Gln Ala Ile Ala Gly Asp Arg Ile Arg Met Phe			
545	550	555	560
atc agg ttt cct aag ttt ctg ctt gaa aag att caa gat cct aaa caa			1728
Ile Arg Phe Pro Lys Phe Leu Leu Glu Lys Ile Gln Asp Pro Lys Gln			
565	570	575	
cta tta ttt gct gtc tcc gga tta cta ctt cat gaa cac aaa aat ggc			1776
Leu Leu Phe Ala Val Tyr Gly Leu Leu Leu His Glu His Lys Asn Ala			
580	585	590	

gta gtc aac ttc tct cta caa aga tgg gaa caa tat gac aaa cct gtg	1824
Val Val Asn Phe Ser Leu Gln Arg Trp Glu Gln Tyr Asp Lys Pro Val	
595 600 605	
cct tct cag gag cct atc gta gta caa tac ggt gtt aga aga tac act	1872
Pro Ser Gln Gln Pro Ile Val Val Gln Tyr Gly Val Arg Arg Tyr Thr	
610 615 620	
att caa cct cta ttt tct caa ggc tct aac agt cct aat aat gtt cac	1920
Ile Gln Pro Leu Phe Ser Gln Gly Ser Asn Ser Pro Asn Asn Val His	
625 630 635 640	
aag tat gaa agg ttt ctg cat cca gat aca gta tca gtc gcc aca tgt	1968
Lys Tyr Glu Arg Phe Leu His Pro Asp Thr Val Ser Val Ala Thr Cys	
645 650 655	
att gct ccc gta gat ttc acc cag tca cct gca att ttt ttc aag cca	2016
Ile Ala Pro Val Asp Phe Thr Gln Ser Pro Ala Ile Phe Phe Lys Pro	
660 665 670	
tca cca aca gat gcc aaa aat att gaa ttg att ggt cac ggt aca ttc	2064
Ser Pro Thr Asp Ala Lys Asn Ile Glu Leu Ile Gly His Gly Thr Phe	
675 680 685	
ctg aac gca gac cat tca aga ata tta gca aag aga gcc att ttg acc	2112
Leu Asn Ala Asp His Ser Arg Ile Leu Ala Lys Arg Ala Ile Leu Thr	
690 695 700	
ggt cat cca ttc aga ttc cac aaa act gtg gtt act gta cgt tac atg	2160
Gly His Pro Phe Arg Phe His Lys Thr Val Val Thr Val Arg Tyr Met	
705 710 715 720	
ttt ttc aga cca gaa gat gtg gaa tgg ttc aag tct atc cca ctg ttc	2208
Phe Phe Arg Pro Glu Asp Val Glu Trp Phe Lys Ser Ile Pro Leu Phe	
725 730 735	
acc aaa tca ggt agt tca ggt ttc att aaa gaa agt ttg ggt aag caa	2256
Thr Lys Ser Gly Arg Ser Gly Phe Ile Lys Glu Ser Leu Gly Thr His	
740 745 750	
ggt tat ttc aag gct aca ttt gat ggt aaa tta tct gcg cag gat gtt	2304
Gly Tyr Phe Lys Ala Thr Phe Asp Gly Lys Leu Ser Ala Gln Asp Val	

755

7ED

765

tgg aat ggt atg taa 2367
 Trp Asn Gly Met
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<212> FFT
<213> Saccharomyces cerevisiae
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Gly Lys Val Glu Lys Glu Pro Val Gly Thr Gly Lys Pro Asp Lys Gln

35 40 45

Val Ser Lys Leu Gln Arg Lys Asn Lys Ala Lys Gln Leu Arg Ala Gln
50 55 60

Arg Ile Leu Asp Ser Ile Glu Asn Arg Lys Leu Phe Glu Gly Lys Asn
65 70 75 80

Gly Ala Afa Lys Ile Ile Thr Ile Val Pro Leu Val Asn Asp Leu Asp

85 90 95

Pro Leu Asp Ile Leu Tyr Lys Leu Leu Lys Cys Ala Asp Asp Glu Gly
100 105 110

Ile Met Val Gln Glu Val Asp Ser Lys Arg Ile Phe Asn Val His Ile
115 120 125

Lys Lys Phe Lys Ser Asn Leu Lys Ile Ile Ile Pro Asp Met Thr Asn
130 135 140

Phe Leu Asn Ile Leu Asp Cys Ala Lys Val Ala Asp Phe Val Val Phe
145 150 155 160

Gly Leu Ser Gly Val Gln Glu Val Asp Glu Glu Phe Gly Glu Gln Ile
165 170 175

Ile Arg Ala Leu Glu Leu Gln Gly Ile Ala Ser Tyr Ile Gly Val Ile
180 185 190

Ser Asn Leu Ser Ala Val His Glu Lys Glu Lys Phe Gln Leu Asp Val
195 200 205

Lys Gln Ser Leu Glu Ser Tyr Phe Lys His Phe Phe Pro Ser Glu Glu
210 215 220

Arg Val Tyr Asn Leu Glu Lys Asn Ser Asp Ala Leu Asn Val Leu Arg
225 230 235 240

Thr Leu Cys Gln Arg Leu Pro Arg Ser Ile Asn Trp Arg Asp Asn Arg
245 250 255

Gly Tyr Val Val Ala Asp Phe Val Asp Phe Val Glu Thr Ser Pro Asp
260 265 270

Ser Gly Asp Leu Val Ile Glu Gly Thr Val Arg Gly Ile Gly Phe Asn
275 280 285

Ala Asn Arg Leu Val His Ile Pro Asp Phe Gly Asp Phe Gln Leu Asn
290 295 300

Lys Ile Glu Lys Ile Ser Glu Ser Ser Gln Lys Arg Lys Ile Ile Lys
305 310 315 320

Glu Lys Ala Thr Asp Ser Leu Ser Leu Glu Leu Asp Leu Gln Thr Val
325 330 335

Phe Glu Ser Asn Met Asn Arg Asp Thr Leu Asp Glu Tyr Ala Pro Cys
340 345 350

Gly Thr Glu Asp Trp Ser Asp Tyr Asp Glu Asp Phe Glu Tyr Asp Gly
355 360 365

Leu Thr Thr Ala Arg Tyr Asp Asp His Gly Phe Leu Pro Gly Arg Glu
370 375 380

Gln Thr Ser Lys Lys Ala Ala Val Pro Lys Gly Thr Ser Asp Tyr Gln
385 390 395 400

Ala Lys Trp Tyr Leu Asp Asp Val Ile Asp Ala Asn Glu Glu Glu Glu
405 410 415

Ala Glu Gln Thr Asn Gly Lys Asp Glu Thr Met Met Gln Ile Asp Asp
420 425 430

Glu Met Met Val Glu Gln Asp Asn Glu Glu Val Ala Gly Asp Glu Gln
435 440 445

Tyr Asp Ile Glu Asp Asn Glu Gly Phe Glu Glu Leu Ser Pro Glu Glu
450 455 460

Glu Glu Arg Gln Leu Arg Glu Phe Arg Asp Met Glu Lys Glu Asp Arg
465 470 475 480

Glu Phe Pro Asp Glu Ile Glu Leu Glu Pro Ser Glu Ser Ala Ile Gln
485 490 495

Arg Leu Lys Arg Tyr Arg Gly Leu Lys Asn Leu Tyr Asn Cys Asp Trp
500 505 510

Gln Val Asp Glu Lys Asp Pro Ser Ser Pro Ala Glu Trp Lys Arg Leu
515 520 525

Leu Arg Ile Gly Asn Tyr Lys Asn Thr Lys Asn Arg Ile Ile Lys Glu
530 535 540

Thr Lys Asn Glu Ala Gln Ala Ile Ala Gly Asp Arg Ile Arg Met Phe
545 550 555 560

Ile Arg Phe Pro Lys Phe Leu Leu Glu Lys Ile Gln Asp Pro Lys Gln
565 570 575

Leu Leu Phe Ala Val Tyr Gly Leu Leu Asn His Glu His Lys Asn Ala
580 585 590

Val Val Asn Phe Ser Leu Gln Arg Trp Glu Gln Tyr Asp Lys Pro Val
595 600 605

Pro Ser Gln Glu Pro Ile Val Val Gln Tyr Gly Val Arg Arg Tyr Thr
610 615 620

Ile Gln Pro Leu Phe Ser Gln Gly Ser Asn Ser Pro Asn Asn Val His
625 630 635 640

Lys Tyr Glu Arg Phe Leu His Pro Asp Thr Val Ser Val Ala Thr Cys
645 650 655

Ile Ala Pro Val Asp Phe Thr Gln Ser Pro Ala Ile Phe Phe Lys Pro
660 665 670

Ser Pro Thr Asp Ala Lys Asn Ile Glu Leu Ile Gly His Gly Thr Pro
675 680 685

Leu Asn Ala Asp His Ser Arg Ile Leu Ala Lys Arg Ala Ile Leu Thr
690 695 700

Gly His Pro Phe Arg Phe His Lys Thr Val Val Thr Val Arg Tyr Met
705 710 715 720

Phe Phe Arg Pro Glu Asp Val Glu Trp Phe Lys Ser Ile Pro Leu Phe
725 730 735

Thr Lys Ser Gly Arg Ser Gly Phe Ile Lys Glu Ser Leu Gly Thr His
740 745 750

Gly Tyr Phe Lys Ala Thr Phe Asp Gly Lys Leu Ser Ala Gln Asp Val
755 760 765

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 770 775 780

Trp Asn Gly Met
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 tct gaa cgg ggg agc aat acc aga aca atg acg tat aaa aat aag ctt 96
 Ser Gln Arg Gly Ser Asn Thr Arg Thr Met Thr Tyr Lys Asn Lys Leu
 20 25 30
 aat ggt tgc ttc gat gac atc cta aaa gtt gga gca gaa atg atg atg 144
 Thr Val Cys Phe Asp Asp Ile Leu Lys Val Gly Ala Gln Met Met Met
 35 40 45
 caa caa cag tta aaa aat gta caa cta gat tot tat ctc gtc aat ggt 192
 Gln Gln Gln Leu Lys Asn Val Gln Leu Asp Ser Tyr Leu Val Asn Gly
 50 55 60
 ttc agt caa tct cag caa aaa tta ttg aaa gag aag gtt aaa tta ttt 240
 Phe Ser Gln Ser Gln Gln Lys Leu Ileu Tyr Glu Lys Val Lys Leu Phe
 65 70 75 80
 cat gga att tta gat gat tta gag act tct cta agc cag agt tct tca 288
 His Gly Ile Leu Asp Asp Leu Glu Thr Ser Leu Ser Gln Ser Ser Ser
 85 90 95

tat tta gaa act ctt act gca ctc gga aaa gaa aag gag aaa gaa aga	336
Tyr Leu Glu Thr Leu Thr Ala Leu Gly Lys Glu Lys Glu Lys Glu Arg	
100 105 110	
gag gaa gct gaa aaa aag agg gct gaa caa gaa aat atg agg aag gtt	384
Glu Glu Ala Glu Lys Lys Arg Ala Gln Gln Glu Asn Met Arg Lys Val	
115 120 125	
aga gaa caa gaa gaa tta aaa aag cga caa gaa ctc gaa gaa gcc tcc	432
Arg Glu Gln Glu Glu Leu Lys Lys Arg Gln Glu Leu Glu Glu Ala Ser	
130 135 140	
caa cag cag caa ctc cag caa aat tca aag gaa aaa aat ggc ctt ggt	480
Gln Gln Gln Gln Leu Gln Gln Asn Ser Lys Glu Lys Asn Gly Leu Gly	
145 150 155 160	
ttg aac ttc tcc aca aca gca cct gcy aac aca acg gat gcc aac ggt	528
Leu Asn Phe Ser Thr Thr Ala Pro Ala Asn Thr Thr Asp Ala Asn Gly	
165 170 175	
tcc aaa gag aat tat caa gaa ctt gga tct ctt caa tca tcc agt caa	576
Ser Lys Glu Asn Tyr Gln Glu Leu Gly Ser Leu Gln Ser Ser Ser Gln	
180 185 190	
aca caa cll gag aac gca aat gct gct aat aac ggt gcc gca ttt tct	624
Thr Gln Leu Glu Asn Ala Asn Ala Ala Asn Asn Gly Ala Ala Phe Ser	
195 200 205	
ccc tta acc act act cga atc caa agc cag cag gcc caa ccc tcg gat	672
Pro Leu Thr Thr Thr Arg Ile Gln Ser Gln Gln Ala Gln Pro Ser Asp	
210 215 220	
gta atg ttc aac gat tta aac tct atg gat att tcg atg ttt tca ggc	720
Val Met Phe Asn Asp Leu Asn Ser Met Asp Ile Ser Met Phe Ser Gly	
225 230 235 240	
cll gaa agl act ggt ttt gac tcc aca gcc ttc aat gcc acg gtg gac	768
Leu Asp Ser Thr Gly Phe Asp Ser Thr Ala Phe Asn Ala Thr Val Asp	
245 250 255	
gaa acc aaa gcc ttt gac gat aat gac tca ggt aac aac tuc aat gac	816

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Glu Thr Lys Gly Phe Asp Asp Asn Asp Ser Gly Asn Asn Tyr Asn Asp	
260	265 270
ala aal all tct tct att gaa aac aac ata aat aat aat aac aat agc	864
Ile Asn Ile Ser Ser Ile Glu Asn Asp Ile Asn Asn Asn Ile Asn Ser	
275	280 285
acc aag aac ggc aag gat aac aac aac gaa agc aac aac aat aac aac	912
Thr Lys Asn Gly Lys Asp Asn Asn Asn Glu Ser Asn Lys Asn Asn Asn	
290	295 300
ggc gat gaa aag aat aag aac aac aac gag gac aac gag aac aac aac	960
Gly Asp Glu Lys Asn Lys Asn Asn Asn Glu Asp Asn Glu Asn Asn Asn	
305	310 315 320
aac agc agt gag aag aac aac aal aat aat aat aat aac aat aac aac	1008
Asn Ser Ser Glu Lys Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn	
325	330 335
aat gac gat aac ggc aac aac aac aac aac aac agt ggg aac gac aat	1056
Asn Asp Asp Asn Gly Asn Asn Asn Asn Asn Asn Ser Gly Asn Asp Asn	
340	345 350
aac aat acc acc aac aac gac agc aat aac aag aac aal lcl alc aal	1104
Asn Asn Thr Thr Asn Asn Asp Ser Asn Asn Lys Asn Asn Ser Ile Thr	
355	360 365
acc gga aat gat aat gaa aat ata gtt aat aat gat tta cca aag acc	1152
Thr Gly Asn Asp Asn Glu Asn Ile Val Asn Asn Asp Leu Pro Thr Thr	
370	375 380
gtt gtt tcc aat cct gga gat aac cct cct cca gcc gac aac ggt gaa	1200
Val Val Ser Asn Pro Gly Asp Asn Pro Pro Pro Ala Asp Asn Gly Glu	
385	390 395 400
gaa tac ttg acc tta aat gat lcc aac gac ctt aat att gac tgg tog	1248
Glu Tyr Leu Thr Leu Asn Asp Phe Asn Asp Leu Asn Ile Asp Trp Ser	
405	410 415
acc act gga gat aat ggc gaa tta gac ctc agc ggc ttc aat ata tag	1296
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20 25 30

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35 40 45

Gln Gln Gln Leu Lys Asn Val Gln Leu Asp Ser Tyr Leu Val Asn Gly
50 55 60

Phe Ser Gln Ser Gln Gln Lys Leu Leu Lys Glu Lys Val Lys Leu Phe
65 70 75 80

His Gly Ile Leu Asp Asp Leu Glu Thr Ser Leu Ser Gln Ser Ser Ser
85 90 95

Tyr Leu Glu Thr Leu Thr Ala Leu Gly Lys Glu Lys Glu Lys Glu Arg
100 105 110

Glu Gln Ala Gln Lys Lys Arg Ala Glu Gln Glu Asn Met Arg Lys Val
115 120 125

Arg Gln Gln Gln Gln Leu Lys Lys Arg Gln Gln Leu Glu Glu Ala Ser

130 135 140

Gln Gln Glu Gln Leu Gln Glu Asn Ser Lys Glu Lys Asn Gly Leu Gly
145 150 155 160

Leu Asn Phe Ser Thr Thr Ala Pro Ala Asn Thr Thr Asp Ala Asn Gly
165 170 175

Ser Lys Glu Asn Tyr Gln Gln Leu Gly Ser Leu Gln Ser Ser Ser Gln
180 185 190

Thr Gln Leu Glu Asn Ala Asn Ala Ala Asn Asn Gly Ala Ala Phe Ser
195 200 205

Pro Leu Thr Thr Thr Arg Ile Gln Ser Glu Gln Ala Glu Pro Ser Asp
210 215 220

Val Met Phe Asn Asp Leu Asn Ser Met Asp Ile Ser Met Phe Ser Gly
225 230 235 240

Leu Asp Ser Thr Gly Phe Asp Ser Thr Ala Phe Asn Ala Thr Val Asp
245 250 255

Glu Thr Lys Gly Phe Asp Asp Asn Asp Ser Gly Asn Asn Tyr Asn Asp
260 265 270

Ile Asn Ile Ser Ser Ile Glu Asn Asn Ile Asn Asn Asn Ile Asn Ser
275 280 285

Thr Lys Asn Gly Lys Asp Asn Asn Asn Glu Ser Asn Lys Asn Asn Asn
290 295 300

Gly Asp Glu Lys Asn Lys Asn Asn Asn Glu Asp Asn Glu Asn Asn Asn
305 310 315 320

Asn Ser Ser Glu Lys Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn Asn
325 330 335

Asn Asp Asp Asn Gly Asn Asn Asn Asn Asn Asn Ser Gly Asn Asp Asn
340 345 350

Asn Asn Thr Thr Asn Asn Asp Ser Asn Asn Lys Asn Asn Ser Ile Thr
355 360 365

Thr Gly Asn Asp Asn Glu Asn Ile Val Asn Asn Asp Leu Pro Thr Thr
370 375 380

Val Val Ser Asn Pro Gly Asp Asn Pro Pro Pro Ala Asp Asn Gly Glu
385 390 395 400

Glu Tyr Leu Thr Ile Asn Asp Phe Asn Asp Leu Asn Ile Asp Trp Ser
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Ser Gln Leu Asn Ile Gln Leu Ser Gln Asp Glu His Ser Gln Val Glu
20 25 30

cag act tgc gtg aaa cta ttg gat tct gga tgt gag aat cca gcg gat 144
Gln Thr Cys Val Lys Leu Leu Asp Ser Gly Cys Glu Asn Pro Ala Asp
35 40 45

gta ttt aga tgc tgc tta gta gct gtt atc caa cag gac aag tat caa 192
Val Phe Arg Arg Cys Leu Val Ala Val Ile Gln Gln Asp Lys Tyr Gln
50 55 60

aag gct tta cat tat tta aaa aaa ttc aac cat ata gct gac aag tac 240
Lys Ala Leu His Tyr Leu Lys Lys Phe Lys His Ile Asp Asp Lys Tyr
65 70 75 80

ggc cgc aaa ttt gcg cta gaa aaa ttg tac att ttc tat aaa ttg aat 288
Gly Arg Lys Phe Ala Leu Glu Lys Leu Tyr Ile Phe Tyr Lys Leu Asn
85 90 95

atg cca gat gaa ttc aac aca ttg tac aca gca att atc aca gat gat 336
Met Pro Asp Glu Phe Asn Thr Leu Tyr Thr Ala Ile Ile Thr Asp Asp
100 105 110

cgc gat aag glu cta aua aag gat atc gag tca ctt aga ggt atc cta 384
Leu Asp Thr Val Leu Lys Lys Asp Gln Glu Ser Leu Arg Gly Ile Leu
115 120 125

cat gtg aga gct aua tat tgt tat aaa aat ggg ctg tac caa gaa gct 432
His Val Arg Ala Gln Tyr Cys Tyr Lys Asn Gly Leu Tyr Gln Gln Ala
130 135 140

ttt aaa ata tat caa cat tta gca agt cac aat gag aag gat cag gat 480
Phe Lys Ile Tyr Gln His Leu Ala Ser His Asn Glu Lys Asp Gln Asp
145 150 155 160

agt caa att gaa ctc tct tgt aac gaa agg gtt ccg cta tcc gtt gcg	528
Ser Gln Ile Glu Leu Ser Cys Asn Glu Arg Val Pro Leu Ser Val Ala	
165 170 175	
aca gag tta atg aac aga taa ccc taa gtc aat cct atg gat gaa tct	576
Thr Gln Leu Met Asn Arg Ser Pro Leu Val Thr Pro Met Asp Glu Ser	
180 185 190	
tcc tac gat tta tta ttc aat gaa taa ttc atc atg gca tcc gta ggc	624
Ser Tyr Asp Leu Leu Phe Asn Glu Ser Phe Ile Met Ala Ser Val Gly	
195 200 205	
aaa tat gac aag gct acc gaa cta tta gaa aaa gcg ctt caa gga gcc	672
Lys Tyr Asp Lys Ala Ile Glu Leu Leu Glu Lys Ala Leu Gln Gly Ala	
210 215 220	
acg aat gaa ggc tat caa aac gat att aat aat att aaa ttg caa tta	720
Thr Asn Glu Gly Tyr Gln Asn Asp Ile Asn Thr Ile Lys Leu Gln Leu	
225 230 235 240	
tca ttt gtt ttg caa atg gtg ggg aaa aat gct caa agt aaa gaa atc	768
Ser Phe Val Leu Gln Met Val Gly Lys Thr Ala Gln Ser Lys Glu Ile	
245 250 255	
tta aag ggc tta ttg cag gaa ctg aaa ggc gat tct cca ttc tct tta	816
Leu Lys Gly Leu Leu Gln Glu Leu Lys Ala Asp Ser Pro Phe Ser Leu	
260 265 270	
att tgt caa aat aac cta aat gcg ttt gtt gat ttc tct aaa tac aat	864
Ile Cys Gln Asn Asn Leu Asn Ala Phe Val Asp Phe Ser Lys Tyr Asn	
275 280 285	
aca aac ttc aat tta ctg tta agg gaa tta aac gta gaa aaa cta aac	912
Thr Asn Phe Asn Leu Leu Leu Arg Glu Leu Asn Val Glu Lys Leu Asn	
290 295 300	
act ttt aat tta caa aac ttc acc cat gaa caa tgg tca aac att caa	960
Thr Phe Asn Leu Gln Thr Phe Thr His Glu Gln Trp Ser Asn Ile Gln	
305 310 315 320	
agg aat gta ctt ttc ctg agt ttg ttc aac aat gtc aaa att cac tct	1008
Arg Asn Val Leu Phe Leu Arg Leu Phe Asn Asn Val Lys Ile His Ser	

325	330	335	
caa gag tcc ctt tta tca aga aag ttc gat aac tac tct aag tta gtt			1056
Gln Glu Ser Leu Leu Ser Arg Thr Phe Asp Lys Tyr Ser Lys Leu Val			
340	345	350	
gac aat gtt act ttg gaa agc tac aag acg cag gcc aag aaa ctt tac			1104
Asp Asn Val Thr Leu Glu Ser Tyr Lys Thr Gln Ala Lys Lys Leu Tyr			
355	360	365	
cac cac act aca aaa acc att tta aat gga aca gat gga aat aag att			1152
His His Thr Thr Lys Thr Ile Leu Ser Gly Thr Asp Gly Ser Thr Ile			
370	375	380	
gga aca tta cta ctg act atc caa ttg cta ata ata gag aag gaa tgg			1200
Gly Ile Leu Leu Leu Thr Ile Gln Leu Leu Ile Ile Glu Lys Glu Trp			
385	390	395	400
gaa aat gct atc aga ata gga gaa tta ttt tta aat gaa agc tgg aac			1248
Glu Asn Ala Ile Arg Ile Gly Glu Leu Phe Leu Asn Glu Ser Trp Lys			
405	410	415	
tug tcc ttt gaa aac ttc aac gat tca caa gcc atc gtg tgt tac atc			1296
Ser Ser Phe Glu Lys Phe Asn Asp Ser Gln Ala Ile Val Cys Tyr Ile			
420	425	430	
tta ttt gaa tta tac aag att aag gga aga aat aac tcc aac aat gtc			1344
Leu Phe Glu Leu Tyr Lys Ile Lys Gly Arg Asn Asn Ser Lys Ser Val			
435	440	445	
ctg ctt aca aca tta ggc tcc gtg aga gtc caa ttg agc gga aac atc			1392
Leu Leu Lys Lys Leu Gly Ser Val Arg Val Gln Leu Ser Gly Lys Ile			
450	455	460	
caa gaa aac ata cca ttt tgg aaa cac gtc ggg ttt gaa tta ttg tcc			1440
Gln Glu Asn Ile Pro Phe Trp Lys His Val Gly Phe Glu Leu Leu Ser			
465	470	475	480
atg ggt aat gct aaa gaa tgg aag gct tta ctc aga gag att tca aac			1488
Met Gly Asn Ala Lys Glu Ser Lys Ala Leu Leu Arg Glu Ile Ser Asn			
485	490	495	

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ttt agt aaa ggc gat gca gat gtc ctt gtt gac aga gtt gtt tgg tca	1536
Phe Ser Lys Gly Asp Ala Asp Val Leu Val Asp Arg Val Val Ser Ser	
510 505 510	

gac tct tlg gat ata gca caa ggt ata gat cta gtg aga gat att gat	1584
Asp Ser Leu Asp Ile Ala Gln Gly Ile Asp Leu Val Arg Asp Ile Asp	
515 520 525	

att gat aaa tta att caa ctt ggt gty aaa ccc tta gaa tgg tca gca	1632
Ile Asp Lys Leu Ile Gln Leu Gly Val Lys Pro Leu Gln Ser Ser Ala	
530 535 540	

aag aga agt aaa aac aac gca gtt agc aaa gtt caa aag aga aaa gtt	1680
Lys Arg Ser Lys Asn Thr Ala Val Ser Tyr Val Gln Lys Arg Lys Val	
545 550 555 560	

tta gag cta aag aag aaa aga aag att aaa cgc ctc gaa aaa ttt tta	1728
Leu Gln Leu Lys Lys Lys Arg Lys Ile Lys Arg Leu Gln Lys Phe Leu	
565 570 575	

caa ggt cgc gac acc tcc aaa tta cct gal cct gaa agg tgg ctg cca	1776
Gln Gly Arg Asp Thr Ser Lys Leu Pro Asp Pro Gln Arg Trp Leu Pro	
580 585 590	

tta aga gac agg act act tat agg cca aag aaa aaa caa caa ggt gca	1824
Leu Arg Asp Arg Ser Thr Tyr Arg Pro Lys Lys Lys Gln Gln Gly Ala	
595 600 605	

aaa caa act caa ggt ggt gtt atg aac aaa aaa tca gaa cag gcc ctt	1872
Lys Gln Thr Gln Gly Gly Ala Met Asn Lys Lys Ser Gln Gln Ala Leu	
610 615 620	

gac ata tca aag aaa ggg aag ccc act gtt aat aaa aag cct aag aac	1920
Asp Ile Ser Lys Lys Gly Lys Pro Thr Val Asn Lys Lys Pro Lys Asn	
625 630 635 640	

aag aag asg ggc cgt aaa tag	1941
Lys Lys Lys Gly Arg Lys	
645	

<211> 646
<212> FET
<213> *Saccharomyces cerevisiae*

<400> 218

Met Lys Glu Ser Lys Lys Met Ala Lys Asp Asn Leu Thr Asn Leu Leu
1 5 10 15

Ser Gln Leu Asn Ile Gln Leu Ser Gln Asp Glu His Ser Gln Val Glu
20 25 30

Gln Thr Cys Val Lys Leu Leu Asp Ser Gly Cys Glu Asn Pro Ala Asp
35 40 45

Val Phe Arg Arg Cys Leu Val Ala Val Ile Gln Gln Asp Lys Tyr Gln
50 55 60

Lys Ala Leu His Tyr Leu Lys Lys Phe Lys His Ile Asp Asp Lys Tyr
65 70 75 80

Gly Arg Lys Phe Ala Leu Glu Lys Leu Tyr Ile Phe Tyr Lys Leu Asn
85 90 95

Met Pro Asp Glu Phe Asn Thr Leu Tyr Thr Ala Ile Ile Thr Asp Asp
100 105 110

Leu Asp Thr Val Leu Lys Lys Asp Ile Glu Ser Leu Arg Gly Ile Leu
115 120 125

His Val Arg Ala Gln Tyr Cys Tyr Lys Asn Gly Leu Tyr Gln Glu Ala
130 135 140

Phe Lys Ile Tyr Gln His Leu Ala Ser His Asn Glu Lys Asp Gln Asp
145 150 155 160

Ser Gln Ile Glu Leu Ser Cys Asn Gln Arg Val Pro Leu Ser Val Ala
165 170 175

Thr Glu Leu Met Asn Arg Ser Pro Leu Val Thr Pro Met Asp Glu Ser
180 185 190

Ser Tyr Asp Leu Leu Phe Asn Glu Ser Phe Ile Met Ala Ser Val Gly
195 200 205

Lys Tyr Asp Lys Ala Ile Glu Leu Leu Glu Lys Ala Leu Gln Gly Ala
210 215 220

Thr Asn Glu Gly Tyr Gln Asn Asp Ile Asn Thr Ile Lys Leu Gln Leu
225 230 235 240

Ser Phe Val Leu Gln Met Val Gly Lys Thr Ala Gln Ser Lys Glu Ile
245 250 255

Leu Lys Gly Leu Leu Gln Glu Leu Lys Ala Asp Ser Pro Phe Ser Leu
260 265 270

Ile Cys Gln Asn Asn Leu Asn Ala Phe Val Asp Phe Ser Lys Tyr Asn
275 280 285

Thr Asn Phe Asn Leu Leu Leu Arg Glu Leu Asn Val Glu Lys Leu Asn
290 295 300

Thr Phe Asn Leu Gln Thr Phe Thr His Glu Gln Trp Ser Asn Ile Gln
305 310 315 320

Arg Asn Val Leu Phe Leu Arg Leu Phe Asn Asn Val Lys Ile His Ser
325 330 335

Gln Glu Ser Leu Leu Ser Arg Thr Phe Asp Lys Tyr Ser Lys Leu Val
340 345 350

Asp Asn Val Thr Leu Glu Ser Tyr Lys Thr Gln Ala Lys Lys Leu Tyr
355 360 365

His His Thr Thr Cys Thr Ile Leu Ser Gly Thr Asp Gly Ser Thr Ile
370 375 380

Gly Ile Leu Leu Leu Thr Ile Gln Leu Leu Ile Ile Glu Lys Glu Trp
385 390 395 400

Glu Asn Ala Ile Arg Ile Gly Glu Leu Phe Leu Asn Glu Ser Trp Lys
405 410 415

Ser Ser Phe Glu Lys Phe Asn Asp Ser Gln Ala Ile Val Cys Tyr Ile
420 425 430

Leu Phe Glu Leu Tyr Lys Ile Lys Gly Arg Asn Asn Ser Lys Ser Val
435 440 445

Leu Leu Lys Lys Leu Gly Ser Val Arg Val Gln Leu Ser Gly Lys Ile
450 455 460

Gln Glu Asn Ile Pro Phe Trp Lys His Val Gly Phe Gln Leu Leu Ser
465 470 475 480

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Met Gly Asn Ala Lys Glu Ser Lys Ala Leu Leu Arg Glu Ile Ser Asn
485 490 495

Phe Ser Lys Gly Asp Ala Asp Val Leu Val Asp Arg Val Val Ser Ser
500 505 510

Asp Ser Leu Asp Ile Ala Gln Gly Ile Asp Leu Val Arg Asp Ile Asp
515 520 525

Ile Asp Lys Leu Ile Gln Leu Gly Val Lys Pro Leu Glu Ser Ser Ala
530 535 540

Lys Arg Ser Lys Asn Thr Ala Val Ser Lys Val Gln Lys Arg Lys Val
545 550 555 560

Leu Glu Leu Lys Lys Lys Arg Lys Ile Lys Arg Leu Glu Lys Phe Leu
565 570 575

Gln Gly Arg Asp Thr Ser Lys Leu Pro Asp Pro Glu Arg Trp Leu Pro
580 585 590

Leu Arg Asp Arg Ser Thr Tyr Arg Pro Lys Lys Lys Gln Gln Gly Ala
595 600 605

Lys Gln Thr Gln Gly Gly Ala Met Asn Lys Lys Ser Glu Gln Ala Leu
610 615 620

Asp Ile Ser Lys Lys Gly Lys Pro Thr Val Asn Lys Lys Pro Lys Asn
625 630 635 640

Lys Lys Lys Gly Arg Lys
645

<210> 219
 <211> 543
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> {1}..(543)

<400> 219
 atg ttc gca act cgc tca ttc tgc cta agc tct tct tta ttc cgt cgg 48
 Met Phe Ala Thr Arg Ser Phe Cys Leu Ser Ser Ser Leu Phe Arg Pro
 1 5 10 15
 gct gcc caa ctg ttg cgc cct gct ggc cgc tct act tta cga aat gtt 96
 Ala Ala Gln Leu Leu Arg Pro Ala Gly Arg Ser Thr Leu Arg Asn Val
 20 25 30
 tgg aga cgc tct att gca acc ggc cat ttg acc cag acg gag gat aat 144
 Trp Arg Arg Ser Ile Ala Thr Glu His Leu Thr Glu Thr Glu Ala Asn
 35 40 45
 tct cgt ctt gct tcc cag cgt gtt cgc cgt cca aat tct cct cat ttg 192
 Ser Arg Leu Ala Ser Gln Arg Val His Arg Pro Asn Ser Pro His Leu
 50 55 60
 act aic tat gaa cct caa ttg act tgg tat cta ecc agt tta cat cgt 240
 Thr Ile Tyr Gln Pro Gln Leu Thr Trp Tyr Leu Ser Ser Leu His Arg
 65 70 75 80
 atc act ggt tgt gtt gtc gcc ggt act ctt tat gct ttc gct atg ggc 288
 Ile Thr Gly Cys Val Val Ala Gly Thr Leu Tyr Ala Phe Ala Met Gly
 85 90 95
 tac ttg gtn gct cct ctc gct gga tac tct ttg gat aca gct acc att 336
 Tyr Leu Val Ala Pro Leu Ala Gly Tyr Ser Leu Asp Thr Ala Thr Ile
 100 105 110
 tct ggt ctt act cag caa gtt ccc acc tgg atc aaa gtt cct gct aag 334

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Ser Gly Leu Ile Gln Gln Val Pro Thr Trp Ile Lys Val Pro Ala Lys
 115 120 125
 ttt gtt att tct tat cct ttg act ttc cac att ttt aac ggt att cgt 432
 Phe Val Ile Ser Tyr Pro Leu Thr Phe His Ile Phe Asn Gly Ile Arg
 130 135 140
 cac ttg atc tgg gat acc acc aag gag tta agt cta aag ggt gtc tat 460
 His Leu Ile Trp Asp Thr Thr Lys Glu Leu Ser Leu Lys Gly Val Tyr
 145 150 155 160
 cgt acc ggt tat gct gtc ctt gcc ctt tcc gtt ttg acc tct ggc tat 528
 Arg Thr Gly Tyr Ala Val Leu Ala Leu Ser Val Leu Thr Ser Gly Tyr
 165 170 175
 ttt gag atg att tag 543
 Phe Ala Met Ile
 180

<210> 220
 <211> 180
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 220

Met Phe Ala Thr Arg Ser Phe Cys Leu Ser Ser Ser Leu Phe Arg Pro
 1 5 10 15

Ala Ala Gln Leu Leu Arg Pro Ala Gly Arg Ser Thr Leu Arg Asn Val
 20 25 30

Trp Arg Arg Ser Ile Ala Thr Glu His Leu Thr Gln Thr Glu Ala Asn
 35 40 45

Ser Arg Leu Ala Ser Gln Arg Val His Arg Pro Asn Ser Pro His Leu
 50 55 60

Thr Ile Tyr Glu Pro Gln Leu Thr Trp Tyr Leu Ser Ser Leu His Arg
65 70 75 80

Ile Thr Gly Cys Val Val Ala Gly Thr Leu Tyr Ala Ile Ala Met Gly
85 90 95

Tyr Leu Val Ala Pro Leu Ala Gly Tyr Ser Leu Asp Thr Ala Thr Ile
100 105 110

Ser Gly Leu Ile Gln Gln Val Pro Thr Trp Ile Lys Val Pro Ala Lys
115 120 125

Phe Val Ile Ser Tyr Pro Leu Thr Phe His Ile Phe Asn Gly Ile Arg
130 135 140

His Leu Ile Trp Asp Thr Thr Lys Glu Leu Ser Leu Lys Gly Val Tyr
145 150 155 160

Arg Thr Gly Tyr Ala Val Leu Ala Leu Ser Val Leu Thr Ser Gly Tyr
165 170 175

Phe Ala Met Ile
180

<210> 221
<211> 262
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1) .. (262)

<400> 221

atg gtc acc cca aga gaa cct aag aag aga acc act aga aag aag aag 40
 Met Val Thr Pro Arg Glu Pro Lys Lys Arg Thr Thr Arg Lys Lys Lys
 1 5 10 15

gac cca aat gcc cct aag agg gct ttg tcc gcc tac atg ttt ttc gct 96
 Asp Pro Asn Ala Pro Lys Arg Ala Leu Ser Ala Tyr Met Phe Phe Ala
 20 25 30

aac gaa aac aga gat att gtt cgt tct gaa aat cca gat atc aca ttt 144
 Asn Glu Asn Arg Asp Ile Val Arg Ser Glu Asn Pro Asp Ile Thr Phe
 35 40 45

gga caa gtc gcc aag aag ctg gct gag aag lgg aag gct cta acg cca 192
 Gly Gln Val Gly Lys Lys Leu Gly Glu Lys Trp Lys Ala Leu Thr Pro
 50 55 60

gag gaa aag cag cct tac gag gcc aag gcc cag gcc gat aag aag aga 240
 Glu Glu Lys Gln Pro Tyr Glu Ala Lys Ala Gln Ala Asp Lys Lys Arg
 65 70 75 80

tat gaa tcc gaa aag gag tta tat aac gcc act ttg gct tag 288
 Tyr Glu Ser Glu Lys Glu Leu Tyr Asn Ala Thr Leu Ala
 85 90

<210> 222

<211> 93

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 222

Met Val Thr Pro Arg Glu Pro Lys Lys Arg Thr Thr Arg Lys Lys Lys
 1 5 10 15

Asp Pro Asn Ala Pro Lys Arg Ala Leu Ser Ala Tyr Met Phe Phe Ala
 20 25 30

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Asn Gln Asn Arg Asp Ile Val Arg Ser Glu Asn Pro Asp Ile Thr Phe
 35 40 45

Gly Gln Val Gly Lys Lys Leu Gly Glu Lys Trp Lys Ala Leu Thr Pro
 50 55 60

Glu Glu Lys Gln Pro Tyr Glu Ala Lys Ala Gln Ala Asp Lys Lys Arg
 65 70 75 80

Tyr Glu Ser Gln Lys Glu Leu Tyr Asn Ala Thr Leu Ala
 85 90

<210> 223

<211> 1110

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> [1]..(1110)

<400> 223

atg aat cag agc gat agc agc ttg ctg gat tta cca ctg gag ata cat 40
 Met Asn Gln Ser Asp Ser Ser Leu Met Asp Leu Pro Leu Glu Ile His
 1 5 10 15

tta tca tta cta gag tac gtg cct aat gac ctt cgt gct gtc aat aac 80
 Leu Ser Leu Leu Glu Tyr Val Pro Asn Gln Leu Arg Ala Val Asn Lys
 20 25 30

tac ttc tac gtc ttg cat aac cac agc tat aag gag aag agt ttg gcg 120
 Tyr Phe Tyr Val Leu His Asn His Ser Tyr Lys Glu Lys Ser Leu Ala
 35 40 45

tgg ata gct gag gac aac tat ata tgg gcc gtc gtc aaa cat tca tta 160
 Trp Ile Ala Gln Asp Asn Tyr Ile Trp Ala Val Val Lys His Ser Leu
 50 55 60

tgt tta tat gtc aag agt ttg gac cca ctt cga cag cat gcc aqa gaa	240
Cys Leu Tyr Val Lys Ser Leu Asp Pro Leu Arg Gln His Ala Arg Glu	
65 70 75 80	
atc att caa gaa acg aag gac cca ggt ttt aat gtg cca ctg tgc atg	288
Ile Ile Gln Glu Thr Lys Glu Pro Gly Phe Asn Val Pro Leu Cys Met	
85 90 95	
act aaa tac alc gca gat tct tgg tat att gta tac aat gcg ctg caa	336
Thr Lys Tyr Ile Ala Asp Ser Trp Tyr Ile Val Tyr Asn Ala Leu Gln	
100 105 110	
tat cct gga aag ata att aat atg gga tgg gac aaa tat acc aaa agt	384
Tyr Pro Gly Lys Ile Ile Asn Met Gly Trp Asp Lys Tyr Thr Lys Ser	
115 120 125	
caa gat tca aat ggt tct cat tct acc agt aac ttt aat agt cgg ccc	432
Glu Asp Ser Asn Gly Ser Asp Ser Thr Ser Asn Phe Asn Ser Arg Pro	
130 135 140	
aag gaa aga act ctt atg cag tgg tgg aca gct lla cct gtt aac ttt	480
Lys Glu Arg Thr Leu Met Gln Ser Leu Thr Ala Leu Pro Val Asn Phe	
145 150 155 160	
tgg tcc agg agg aag gac gag ccc aca ccg gta aac gtt tgg ttt tat	528
Trp Ser Arg Arg Lys Asp Glu Pro Thr Pro Val Asn Val Trp Phe Tyr	
165 170 175	
gta aaa aat gag cac gtt gct aga tac aca ccg aac att att acg gaa	576
Val Lys Asn Ala His Val Ala Arg Tyr Ile Pro Lys Ile Ile Thr Glu	
180 185 190	
ata ggc ata tgc aac tat ggg ccg aag cag atc gtg gca agt gca gga	624
Ile Gly Ile Cys Asn Tyr Gly Pro Lys Gln Ile Val Ala Ser Ala Gly	
195 200 205	
tat atc aac gaa ttg ata aca tct gaa gga ata taa tgt gll aac cta	672
Tyr Ile Asn Glu Leu Ile Thr Ser Glu Gly Ile Tyr Cys Val Asn Leu	
210 215 220	
ggc cac ctt ccc agg cta tac gat gag caa att ttt gaa ggc act gga	720

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 224

Met Asn Gln Ser Asp Ser Ser Leu Met Asp Leu Pro Leu Glu Ile His

1 5 10 15

Leu Ser Leu Leu Glu Tyr Val Pro Asn Glu Leu Arg Ala Val Asn Lys

20 25 30

Tyr Phe Tyr Val Leu His Asn His Ser Tyr Lys Glu Lys Ser Leu Ala

35 40 45

Trp Ile Ala Glu Asp Asn Tyr Ile Trp Ala Val Val Lys His Ser Leu

50 55 60

Cys Leu Tyr Val Lys Ser Leu Asp Pro Leu Arg Gln His Ala Arg Glu

65 70 75 80

Ile Ile Gln Gln Thr Lys Gln Pro Gly Phe Asn Val Pro Leu Cys Met

85 90 95

Thr Lys Tyr Ile Ala Asp Ser Trp Tyr Ile Val Tyr Asn Ala Leu Gln

100 105 110

Tyr Pro Gly Lys Ile Ile Asn Met Gly Trp Asp Lys Tyr Thr Lys Ser

115 120 125

Gln Asp Ser Asn Gly Ser Asp Ser Thr Ser Asn Phe Asn Ser Arg Pro

130 135 140

Lys Glu Arg Thr Leu Met Gln Ser Leu Thr Ala Leu Pro Val Asn Phe

145 150 155 160

 Trp Ser Arg Arg Lys Asp Glu Pro Thr Pro Val Asn Val Trp Phe Tyr
 165 170 175

 Val Lys Asn Ala His Val Ala Arg Tyr Ile Pro Lys Ile Ile Thr Glu
 180 185 190

 Ile Gly Ile Cys Asn Tyr Gly Pro Lys Glu Ile Val Ala Ser Ala Gly
 195 200 205

 Tyr Ile Asn Glu Leu Ile Thr Ser Glu Gly Ile Tyr Cys Val Asn Leu
 210 215 220

 Gly His Leu Pro Arg Leu Tyr Asp Glu Gln Ile Phe Glu Gly Thr Gly
 225 230 235 240

 Thr Thr His Leu Pro Leu Glu Leu Lys Ala Ile Asp Arg Thr Asp Ser
 245 250 255

 Asp Val Cys Ile Asn Gly Asp Leu Val Leu Leu Gly Tyr Asp Phe Ile
 260 265 270

 Pro Tyr Gln Ile Ser Lys Pro Trp Leu Leu Phe Arg Ile Glu Pro Val
 275 280 285

 Asn Ser Ile Glu Ala Ile Phe Asn Tyr Ser Glu Cys Ser Phe Ser Tyr
 290 295 300

 Gln Phe Ala Trp Ser Leu Ala Cys Leu Gln Ser Glu Glu Lys Ile Ser
 305 310 315 320

Phe Pro Arg Asp Thr Ile Ile Gly His Gly Leu Pro Tyr Lys Pro Ser
 325 330 335

Lys Leu Ile Arg Ile Phe Val Tyr Lys His Pro Glu Gln Lys Glu Asp
 340 345 350

Leu Gly Gln Glu Ile Ala Leu Pro Asn Trp Asn Thr Pro Tyr Leu Arg
 355 360 365

Arg

<210> 225
 <211> 353
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (333)

<400> 235
 atg tca tca cca ata aat gat cgt cca aca cat gaa ctg tct aga gca 48
 Met Ser Ser Gln Ile Ile Asp Arg Pro Lys His Glu Leu Ser Arg Ala
 1 5 10 15
 gaa tta gag gaa cta gaa gaa ttt gaa ttc aaa cat ggt cca atg tcc 96
 Glu Leu Glu Glu Leu Clu Glu Phe Glu Phe Lys His Gly Pro Met Ser
 20 25 30
 ctg ata aat gat gct atg gtg aca aga aca cct gty ata atc tca tta 144
 Leu Ile Asn Asp Ala Met Val Thr Arg Thr Pro Val Ile Ile Ser Leu
 35 40 45
 aga aac aat cat aaa ata ata gag aga gtg aaa gct ttc gac agg cat 192
 Arg Asn Asn His Lys Ile Ile Ala Arg Val Lys Ala Phe Asp Arg His

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50	55	60	
agt aat atg gtt tta gaa aat gtg aag gag att tgg aca gag aag aag	240		
Cys Asn Met Val Leu Glu Asn Val Lys Glu Leu Trp Thr Glu Lys Lys			
65	70	75	80
ggc aaa aat gta att aat cgg gaa aga ttc ata agt aaa cta ttc tta	288		
Gly Lys Asn Val Ile Asn Arg Glu Arg Phe Ile Ser Lys Leu Phe Leu			
85	90	95	
aga ggt gat tca gtc atc gtc gtg tta aaa acc cct gll gag taa	333		
Arg Gly Asp Ser Val Ile Val Val Leu Lys Thr Pro Val Glu			
100	105	110	
<210>	226		
<211>	110		
<212>	PRF		
<213>	<i>Saccharomyces cerevisiae</i>		
<400>	226		
Met Ser Ser Gln Ile Ile Asp Arg Pro Lys His Glu Leu Ser Arg Ala			
1	5	10	15
Glu Leu Glu Glu Leu Glu Gln Phe Glu Phe Lys His Gly Pro Met Ser			
20	25	30	
Leu Ile Asn Asp Ala Met Val Thr Arg Thr Pro Val Ile Ile Ser Leu			
35	40	45	
Arg Asn Asn His Lys Ile Ile Ala Arg Val Lys Ala Phe Asp Arg His			
50	55	60	
Cys Asn Met Val Leu Glu Asn Val Lys Glu Leu Trp Thr Glu Lys Lys			
65	70	75	80

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Gly Lys Asn Val Ile Asn Arg Glu Arg Phe Ile Ser Lys Leu Phe Leu
 85 90 95

Arg Gly Asp Ser Val Ile Val Val Leu Lys Thr Pro Val Glu
 100 105 110

<210> 237

<211> 2184

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2184)

<400> 127

atg aat gat tgg cat gag tcc aat gcc gcc acc aag tca acc tat tgt 48
 Met Asn Asp Trp His Glu Phe Asn Ala Ala Ile Lys Ser Ile Tyr Cys
 1 5 10 15

aat gca gaa ggt gac tca agc agt ata att aat aga ttg gtt gcc ttg 96
 Asn Ala Glu Gly Asp Ser Ser Ser Ile Ile Asn Arg Leu Val Gly Leu
 20 25 30

gcc atg aaa agc gaa gat tcc acg tcc att gag gcc gtt tta gtt ttg 144
 Ala Met Lys Ser Glu Asp Ser Thr Phe Ile Glu Ala Val Leu Val Leu
 35 40 45

aaa gaa aat gtg tgg aaa gla gat aaa caa tta aga ttt tta tgg ctt 192
 Lys Glu Asn Val Ser Lys Val Asp Lys Gln Leu Arg Phe Leu Trp Leu
 50 55 60

acc tca act att aat tca agg ttt tat ccc cct ata cct atc tca gaa 240
 Thr Ser Thr Ile Asn Ser Arg Phe Tyr Pro Pro Ile Pro Ile Ser Glu
 65 70 75 80

gcc tca cag gtt tct tgg aat aaa acc gaa tat tgc gca cct ggt acc 288
 Ala Ser Pro Val Ser Trp Asn Lys Thr Glu Tyr Cys Ala Pro Gly Thr
 85 90 95

gaa gaa cta caa ugg cgt tat cca ggg aga gcc aag tta cag aat gaa Glu Glu Leu Gln Arg Arg Tyr Pro Gly Arg Ala Lys Leu Gln Asn Glu 100 105 110	336
gaa gac tat tca ggc gga ata gaa caa tgc cga gat gtg cca gat tgc Glu Asp Tyr Ser Gly Gly Ile Glu Gln Cys Arg Asp Val Pro Asp Cys 115 120 125	334
tca tta ggt gct tct cta att aac ctt agg cct aag aac ttg aat ctc Ser Leu Val Ala Ser Leu Ile Asn Leu Arg Ser Lys Asn Leu Asn Leu 130 135 140	432
cct cta att aac caa ata tca tca act aaa tat cac gtc aat tta agt Pro Leu Ile Lys Gln Ile Ser Ser Thr Lys Tyr His Val Asn Leu Ser 145 150 155 160	490
tct aac gga agc aac aaa aag cta gtg aca gta gat att tgg cag aac Phe Asn Gly Ser Asn Lys Arg Leu Val Thr Val Asp Ile Ser Gln Ile 165 170 175	528
cca acc leu gtg gat ggc aca cac att cct tta aag agt aac gat att Pro Thr Ser Val Asp Gly Lys Gln Leu Ser Leu Lys Ser Asn Asp Ile 180 185 190	576
tgg gac aac att ggc gag cct gca tta ctg ctt gtt tct aca gga aca Ser Asp Lys Ile Gly Glu Leu Ala Leu Leu Leu Val Ser Lys Gly Thr 195 200 205	624
tat tcc acg gat ggc tca aat att agt ata gaa act tac cgc tta agt Tyr Ser Thr Asp Gly Ser Asn Ile Ser Ile Asp Thr Tyr Arg Leu Ser 210 215 220	672
ggc ttc tta cca gag ata aca caa gta aac ayc tat cct ttc gaa aaa Gly Phe Asn Pro Glu Ile Thr Gln Val Asn Ser Tyr Pro Phe Glu Lys 225 230 235 240	720
tta tgg aag cct cac aaa tct aat tta hgt ctg atg ggc gct ggc acc Leu Trp Lys Phe His Lys Ser Asn Leu Cys Leu Met Gly Ala Gly Thr 245 250 255	768
ggc aat cgt tcc aat gac atg ata aag ccc cta gct gag aac cat gat	816

Gly Asn Arg Ser Asn Asp Met Ile Lys Pro Leu Val Glu Asn His Asp	
250	265
270	
tac tct ata att gat atc acg tat gat tct agg cta gta aaa ttg cga	864
Tyr Ser Ile Ile Asp Ile Phe Tyr Asp Ser Arg Leu Val Lys Leu Arg	
275	280
285	
gat ccg agg aac tgg gca cta aat gtt gaa atc agc tat gaa cag tat	912
Asp Pro Arg Asn Ser Ala Leu Asn Val Glu Ile Ser Tyr Glu Gln Tyr	
290	295
300	
tta aaa aat ttc aaa caa ctt tat ctt aat tgg aac caa gaa aaa tta	960
Leu Lys Asn Phe Lys Gln Leu Tyr Leu Asn Trp Asn Gln Glu Lys Leu	
305	310
315	320
ttc aaa cgt tct cag gta ctt cat ttt cgg tac gal acg tca cgc tac	1008
Phe Lys Arg Ser Gln Val Leu His Phe Arg Tyr Asp Thr Ser Arg Tyr	
325	330
335	
aat aaa ttt tct atc gtt gca gat aac cct tta ttt cac ctg gta aac	1056
Asn Lys Phe Ser Ile Val Ala Asp Lys Pro Leu Phe His Leu Val Asn	
340	345
350	
aat tct aaa gtg aca gag acg gta tgg tta ttg cta gaa tcc cat ttg	1104
Asn Ser Lys Val Thr Glu Thr Val Trp Leu Leu Leu Gln Ser His Leu	
355	360
365	
caa gat gaa ggc agc caa gaa aat cgg tca gtt tcc ttt ttg aat gag	1152
Gln Asp Glu Gly Ser Gln Glu Asn Arg Ser Val Ser Phe Leu Asn Glu	
370	375
380	
gct ccc gaa tgc ata att tgt cca att gaa cct cca gta gan tgc ggt	1200
Ala Pro Glu Cys Ile Ile Cys Pro Ile Glu Pro Pro Val Glu Cys Gly	
385	390
395	400
ggc aat cac att gga ctt cag ctg gta aag ttg aga tta gal gct gag	1248
Gly Asn His Ile Gly Leu Gln Leu Val Lys Leu Arg Leu Asp Ala Glu	
405	410
415	
act gag agg tta ctg tat tgt tat tca cca cca aac aac aat ttc agt	1296
Thr Glu Arg Leu Leu Tyr Cys Tyr Ser Thr Thr Asn Asn Asn Phe Ser	
420	425
430	

att caa tat ttc tca gtt gtg aag gaa ata tgt ttt caa aga ttg aaa	1344
Ile His Ser Phe Ser Val Val Lys Glu Ile Cys Phe Gln Arg Leu Lys	
435 440 445	
gat aca aac agt ctt ttc gcc aaa gtc ctt ttc tct ttt cct tat gaa	1392
Asp Thr Lys Ser Leu Phe Ala Lys val Leu Phe Ser Phe Pro Tyr Glu	
450 455 460	
ata gag gga aaa gcc tca ttt gat act cgt aat ttt ttt caa aat cag	1440
Ile Glu Gly Lys Ala Ser Phe Asp Thr Cys Asn Phe Phe Gln Asn Pro	
465 470 475 480	
act ttt gag ttg gaa gtc aac tct gaa caa gat tat caa gta ctt atg	1488
Thr Phe Glu Leu Glu Val His Ser Gln Gln Asp Tyr Gln Val Leu Met	
485 490 495	
gac gcc gca tgt atc tca act agc tca cat gat tta att aac atc caa	1536
Asp Ala Ala Cys Ile Ser Thr Ser Ser His Asp Leu Ile Asn Ile Gln	
500 505 510	
gta cat cat ttt act gcc cat gaa ttg ata aag cca ata atg ttt gat	1584
Val Tyr Tyr Phe Asn Asp Tyr Glu Leu Ile Lys Pro Ile Met Phe Asp	
515 520 525	
aac caa tat cag ccc ggg cag ggc ctt aac caa gcc gtg ccc atc tta	1632
Asn His Tyr Gln Pro Gly Gln Gly Leu Lys Gln Asp Val Pro Ile Leu	
530 535 540	
act aat gtc aaa tat atg att gta tgc tca act tac ggc cct cca gcc	1680
Thr Asn Val Lys Tyr Met Ile Val Cys Ser Thr Tyr Gly Pro Pro Ala	
545 550 555 560	
tca acg gaa ttt gaa tta ctt gcc tcc ata cgg tta tcc tct tca tgg	1728
Ser Thr Glu Phe Glu Leu Leu Ala Ser Ile Arg Leu Ser Ser Ser Trp	
565 570 575	
agg tta ata tct gga ata act tta cgg agt gtt aac ttg ata tac ggt	1776
Arg Leu Ile Ser Gly Ile Thr Leu Arg Ser Val Asn Leu Ile Tyr Gly	
580 585 590	
act tat cca tat cat tgt cgc aac agg ttc cat tgg aag gaa act tca	1824

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Thr Tyr Pro Tyr His Cys Arg Asn Arg Phe His Trp Lys Glu Thr Ser
 595 600 605

gac aac ctt aac att cag atg act ttg cca acc aac aag tat tct acg 1872
 Asp Lys Leu Lys Ile Glu Met Thr Leu Pro Thr Lys Lys Tyr Ser Thr
 610 615 620

aac aac ctt ttt ata cgt gta gta ccc ggg gaa tca tca gca cga tta 1920
 Asn Lys Leu Phe Ile Arg Val Val Pro Val Glu Ser Ser Ala Arg Leu
 625 630 635 640

agg atg cga tgt aat att ttc gag cct gaa tca gct ctc tgt gtt tat 1968
 Arg Met Arg Cys Asn Ile Phe Glu Pro Glu Ser Ala Leu Cys Val Tyr
 645 650 655

gaa tgt cca gag tat aag aca tgt cca tct ggg ggc acc gtt ata cct 2016
 Glu Cys Gln Glu Tyr Arg Thr Cys Pro Ser Gly Gly Ile Val Ile Pro
 660 665 670

gat cag gaa gtc tct cgt acg aac att gtt gta ttg atg ata gaa aga 2064
 Asp Leu Glu Val Ser Arg Thr Asn Ile Val Val Leu Met Ile Glu Arg
 675 680 685

agt gta cct att ccc agt tgt tta cct acg gaa gga cca ttg gat gaa 2112
 Ser Val Pro Ile Ser Ser Cys Leu Pro Thr Glu Gly Gln Leu Asp Glu
 690 695 700

ttg gag ttg ttc gtt ggg tcc agt caa aac atc aga att gaa aac tac 2160
 Leu Glu Leu Phe Val Gly Ser Ser Gln Lys Ile Arg Ile Glu Lys Tyr
 705 710 715 720

tcc gat gat ggg ata cca aac taa 2208
 Ser Asp Asp Val Ile Pro Lys
 725

<210> 228

<211> 727

<212> FRT

<213> Saccharomyces cerevisiae

<400> 228

Met Asn Asp Trp His Glu Phe Asn Ala Ala His Lys Ser Ile Tyr Cys
1 5 10 15

Asn Ala Glu Gly Asp Ser Ser Ser Ile Ile Asn Arg Leu Val Gly Leu
20 25 30

Ala Met Lys Ser Glu Asp Ser Thr Phe Ile Glu Ala Val Leu Val Leu
35 40 45

Lys Glu Asn Val Ser Lys Val Asp Lys Glu Leu Arg Phe Leu Trp Leu
50 55 60

Thr Ser Thr Ile Asn Ser Arg Phe Tyr Pro Pro Ile Pro Ile Ser Glu
65 70 75 80

Ala Ser Pro Val Ser Trp Asn Lys Thr Glu Tyr Cys Ala Pro Gly Thr
85 90 95

Glu Glu Leu Gln Arg Arg Tyr Pro Gly Arg Ala Lys Leu Gln Asn Glu
100 105 110

Glu Asp Tyr Ser Gly Gly Ile Glu Gln Cys Arg Asp Val Pro Asp Cys
115 120 125

Ser Leu Val Ala Ser Leu Ile Asn Leu Arg Ser Lys Asn Leu Asn Leu
130 135 140

Pro Leu Ile Lys Gln Ile Ser Ser Thr Lys Tyr His Val Asn Leu Ser
145 150 155 160

Phe Asn Gly Ser Asn Lys Arg Leu Val Thr Val Asp Ile Ser Gln Ile

165

170

175

Pro Thr Ser Val Asp Gly Lys Gln Leu Ser Leu Lys Ser Asn Asp Ile
 180 195 190

Ser Asp Lys Ile Gly Glu Ser Ala Leu Leu Leu Val Ser Lys Gly Thr
 195 200 205

Tyr Ser Thr Asp Gly Ser Asn Phe Ser Ile Asp Thr Tyr Arg Leu Ser
 210 215 220

Gly Phe Leu Pro Glu Ile Thr Gln Val Asn Ser Tyr Pro Phe Glu Lys
 225 230 235 240

Leu Trp Lys Phe His Lys Ser Asn Leu Cys Leu Met Gly Ala Gly Thr
 245 250 255

Gly Asn Arg Ser Asn Asp Met Ile Lys Pro Leu Val Glu Asn His Asp
 260 265 270

Tyr Ser Ile Ile Asp Ile Thr Tyr Asp Ser Arg Leu Val Lys Leu Arg
 275 280 285

Asp Pro Arg Asn Ser Ala Leu Asn Val Glu Ile Ser Tyr Glu Gln Tyr
 290 295 300

Leu Lys Asn Phe Lys Gln Leu Tyr Leu Asn Trp Asn Gln Glu Lys Leu
 305 310 315 320

Phe Lys Arg Ser Gln Val Leu His Phe Arg Tyr Asp Thr Ser Arg Tyr
 325 330 335

Asn Lys Phe Ser Ile Val Ala Asp Lys Pro Leu Phe His Leu Val Asn
340 345 350

Asn Ser Lys Val Thr Glu Thr Val Trp Leu Leu Leu Glu Ser His Leu
355 360 365

Gln Asp Glu Gly Ser Gln Gln Asn Arg Ser Val Ser Phe Leu Asn Gln
370 375 380

Ala Pro Glu Cys Ile Ile Cys Pro Ile Glu Pro Pro Val Glu Cys Gly
385 390 395 400

Gly Asn His Ile Gly Leu Gln Leu Val Lys Leu Arg Leu Asp Ala Gln
405 410 415

Thr Glu Arg Leu Leu Tyr Cys Tyr Ser Thr Thr Asn Asn Asn Phe Ser
420 425 430

Ile His Ser Phe Ser Val Val Lys Glu Ile Cys Phe Gln Arg Leu Lys
435 440 445

Asp Thr Lys Ser Leu Phe Ala Lys Val Leu Phe Ser Phe Pro Tyr Glu
450 455 460

Ile Gln Gly Lys Ala Ser Phe Asp Thr Cys Asn Phe Ile Gln Asn Pro
465 470 475 480

Thr Phe Glu Leu Glu Val His Ser Glu Gln Asp Tyr Gln Val Leu Met
485 490 495

Asp Ala Ala Cys Ile Ser Thr Ser Ser His Asp Leu Ile Asn Ile Gln

500	505	510
Val Tyr Tyr Phe Asn Asp Tyr Glu Leu Ile Lys Pro Ile Met Phe Asp		
515	520	525
Asn His Tyr Gln Pro Gly Gln Gly Leu Lys Gln Asp Val Pro Ile Leu		
530	535	540
Thr Asn Val Lys Tyr Met Cys Val Cys Ser Thr Tyr Gly Pro Pro Ala		
545	550	555
Ser Thr Glu Phe Glu Leu Leu Ala Ser Ile Arg Leu Ser Ser Ser Trp		
565	570	575
Arg Leu Ile Ser Gly Ile Thr Leu Arg Ser Val Asn Leu Ile Tyr Gly		
580	585	590
Thr Tyr Pro Tyr His Cys Arg Asn Arg Phe His Trp Lys Glu Thr Ser		
595	600	605
Asp Lys Leu Lys Ile Gln Met Thr Leu Pro Thr Lys Lys Tyr Ser Thr		
610	615	620
Asn Lys Leu Phe Ile Arg Val Val Pro Val Glu Ser Ser Ala Arg Leu		
625	630	635
Arg Met Arg Cys Asn Ile Phe Glu Pro Glu Ser Ala Leu Cys Val Tyr		
645	650	655
Glu Cys Gln Glu Tyr Arg Thr Cys Pro Ser Gly Gly Ile Val Ile Pro		
660	665	670

Asp Leu Glu Val Ser Arg Thr Asn Ile Val Val Leu Met Ile Glu Arg
 675 680 685

Ser Val Pro Ile Ser Ser Cys Leu Pro Thr Glu Gly Gln Leu Asp Glu
 690 695 700

Leu Glu Leu Phe Val Gly Ser Ser Gln Lys Ile Arg Ile Glu Lys Tyr
 705 710 715 720

Ser Asp Asp Val Ile Pro Lys
 725

<210> 229

<211> 2223

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(2223)

<400> 220

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 Met Asp Arg Gly Arg Trp Cys Phe Leu Val Ser Val Ser Ser Arg Ile
 1 5 10 15

atg aat ctg caa gaa cta tta gag aag gta cag ctg ttg tta cag tat 96
 Met Asn Leu Gln Glu Leu Leu Ala Lys Val Pro Leu Leu Leu Ser Tyr
 20 25 30

cag acc att att cta tcc agt aat cag atc gta cct tcc cat aat gat 144
 Pro Thr Ile Ile Leu Ser Ser Asn Leu Ile Val Pro Ser His Asn Asp
 35 40 45

ctc ata tca cga gca gcc tct aca tca gca gca gag tat gct gac gaa 192
 Leu Ile Ser Arg Ala Ala Ser Thr Ser Ala Ala Glu Tyr Ala Asp Glu

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50	55	60	
aag cta ata ttt ttc agt acc gat cac gcc acc aga ctg att ttt ctg			240
Lys Leu Ile Phe Phe Ser Thr Asp His Ala Ile Arg Leu Ile Phe Leu			
65	70	75	80
cca acc ttc gta gct tct tcc ttt aac cta ttt gcg cac tat ttt aac			268
Pro Thr Phe Val Ala Ser Ser Phe Asn Leu Phe Ala His Tyr Phe Asn			
	85	90	95
llu ulc aat tac tct agc cga agg aag tat tat gtt tta ttt act gca			336
Phe Ile Asn Tyr Ser Ser Arg Arg Lys Tyr Tyr Val Leu Phe Thr Ala			
	100	105	110
att tat ttc cta tcc ata ttg act gcg att ttc cat cca att cag tca			384
Ile Tyr Phe Leu Ser Ile Leu Thr Ala Ile Phe His Pro Ile Gln Ser			
	115	120	125
aca tgc atc act cta ttg att atc sag ctc ctg act acc gcc gat gag			432
Thr Cys Ile Thr Leu Leu Ile Ile Lys Leu Leu Thr Thr Ala Asp Gln			
	130	135	140
tct tgg cca aaa att gcc ctc aat ttc aag acc att ttg aaa acc ttt			480
Ser Ser Pro Lys Ile Ala Leu Asn Phe Lys Thr Ile Leu Lys Thr Phe			
145	150	155	160
gtt ccc ttt att act tta acc tta gtt ata ttg cgt tgg gat cct tct			528
Val Pro Phe Ile Thr Leu Thr Leu Val Ile Leu Arg Trp Asp Pro Ser			
	165	170	175
ttt gat gcc agc tca gga gat gtg aac aaa att tct acg tct ttg gcc			576
Phe Asp Ala Ser Ser Gly Asp Val Asn Lys Ile Ser Thr Ser Leu Ala			
	180	185	190
gca tat gct ctc tta ata tta acg cta aga tat gca tca ccg ctg ata			624
Ala Tyr Ala Leu Leu Ile Leu Thr Leu Arg Tyr Ala Ser Pro Leu Ile			
	195	200	205
tta tcy acy tta tca agt agc ata ggt gtt gtt tcc aaa gac acc agc			672
Leu Ser Thr Leu Ser Ser Ser Ile Gly Val Val Ser Lys Asp Thr Ser			
210	215	220	

5380762

gtc gca cag cat tcg ata agt aga aat aag aga ttt ccg cta att ctc	720
Val Ala Gln His Ser Ile Ser Arg Asn Lys Arg Phe Pro Leu Ile Leu	
225 230 235 240	
gtg tta cng att ttt tcc att gat ctt ttg tat cta atg act ata gtt	768
Val Leu Pro Ile Phe Ser Phe Val Leu Leu Tyr Leu Met Thr Ile Val	
245 250 255	
aac aag act tac aat atc cag tta tta atg gta ttt gtg ttt ttt gga	816
Asn Lys Thr Tyr Asn Ile Gln Leu Leu Met Val Phe Val Phe Phe Gly	
260 265 270	
tgt ctg tcc att ttc ttt tta tcg tta aaa gat ttg ttc aca gag gat	864
Cys Leu Ser Ile Phe Phe Leu Ser Leu Lys Asp Leu Phe Thr Glu Asp	
275 280 285	
gga aat caa aag aag gga ggc cag gag gat gaa tat tgt cgt atg ttt	912
Gly Asn Gln Lys Lys Gly Gly Gln Glu Asp Glu Tyr Cys Arg Met Phe	
290 295 300	
gac ata aag tac atg att tcc tat tta tgg ctg aca agg tcc acc att	960
Asp Ile Lys Tyr Met Ile Ser Tyr Leu Trp Leu Thr Arg Phe Thr Ile	
305 310 315 320	
tta ttg aca ggc ata atg gct att gta gta cat ttt tta tcg tcc aat	1008
Leu Leu Thr Gly Ile Met Ala Ile Val Val His Phe Leu Ser Phe Asn	
325 330 335	
gaa att act tct tcc atc aaa act gat ttg tta agt tta ctt ttg gtc	1056
Glu Ile Thr Ser Ser Ile Lys Thr Asp Leu Leu Ser Leu Leu Phe Val	
340 345 350	
gta gtg gca gaa tat gtt tcc agt ttc tct aac aaa caa cct gat tgg	1104
Val Val Ala Glu Tyr Val Ser Ser Phe Ser Asn Lys Gln Pro Asp Ser	
355 360 365	
gac tcc cat aat cat gca cat cac cat tcc cat cta acc gat tca ttg	1152
His Ser His Asn His Ala His His His Ser His Leu Thr Asp Ser Leu	
370 375 380	
cct ctc gaa aat gaa agt atg ttc aaa caa atg gca ttg aat aag gac	1200
Pro Leu Glu Asn Glu Ser Met Phe Lys Gln Met Ala Leu Asn Lys Asp	

385	390	395	400	
acc agg tcc att ttt ccg ttt tta ttg ttg aat acc gct ttc atg ttt	1240			
Thr Arg Ser Ile Phe Ser Phe Leu Leu Leu Asn Thr Ala Phe Met Phe				
405	410	415		
gta caa ctt tta tat tcc ttt cgt leu aaa taa ttg ggc tta tta tct	1296			
Val Glu Leu Leu Tyr Ser Phe Arg Ser Lys Ser Leu Gly Leu Leu Ser				
420	425	430		
gat ccg ttg cat atg gcc tta gat tgc aca tct ttg ctc tta ggt cta	1344			
Asp Ser Leu His Met Ala Leu Asp Cys Thr Ser Leu Leu Leu Gly Leu				
435	440	445		
att gct ggt gta ttg acc aag aaa cca gca agt gal aaa ttc cct ttc	1392			
Ile Ala Gly Val Leu Thr Lys Lys Pro Ala Ser Asp Lys Phe Pro Phe				
450	455	460		
ggc cta aat tat ctt ggt acc ttg gca ggt ttc acc aat ggt gct ctg	1440			
Gly Leu Asn Tyr Leu Gly Thr Leu Ala Gly Phe Thr Asn Gly Val Leu				
465	470	475	480	
tta ctc ggc ata gtg tgc ggt atc ttt gtg gag gca att gag aga aat	1488			
Leu Leu Gly Ile Val Cys Gly Ile Phe val Glu Ala Ile Glu Arg Ile				
485	490	495		
ttc aac ccc att cat ctt cat gca aca aat gag ttg ttg gtt gtt gct	1536			
Phe Asn Pro Ile His Leu His Ala Thr Asn Glu Leu Leu Val Val Ala				
500	505	510		
acg tta ggc tta tta gtg aac ctt gta ggt ttg ttt gcc ttc gag cat	1584			
Thr Leu Gly Leu Leu Val Asn Leu Val Gly Leu Phe Ala Phe Asp His				
515	520	525		
ggc gca cat gat cat ggt ggt act gat aat gaa aac atg aag ggg att	1632			
Gly Ala His Asp His Gly Gly Thr Asp Asn Glu Asn Met Lys Gly Ile				
530	535	540		
ttt tta cat ata ttg gca gat aca tta ggt tct gtt ggc gtt gtt att	1680			
Phe Leu His Ile Leu Ala Asp Thr Leu Gly Ser Val Gly Val Val Ile				
545	550	555	560	

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tgc acg tta tta alc aag tta aca cag tgg cca att ttt gat ccg atc	1728
Ser Thr Leu Leu Ile Lys Leu Thr His Trp Pro Ile Phe Asp Pro Ile	
565 570 575	
ccc tct tta tta att ggt tcc ttg att tta ctt agc gat ctg ccc ctg	1776
Ala Ser Leu Leu Ile Gly Ser Leu Ile Leu Leu Ser Ala Leu Pro Leu	
580 585 590	
cta aaa tct act tcc gca aat att tta cta aga ctg gat gac aag aag	1824
Leu Lys Ser Thr Ser Ala Asn Ile Leu Leu Arg Leu Asp Asp Lys Lys	
595 600 605	
cat aat cta gta aag agt ggc cta aac cag att tca acg acg cca gga	1872
His Asn Leu Val Lys Ser Ala Leu Asn Gln Ile Ser Thr Thr Pro Gly	
610 615 620	
atc aca ggt tat aca act cct aga ttt tgg ccg aca gag tca ggc agt	1920
Ile Thr Gly Tyr Thr Thr Pro Arg Phe Trp Pro Thr Glu Ser Gly Ser	
625 630 635 640	
tcc ggg cat tca cat gca cac acc cat tct cat gca gag aat cat agc	1968
Ser Gly His Ser His Ala His Thr His Ser His Ala Glu Asn His Ser	
645 650 655	
cat gag cat cat cat gat cag aac aac ggt tca cca gaa cac ccg agc	2016
His Glu His His His Asp Gln Lys Asn Gly Ser Gln Glu His Pro Ser	
660 665 670	
ttg gtc ggc tat att cat gta cag tat gta gac ggc gag aat tag aca	2064
Leu Val Gly Tyr Ile His Val Gln Tyr Val Asp Gly Glu Asn Ser Thr	
675 680 685	
att atc aag aaa aga gtt gaa aaa ata ttc gaa aat gtg tgc att aaa	2112
Ile Ile Lys Lys Arg Val Gln Lys Ile Phe Glu Asn Val Ser Ile Lys	
690 695 700	
gcg tgg gta caa gtt gag cct caa aat tcc act tgt tgg tgc ccg gct	2160
Ala Trp Val Gln Val Glu Pro Gln Asn Ser Thr Cys Trp Cys Arg Ala	
705 710 715 720	
act tct atg aac aca att tca gct aac ccg aat tct tta ccg cta cag	2208
Thr Ser Met Asn Thr Ile Ser Ala Asn Pro Asn Ser Leu Pro Leu Gln	

725

730

735

cct acc gca aat tga

2223

Pro Ile Ala Asn

740

<210> 230

<211> 740

<212> PRT

<213> Saccharomyces cerevisiae

<400> 230

Met Asp Arg Gly Arg Trp Cys Phe Leu Val Ser Val Ser Ser Arg Ile

1

5

10

15

Met Asn Leu Gln Glu Leu Leu Ala Lys Val Pro Leu Leu Leu Ser Tyr

20

25

30

Pro Thr Ile Ile Leu Ser Ser Asn Leu Ile Val Pro Ser His Asn Asp

35

40

45

Leu Ile Ser Arg Ala Ala Ser Thr Ser Ala Ala Glu Tyr Ala Asp Glu

50

55

60

Lys Leu Ile Phe Phe Ser Thr Asp His Ala Ile Arg Leu Ile Phe Leu

65

70

75

80

Pro Thr Phe Val Ala Ser Ser Phe Asn Leu Phe Ala His Tyr Phe Asn

85

90

95

Phe Ile Asn Tyr Ser Ser Arg Arg Lys Tyr Tyr Val Leu Phe Thr Ala

100

105

110

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Ile Tyr Phe Leu Ser Ile Leu Thr Ala Ile Phe His Pro Ile Gln Ser
115 120 125

Thr Cys Ile Thr Leu Leu Ile Ile Lys Leu Leu Thr Thr Ala Asp Gln
130 135 140

Ser Ser Pro Lys Ile Ala Leu Asn Phe Lys Thr Ile Leu Lys Thr Phe
145 150 155 160

Val Pro Phe Ile Thr Leu Thr Leu Val Ile Leu Arg Trp Asp Pro Ser
165 170 175

Phe Asp Ala Ser Ser Gly Asp Val Asn Lys Ile Ser Thr Ser Leu Ala
180 185 190

Ala Tyr Ala Leu Leu Ile Leu Thr Leu Arg Tyr Ala Ser Pro Leu Ile
195 200 205

Leu Ser Thr Leu Ser Ser Ser Ile Gly Val Val Ser Lys Asp Thr Ser
210 215 220

Val Ala Gln His Ser Ile Ser Arg Asn Lys Arg Phe Pro Leu Ile Leu
225 230 235 240

Val Leu Pro Ile Phe Ser Phe Val Leu Leu Tyr Leu Met Thr Ile Val
245 250 255

Asn Lys Thr Tyr Asn Ile Gln Leu Leu Met Val Phe Val Phe Phe Gly
260 265 270

Cys Leu Ser Ile Phe Phe Leu Ser Leu Lys Asp Leu Phe Thr Glu Asp
275 280 285

Gly Asn Gln Lys Lys Gly Gly Gln Glu Asp Glu Tyr Cys Arg Met Phe
290 295 300

asp Ile Lys Tyr Met Ile Ser Tyr Leu Trp Leu Thr Arg Phe Thr Ile
305 310 315 320

Leu Leu Thr Gly Ile Met Ala Ile Val Val His Phe Leu Ser Phe Asn
325 330 335

Glu Ile Thr Ser Ser Ile Lys Thr Asp Leu Leu Ser Leu Leu Phe Val
340 345 350

Val Val Ala Glu Tyr Val Ser Ser Phe Ser Asn Lys Gln Pro Asp Ser
355 360 365

His Ser His Asn His Ala His His His Ser His Leu Thr Asp Ser Leu
370 375 380

Pro Leu Gln Asn Glu Ser Met Phe Lys Gln Met Ala Leu Asn Lys Asp
385 390 395 400

Thr Arg Ser Ile Phe Ser Phe Leu Leu Leu Asn Thr Ala Phe Met Phe
405 410 415

Val Gln Leu Leu Tyr Ser Phe Arg Ser Lys Ser Leu Gly Leu Leu Ser
420 425 430

Asp Ser Leu His Met Ala Leu Asp Cys Thr Ser Leu Leu Leu Gly Leu
435 440 445

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Thr Ala Gly Val Leu Thr Lys Lys Pro Ala Ser Asp Lys Phe Pro Phe
450 455 460

Gly Leu Asn Tyr Leu Gly Thr Leu Ala Gly Phe Thr Asn Gly Val Leu
465 470 475 480

Leu Leu Gly Ile Val Cys Gly Ile Phe Val Glu Ala Thr Glu Arg Ile
485 490 495

Phe Asn Pro Ile His Leu His Ala Thr Asn Glu Leu Leu Val Val Ala
500 505 510

Thr Leu Gly Leu Leu Val Asn Leu Val Gly Leu Phe Ala Phe Asp His
515 520 525

Gly Ala His Asp His Gly Gly Thr Asp Asn Glu Asn Met Lys Gly Thr
530 535 540

Phe Leu His Ile Leu Ala Asp Thr Leu Gly Ser Val Gly Val Val Thr
545 550 555 560

Ser Thr Leu Leu Ile Lys Leu Thr His Trp Pro Ile Phe Asp Pro Ile
565 570 575

Ala Ser Leu Leu Ile Gly Ser Leu Ile Leu Leu Ser Ala Leu Pro Leu
580 585 590

Leu Lys Ser Thr Ser Ala Asn Ile Leu Leu Arg Leu Asp Asp Lys Lys
595 600 605

His Asn Leu Val Lys Ser Ala Leu Asn Glu Ile Ser Thr Thr Pro Gly
610 615 620

Ile Thr Gly Tyr Thr Thr Pro Arg Phe Trp Pro Thr Glu Ser Gly Ser
525 530 535 540

Ser Gly His Ser His Ala His Thr His Ser His Ala Glu Asn His Ser
645 650 655

His Glu His His His Asp Gln Lys Asn Gly Ser Gln Glu His Pro Ser
660 665 670

Leu Val Gly Tyr Ile His Val Gln Tyr Val Asp Gly Glu Asn Ser Thr
675 680 685

Ile Ile Lys Lys Arg Val Glu Lys Ala Phe Glu Asn Val Ser Ile Lys
690 695 700

Ala Trp Val Gln Val Glu Pro Gln Asn Ser Thr Cys Trp Cys Arg Ala
705 710 715 720

Thr Ser Met Asn Thr Ile Ser Ala Asn Pro Asn Ser Leu Pro Leu Gln
725 730 735

Pro Ile Ala Asn
740

<210> 231

<211> 591

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (591)

<400> 211

atg aaa cag ata gtc aaa aga agc cat gcc atc aga ata gll gca gca 48
Met Lys Gln Ile Val Lys Arg Ser His Ala Ile Arg Ile Val Ala Ala
1 5 10 15

tta gga atc ata ggc ctg tgg atg cll lle leg tot aat gaa cta tcc 96
Leu Gly Ile Ile Gly Leu Trp Met Phe Phe Ser Ser Asn Glu Leu Ser
20 25 30

atc gct acg ccg ggc cta atc aag gag aag tot ggt ata gat gaa gty 144
Ile Ala Thr Pro Gly Leu Ile Lys Ala Lys Ser Gly Ile Asp Glu Val
35 40 45

caa ggg gag gct gct gag aag aac gac gct cgg ttg aaa gag atc gag 192
Gln Gly Ala Ala Ala Glu Lys Asn Asp Ala Arg Leu Lys Glu Ile Glu
50 55 60

aag caa acc att atg cca ttg atg gcc gat gat aag gag aag aag gaa 240
Lys Gln Thr Ile Met Pro Leu Met Gly Asp Asp Lys Val Lys Lys Glu
65 70 75 80

gtg ggc agg gag tgg tgg aag tac ttc cat acc ctg ctg gcc cgt ttt 288
Val Gly Arg Ala Ser Trp Lys Tyr Phe His Thr Leu Leu Ala Arg Phe
85 90 95

ccg gac gag cct act cct gaa gaa aga gag aaa ctg caa acg ttt att 336
Pro Asp Glu Pro Thr Pro Glu Glu Arg Glu Lys Leu His Thr Phe Ile
100 105 110

ccg ttg tat gca gaa ctg tat cca tgc ggg gaa tgt tca tat cac ttt 384
Gly Leu Tyr Ala Glu Leu Tyr Pro Cys Gly Glu Cys Ser Tyr His Phe
115 120 125

gta aag ttg att gag aag tal ccc gta cag aca tct agc agg acg gct 432
Val Lys Leu Ile Glu Lys Tyr Pro Val Gln Thr Ser Ser Arg Thr Ala
130 135 140

gcc gca atg tgg gga tgc cac att cac aac aag gtg aac gaa tac cta 480
Ala Ala Met Thr Gly Cys His Ile His Asn Lys Val Asn Glu Tyr Leu
145 150 155 160

aag aaa gac ata tat gac tgt ggt acc atc ctg gag gac tac cat tgt 528
 Lys Lys Asp Ile Tyr Asp Cys Ala Thr Ile Leu Glu Asp Tyr Asp Cys
 165 170 175

gga tgt agt gac agc gac ggt aaa cgc gtg tct ctc gag aag gag gct 576
 Gly Cys Ser Asp Ser Asp Gly Lys Arg Val Ser Leu Glu Tyr Glu Ala
 180 185 190

aaa cag cac ggt tga 591
 Lys Glu His Gly
 195

<210> 232
 <211> 196
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 232

Met Lys Glu Ile Val Lys Arg Ser His Ala Ile Arg Ile Val Ala Ala
 1 5 10 15

Leu Gly Ile Ile Gly Leu Trp Met Phe Phe Ser Ser Asn Glu Leu Ser
 20 25 30

Ile Ala Thr Pro Gly Leu Ile Lys Ala Lys Ser Gly Ile Asp Glu Val
 35 40 45

Gln Gly Ala Ala Ala Glu Lys Asn Asp Ala Arg Leu Lys Glu Ile Glu
 50 55 60

Lys Glu Thr Ile Met Pro Leu Met Gly Asp Asp Lys Val Lys Lys Glu
 65 70 75 80

Val Gly Arg Ala Ser Trp Lys Tyr Phe His Thr Leu Leu Ala Arg Phe

Pro Asp Glu Pro Thr Pro Glu Glu Arg Glu Lys Leu His Thr Phe Ile
100 105 110

Gly Leu Tyr Ala Glu Leu Tyr Pro Cys Gly Glu Cys Ser Tyr His Phe
115 120 125

Val Lys Leu Ile Glu Lys Tyr Pro Val Glu, Thr Ser Ser Arg Thr Ala
130 135 140

Ala Ala Met Trp Gly Cys His Ile His Asn Lys Val Asn Glu Tyr Leu
145 150 155 160

Lys Lys Asp Ile Tyr Asp Cys Ala Thr Ile Leu Glu Asp Tyr Asp Cys
165 170 175

Gly Cys Ser Asp Ser Asp Gly Lys Arg Val Ser Leu Glu Lys Glu Ala
180 185 190

Lys Gln His Gly
195

<210> 233
<211> 1986
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1) .. (1986)

<400> 233

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atg ggc aca cag ttt cga aga aat gtc cag aac caa cag agt gat tct	18
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser	
1 5 10 15	
gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga	36
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg	
20 25 30	
aac cac att cat cat caa cag gga tta ggc cat aag aga agc agg ggt	144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly	
35 40 45	
att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac aag	192
Ile Ser Gly Ser Ala Tyr Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg	
50 55 60	
aaa aga gac ggg aac ggt aga aaa cgt tgg cga gat tcc aga aga ctg	240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
65 70 75 80	
att ttc att ctt ggt cca ttc tta ggt gta ctt ttg cag tct agc ttt	288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
85 90 95	
ggc ggt tat cat gtt cat aat aac gat agc gac ttg ttt gac aac ttt	336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	
100 105 110	
gla aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa cat gtc	384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val	
115 120 125	
ctc cca caa ggt ata agt tgg ttt att gat gat att cag gct ggt aac	432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn	
130 135 140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Gln Asn Phe Ala Val Gly	
145 150 155 160	
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val	

165	170	175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att			576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Gln Ser Trp Gly Val Ile			
180	185	190	
gga gac gac gag tgc gat agt tct ggc cat ttt cgt aaa cgg ctg tgg			624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			
195	200	205	
gga agt ttt tac atg ctg aga aca atg gtt atg gal aaa gtt tgt tgg			672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			
210	215	220	
ttg aac cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac			720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn			
225	230	235	240
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc			768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			
245	250	255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att			816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile			
260	265	270	
ggc tac gaa ccc aat aaa atg acg agt gct ggc tac gat tgg agg ctt			864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu			
275	280	285	
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag			912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
290	295	300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aca gtt tgt tta			960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
305	310	315	320
atg gga cat tct arg ggt cct cag att atc ttt tac ttt atg aac tgg			1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			
325	330	335	

gtc gag gct gaa ggc ccc ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val	
340 345 350	
aac gaa cac ata gat tca ttc att aat gca gca ggg aag ctt ctg ggc	1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	
355 360 365	
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc	1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	
370 375 380	
att caa cta aat aag tta gcc atg tat ggt ttg gaa aag ttc ttc tca	1200
Ile Glu Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	
385 390 395 400	
aga att gag aga gta aaa atg tta caa aag tgg ggt ggt ata cca tca	1248
Arg Ile Glu Arg Val Lys Met Leu Glu Thr Trp Gly Gly Ile Pro Ser	
405 410 415	
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct	1296
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser	
420 425 430	
tca gag gat gca ttg aat aac aac acc gac aca tac ggc aat ttc att	1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile	
435 440 445	
cca tta gaa agg aat aag agc gat gct ttc aac aaa aat ttg aca atg	1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met	
450 455 460	
aau gac gcc att aac atg aca tta tgg ata tca cct gaa tgg ctg caa	1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Glu	
465 470 475 480	
aga aga gta cat gag cag tac tgg ttc ggc tat tcc aag aat gaa gaa	1488
Arg Arg Val His Glu Glu Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu	
485 490 495	
caa tta aga aaa aat gag cta cac cac aag cac tgg tgg aat cca atg	1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met	

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500	505	510	
gaa gta cca att cca gaa gct ccc cac atg aaa atc tat tgt ata cac			1584
Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr			
515	520	525	
ggg gtg aac aac cca act gaa agy gca tat gta tat aag gaa gag ggt			1632
Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp			
530	535	540	
gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag cca cct			1680
Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro			
545	550	555	560
gta ttc ctc acc gag ggg gac gga acc gtt ccg ctg gtg gcy cat caa			1728
Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser			
565	570	575	
atg tgt cac aac tgg gcc cag ggt gct tca ccg tac aac cct gcc gga			1776
Met Cys His Lys Thr Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly			
580	585	590	
att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat			1824
Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp			
595	600	605	
ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctg ggc agc			1872
Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser			
610	615	620	
gcy gag ttg aac gat cac atc ttg aaa att gca agc ggt aat ggc gat			1920
Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp			
625	630	635	640
ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag			1968
Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln			
645	650	655	
atg ccc ttc cca atg taa			1986
Met Pro Phe Pro Met			
660			

<210> 234

<211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 234

Met	Gly	Thr	Leu	Phe	Arg	Arg	Asn	Val	Gln	Asn	Gln	Lys	Ser	Asp	Ser
1				5					10					15	

Asp	Glu	Asn	Asn	Lys	Gly	Gly	Ser	Val	His	Asn	Lys	Arg	Glu	Ser	Arg
			20					25					30		

Asn	His	Ile	His	His	Gln	Gln	Gly	Leu	Gly	His	Lys	Arg	Arg	Arg	Gly
		35					40						45		

Ile	Ser	Gly	Ser	Ala	Lys	Arg	Asn	Gln	Arg	Gly	Lys	Asp	Phe	Asp	Arg
	50					55					60				

Lys	Arg	Asp	Gly	Asn	Gly	Arg	Lys	Arg	Trp	Arg	Asp	Ser	Arg	Arg	Leu
65					70				75					80	

Ile	Phe	Ile	Leu	Gly	Ala	Phe	Asn	Gly	Val	Leu	Leu	Pro	Phe	Ser	Phe
			85						90					95	

Gly	Ala	Tyr	His	Val	His	Asn	Ser	Asp	Ser	Asp	Leu	Phe	Asp	Asn	Phe
			100					105					110		

Val	Asn	Phe	Asp	Ser	Leu	Lys	Val	Tyr	Leu	Asp	Asp	Trp	Lys	Asp	Val
		115					120					125			

Leu	Pro	Gln	Gly	Ile	Ser	Ser	Phe	Ile	Asp	Asp	Ile	Gln	Ala	Gly	Asn
	130						135					140			

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
145 150 155 160

Lys Glu Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
195 200 205

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
210 215 220

Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
225 230 235 240

Phe Thr Leu Arg Ala Ala Glu Gly Phe Glu Ser Thr Asp Tyr Phe Ile
245 250 255

Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Glu Asn Leu Gly Val Ile
260 265 270

Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
275 280 285

Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
290 295 300

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Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
305 310 315 320

Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
325 330 335

Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
340 345 350

Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
355 360 365

Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
370 375 380

Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
385 390 395 400

Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
405 410 415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
420 425 430

Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
435 440 445

Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
450 455 460

Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
465 470 475 480

Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
485 490 495

Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
515 520 525

Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
530 535 540

Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
545 550 555 560

Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
565 570 575

Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
580 585 590

Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
595 600 605

Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
610 615 620

Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
625 630 635 640

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Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

Met Pro Phe Pro Met
 660

<210> 235
 <211> 1164
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (1164)

<400> 235
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 Met Glu Gln Asn Arg Phe Lys Lys Glu Thr Lys Thr Cys Ser Ala Ser
 1 5 10 15
 tgg cag cgc gcc cag cag tgg aag atg tgt gag aca gat cgc ctc gaa 96
 Trp Pro Arg Ala Pro Gln Ser Thr Leu Lys Ala Thr Asp Arg Leu Glu
 20 25 30
 ctc aca tac gat gtg tac act agc gca gag cgg caa cgc cgc tct agc 144
 Leu Thr Tyr Asp Val Tyr Thr Ser Ala Glu Arg Gln Arg Arg Ser Arg
 35 40 45
 act gcc act aag ctt aac ctt gtg ttt ttg cac ggc agc ggc atg agc 192
 Thr Ala Thr Arg Leu Asn Leu Val Phe Leu His Gly Ser Gly Met Ser
 50 55 60
 aag gtg gta tgg gag tac tat ttg cag cgt ctg gta gcc gcc gat ggc 240
 Lys Val Val Trp Glu Tyr Tyr Leu Pro Arg Leu Val Ala Ala Asp Ala
 65 70 75 80
 gag ggc aat tat gcc atc gac aag gtc ttg ttg atc gac cag gtt aac 288
 Glu Gly Asn Tyr Gcc Ile Asp Lys Val Leu Leu Ile Asp Gln Val Asn
 85 90 95

cac ggt gat tct gug gta cgc aac cgc ggc aga ctc ggc acc aat ttc	336
His Gly Asp Ser Ala Val Arg Asn Arg Gly Arg Leu Gly Thr Asn Phe	
100 105 110	
auc tgg atc gac ggg gcc cgc gac gtg ctc aag att gcc asa tgc gag	384
Asn Trp Ile Asp Gly Ala Arg Asp Val Leu Lys Ile Ala Thr Cys Glu	
115 120 125	
ttg ggt agt att gac agc cac cug gca cta aac gta gtc atc ggc cac	432
Leu Gly Ser Ile Asp Ser His Pro Ala Leu Asn Val Val Ile Gly His	
130 135 140	
tgc atg ggc ggg ttc cag gcc ctt gng tgt gac gtc ctg cag acc aat	480
Ser Met Gly Gly Phe Gln Ala Leu Ala Cys Asp Val Leu Gln Pro Asn	
145 150 155 160	
ctg ttt cat ttg ctc atc ttc atc gag cct gta gta atc aca cgg aaa	528
Leu Phe His Leu Leu Ile Leu Ile Glu Pro Val Val Ile Thr Arg Lys	
165 170 175	
gcc atc ggc gcc ggg agg cca ggg ctt cug ccc gcc tct cgg cag atc	576
Ala Ile Gly Ala Gly Arg Pro Gly Leu Pro Pro Asp Ser Pro Gln Ile	
180 185 190	
cca gaa aat ctt tat aac tcc cta cgt tta aag acg tgc gac cct ttc	624
Pro Glu Asn Leu Tyr Asn Ser Leu Arg Leu Lys Thr Cys Asp His Phe	
195 200 205	
gct aac gag tcc gaa tat gta aaa tat atg agg aac ggt tcc ttt ttt	672
Ala Asn Glu Ser Glu Tyr Val Lys Tyr Met Arg Asn Gly Ser Phe Phe	
210 215 220	
acc aat gcg cag agc caa atc ctg caa aac atc atc gat ttt gag agg	720
Thr Asn Ala His Ser Gln Ile Leu Gln Asn Ile Ile Asp Phe Glu Arg	
225 230 235 240	
aca aaa gcc tct gga gac gat gaa gat ggt gga ccc gtt cgc acg aag	768
Thr Lys Ala Ser Gly Asp Asp Glu Asp Gly Gly Pro Val Arg Thr Lys	
245 250 255	
atg gag cag gct caa aat ctc ctc tgc tac atg aac atg cag act ttt	816

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Met	Glu	Gln	Ala	Gln	Asn	Leu	Leu	Cys	Tyr	Met	Asn	Met	Gln	Thr	Phe		
			260					265					270				
ggc	act	ttc	ctg	alc	agg	aat	gtg	aag	ttt	ctg	agg	aag	agg	act	alc	864	
Ala	Pro	Phe	Leu	Ile	Ser	Asn	Val	Lys	Phe	Val	Arg	Lys	Arg	Thr	Ile		
			275				280					285					
cac	att	gtg	ggc	ggc	cgc	tcg	aac	tgg	tgt	cct	cgc	caa	aat	cag	ctg	912	
His	Ile	Val	Gly	Ala	Arg	Ser	Asn	Trp	Cys	Pro	Pro	Gln	Asn	Gln	Leu		
			290				295					300					
ttt	ttg	cag	aaa	act	ctc	cag	aac	tac	cal	cgc	gat	gtc	att	ccc	ggc	960	
Phe	Leu	Glu	Lys	Thr	Leu	Gln	Asn	Tyr	His	Leu	Asp	Val	Ile	Pro	Gly		
305						310				315			320				
ggc	tcg	cac	ttg	gtc	aac	gtt	gag	gct	cgc	gac	ctg	gtg	alc	gag	agg	1008	
Gly	Ser	His	Leu	Val	Asn	Val	Glu	Ala	Pro	Asp	Leu	Val	Ile	Glu	Arg		
			325				330					335					
att	aat	cac	cac	atc	cac	gag	ttt	gtc	ctt	acc	tcg	cgc	ctg	cag	tcg	1056	
Ile	Asn	His	His	Ile	His	Glu	Phe	Val	Leu	Thr	Ser	Pro	Leu	Gln	Ser		
			340				345					350					
tca	cac	att	cgc	caa	ttg	acc	ctt	gaa	gaa	aga	gag	gtg	atg	ttt	gac	1104	
Ser	His	Ile	Pro	Gln	Leu	Thr	Leu	Glu	Glu	Arg	Ala	Val	Met	Phe	Asp		
			355				360					365					
agg	gct	ttc	gac	tgc	ttc	aag	aat	gaa	gct	ttg	gtc	aaa	aag	act	aac	1152	
Arg	Ala	Phe	Asp	Ser	Phe	Lys	Asn	Glu	Ala	Leu	Val	Lys	Thr	Thr	Lys		
			370				375					380					
caa	aaa	ctg	taa													1164	
Gln	Lys	Leu															
385																	

<210> 236

<211> 387

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 236

Met Glu Gln Asn Arg Phe Lys Lys Glu Thr Lys Thr Cys Ser Ala Ser
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Trp Pro Arg Ala Pro Gln Ser Thr Leu Cys Ala Thr Asp Arg Leu Glu
 20 25 30

Leu Thr Tyr Asp Val Tyr Thr Ser Ala Glu Arg Gln Arg Arg Ser Arg
 35 40 45

Thr Ala Thr Arg Leu Asn Leu Val Phe Leu His Gly Ser Gly Met Ser
 50 55 60

Lys Val Val Trp Glu Tyr Tyr Leu Pro Arg Leu Val Ala Ala Asp Ala
 65 70 75 80

Glu Gly Asn Tyr Ala Ile Asp Lys Val Leu Leu Ile Asp Gln Val Asn
 85 90 95

His Gly Asp Ser Ala Val Arg Asn Arg Gly Arg Leu Gly Thr Asn Phe
 100 105 110

Asn Trp Ile Asp Gly Ala Arg Asp Val Leu Lys Ile Ala Thr Cys Glu
 115 120 125

Leu Gly Ser Ile Asp Ser His Pro Ala Leu Asn Val Val Ile Gly His
 130 135 140

Ser Met Gly Gly Phe Gln Ala Leu Ala Cys Asp Val Leu Gln Pro Asn
 145 150 155 160

Leu Phe His Leu Leu Ile Leu Ile Glu Pro Val Val Ile Thr Arg Lys

165

170

175

Ala Ile Gly Ala Gly Arg Pro Gly Leu Pro Pro Asp Ser Pro Gln Phe
180 185 190

Pro Glu Asn Leu Tyr Asn Ser Leu Arg Leu Lys Thr Cys Asp His Phe
195 200 205

Ala Asn Glu Ser Glu Tyr Val Lys Tyr Met Arg Asn Gly Ser Phe Phe
210 215 220

Thr Asp Ala His Ser Gln Phe Leu Gln Asn Phe Phe Asp Phe Glu Arg
225 230 235 240

Thr Lys Ala Ser Gly Asp Asp Glu Asp Gly Gly Pro Val Arg Thr Lys
245 250 255

Met Glu Glu Ala Glu Asn Leu Leu Cys Tyr Met Asn Met Glu Thr Phe
260 265 270

Ala Pro Phe Leu Ile Ser Asn Val Lys Phe Val Arg Lys Arg Thr Ile
275 280 285

His Phe Val Gly Ala Arg Ser Asn Trp Cys Pro Pro Gln Asn Gln Leu
290 295 300

Phe Leu Gln Lys Thr Leu Gln Asn Tyr His Leu Asp Val Ile Pro Gly
305 310 315 320

Gly Ser His Leu Val Asn Val Glu Ala Pro Asp Leu Val Ile Glu Arg
325 330 335

Ile Asn His His Ile His Glu Phe Val Leu Thr Ser Pro Leu Gln Ser
 340 345 350

Ser His Ile Pro Gln Leu Thr Leu Gln Glu Arg Ala Val Met Phe Asp
 355 360 365

Arg Ala Phe Asp Ser Phe Lys Asn Glu Ala Asn Val Lys Thr Thr Lys
 370 375 380

Gln Lys Leu
 385

<210> 237
 <211> 1939
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1939)

<400> 237
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 Met Ser Ser Gln Phe Phe Leu Lys Thr Ser Gln Asp Ile Glu Leu Phe
 1 5 10 15
 caa agc tac cca act ttt gag caa tcc aac aca aac tcc aag gat ttc 96
 Gln Ser Tyr Pro Thr Phe Glu Gln Ser Asn Thr Asn Ser Lys Asp Phe
 20 25 30
 cct gtc att tcc tgg gtt tta tgg cca tgt ggc aga ttt ttg gat tta 144
 Pro Val Ile Ser Ser Val Leu Ser Pro Cys Gly Arg Phe Leu Ala Leu
 35 40 45
 tct acg aag gag aac gtc aaa gtt ttt aca ggt cca tgt ttg gat aac 192
 Ser Thr Lys Glu Asn Val Lys Val Phe Thr Gly Pro Cys Leu Asp Asn

50	55	60	
gll cta tta acc atg aag ttg tcc gac gtc tat gac cta cac ttc	240		
Val Leu Leu Thr Met Lys Leu Ser Asp Val Tyr Asp Leu His Phe Ser			
65	70	75	80
cca gca ggt aac tac tta agc act tgg gag aga gcg tct ata cca gac	280		
Pro Ala Gly Asn Tyr Leu Ser Thr Trp Glu Arg Ala Ser Ile Gln Asp			
85	90	95	
cca aat cac aag aac gll aca gtt tgg tat ttg aat aaa cca ttt aag	320		
Pro Asn His Phe Asn Val Lys Val Trp Tyr Leu Asn Lys Pro Phe Lys			
100	105	110	
aaa gal tgc gtt tgg gag gat ata gtc cct gct tac gaa tat cca ggc	360		
Lys Asp Cys Val Ser Gln Asp Ile Val Pro Ala Tyr Glu Tyr Gln Ala			
115	120	125	
aaa tcc caa agc ggt tgg ctt tta caa ttc tcc aca tta gac aat tat	400		
Lys Ser Gln Ser Gly Trp Phe Leu Gln Phe Ser Lys Leu Asp Asn Tyr			
130	135	140	
ccg cta aga ctt ttt aaa cac gac ttg aag atc gtt aca tta agc tcc	440		
Gly Leu Arg Leu Phe Lys His Asp Leu Lys Ile Val Lys Leu Ser Ser			
145	150	155	160
gct aat ggc gac aat ttc gac ttc caa tct ccg ttt gct gtc ttg tct	520		
Ala Asn Ala Asp Asn Phe Asp Phe Glu Ser Pro Phe Ala Val Leu Ser			
165	170	175	
gal gat gaa aag tcc caa cat ttc acc acc tac cta atc cct cca gct	560		
Asp Asp Glu Thr Ser Gln His Phe Thr Thr Tyr Leu Ile Ser Pro Ala			
180	185	190	
gaa cat cca aca att tgt act ttc aca cca gaa aag ggt ggt aac ccg	600		
Glu His Pro Thr Ile Cys Thr Phe Thr Pro Glu Lys Gly Gly Lys Pro			
195	200	205	
gct caa tta acc ata tgg gcc ctc tct gaa ggt aaa atc acc aag aac	640		
Ala Gln Leu Ile Ile Trp Ala Asn Ser Glu Gly Lys Ile Thr Lys Lys			
210	215	220	

atc	gac	tcg	aaa	act	ttc	tcc	aaa	gct	gat	tcc	tgc	caa	ctg	aaa	tgg	720
Ile	Ala	Ser	Iys	Thr	Phe	Phe	Lys	Ala	Asp	Ser	Cys	Gln	Leu	Lys	Trp	
225					230					235					240	
aac	cca	tta	ggg	aat	gct	att	tta	tgt	tta	gct	att	act	gat	ttt	gat	768
Asn	Pro	Leu	Gly	Asn	Ala	Ile	Leu	Cys	Leu	Ala	Ile	Thr	Asp	Phe	Asp	
				245					250					255		
tcg	tca	aac	aaa	tca	tat	tat	ggg	gaa	aac	aca	cta	tac	tta	ctg	tct	816
Ser	Ser	Asn	Lys	Ser	Tyr	Tyr	Gly	Glu	Asn	Thr	Leu	Tyr	Leu	Leu	Ser	
			260					265					270			
ttc	caa	ggg	gac	aac	ggg	act	tty	ggg	ggg	aac	tct	gta	ggt	gtt	tct	864
Phe	Gln	Gly	Val	Asn	Gly	Thr	Leu	Gly	Gly	Asn	Ser	Val	Arg	Val	Ser	
			275				280						285			
tta	acc	act	ggg	cct	gtc	cac	gat	ttc	act	tgg	tgg	cca	act	tca	agg	912
Leu	Thr	Thr	Gly	Pro	Val	His	Asp	Phe	Thr	Trp	Ser	Pro	Thr	Ser	Arg	
			290				295					300				
cca	ttc	ggg	gtc	atc	gct	ggg	tac	atg	cca	gca	acc	att	tcc	ttc	ttt	960
Gln	Phe	Gly	Val	Ile	Ala	Gly	Tyr	Met	Pro	Ala	Thr	Ile	Ser	Phe	Phe	
305					310					315					320	
gac	tta	aga	ggg	aat	gtt	gac	cac	tca	tta	cct	caa	caa	gac	aaa	aat	1008
Asp	Leu	Arg	Gly	Asn	Val	Val	His	Ser	Leu	Pro	Gln	Gln	Ala	Lys	Asn	
				325						330				335		
acc	atg	ctt	ttc	tct	ccc	tct	ggg	cac	tac	att	ctt	atc	gac	ggg	tct	1056
Thr	Met	Leu	Phe	Ser	Pro	Ser	Gly	His	Tyr	Ile	Leu	Ile	Ala	Gly	Phe	
				340				345					350			
ggc	aac	tta	cag	ggc	tcc	gtg	gaa	atc	cta	gat	cgt	cic	gac	cca	tcc	1104
Gly	Asn	Leu	Gln	Gly	Ser	Val	Glu	Ile	Leu	Asp	Arg	Leu	Asp	Lys	Phe	
			355				360					365				
aag	tgc	gtg	agt	aaa	ttt	gac	gct	acc	aac	act	tct	gtc	tgc	aaa	tgg	1152
Lys	Cys	Val	Ser	Lys	Phe	Asp	Ala	Thr	Asn	Thr	Ser	Val	Cys	Lys	Trp	
			370				375				380					
tca	ccg	ggg	gga	gaa	ttt	atc	atg	aca	gct	acc	act	tca	cca	aga	ttg	1200
Ser	Pro	Gly	Gly	Glu	Phe	Ile	Met	Thr	Ala	Thr	Thr	Ser	Pro	Arg	Leu	

385		390		395		400	
aga gtc gat aac ggc gtt aaa ata tgg cat gta tca ggc tct tta gta							1244
Arg Val Asp Asn Gly Val Lys Ile Trp His Val Ser Gly Ser Leu Val							
	405		410		415		
ttt gtc aaa gag ttc aag gag ctt ttg aag gta gac tgg agg tca cca							1296
Phe Val Lys Glu Phe Lys Glu Leu Leu Lys Val Asp Trp Arg Ser Pro							
	420		425		430		
tgt aac tac aaa act ttg gaa aac aaa gac gaa gca ttt ttc gag aac							1344
Cys Asn Tyr Lys Thr Leu Glu Asn Lys Asp Glu Ala Phe Phe Glu Asn							
	435		440		445		
cat atc att aat aac tgg gaa ccg cta cct gat tgg acc aca tct tca							1392
His Ile Ile Asn Asn Trp Glu Pro Leu Pro Asp Ser Thr Thr Ser Ser							
	450		455		460		
ctt gat cct aaa ata tcc aat aaa tca gaa ttg caa ata cat tct agc							1440
Leu Asp Pro Lys Ile Ser Asn Lys Ser Glu Leu Gln Ile His Ser Ser							
	465		470		475		480
glt caa gag tac ata agt caa caa cca agc aga gaa gca agc tcc aat							1488
Val Gln Glu Tyr Ile Ser Gln His Pro Ser Arg Glu Ala Ser Ser Asn							
	485		490		495		
gga aac gga tct aag gcc aaa gct gga ggc gct tat aaa cca cct cac							1536
Gly Asn Gly Ser Lys Ala Lys Ala Gly Gly Ala Tyr Tyr Pro Pro His							
	500		505		510		
gca aga aga aca ggc ggt gga cgt att gtc ccc gga gtt cct cct ggt							1584
Ala Arg Arg Thr Gly Gly Gly Arg Ile Val Pro Gly Val Pro Pro Gly							
	515		520		525		
gca gca aag aag acc atc cca ggg cta gtt ccg ggc atg agt gcc aac							1632
Ala Ala Lys Lys Thr Ile Pro Gly Leu Val Pro Gly Met Ser Ala Asn							
	530		535		540		
aag gac gcc aac acc aag aac agg aga aga aga gcc aat aaa aag tca							1680
Lys Asp Ala Asn Thr Lys Asn Arg Arg Arg Arg Ala Asn Lys Lys Ser							
	545		550		555		560

566/762

agt gaa aag tca cct gat tct act cag gcc cca tct gct cct gcc tcc 1728
 Ser Glu Thr Ser Pro Asp Ser Thr Pro Ala Pro Ser Ala Pro Ala Ser
 565 570 575

aca aat gcc ccc aca aac aat aaa gaa act tct cca gag gag aag aaa 1776
 Thr Asn Ala Pro Thr Asn Asn Lys Glu Thr Ser Pro Glu Glu Lys Lys
 580 585 590

ala aya tct tta cta aag aaa tta aag gct att gaa acc ttg aag gaa 1824
 Ile Arg Ser Leu Leu Lys Lys Leu Arg Ala Ile Glu Thr Leu Lys Glu
 595 600 605

aga cag gcc glc ggc gac aaa cta gaa gat acg caa gtt cta aaa att 1872
 Arg Glu Ala Val Gly Asp Lys Leu Glu Asp Thr Gln Val Leu Lys Ile
 610 615 620

caa act gaa gaa aaa gtg ttg aaa gat ttg gaa aag ttg ggt tgg aag 1920
 Gln Thr Glu Glu Lys Val Leu Lys Asp Leu Glu Lys Leu Gly Trp Lys
 625 630 635 640

gat gaa caa 1929
 Asp Glu

<210> 238

<211> 642

<212> FRT

<213> *Saccharomyces cerevisiae*

<400> 238

Met Ser Ser Gln Phe Phe Leu Lys Thr Ser Gln Asp Ile Glu Leu Phe
 1 5 10 15

Gln Ser Tyr Pro Thr Phe Gln Gln Ser Asn Thr Asn Ser Lys Asp Phe
 20 25 30

Pro Val Ile Ser Ser Val Leu Ser Pro Cys Gly Arg Phe Leu Ala Leu
 35 40 45

Ser Thr Lys Gln Asn Val Lys Val Phe Thr Gly Pro Cys Leu Asp Asn
50 55 60

Val Leu Leu Thr Met Lys Leu Ser Asp Val Tyr Asp Leu His Phe Ser
65 70 75 80

Pro Ala Gly Asn Tyr Leu Ser Thr Trp Glu Arg Ala Ser Ile Gln Asp
85 90 95

Pro Asn His Lys Asn Val Lys Val Trp Tyr Leu Asn Lys Pro Phe Lys
100 105 110

Lys Asp Cys Val Ser Glu Asp Ile Val Pro Ala Tyr Glu Tyr Gln Ala
115 120 125

Lys Ser Gln Ser Gly Trp Phe Leu Gln Phe Ser Lys Leu Asp Asn Tyr
130 135 140

Gly Leu Arg Leu Phe Lys His Asp Leu Lys Ile Val Lys Leu Ser Ser
145 150 155 160

Ala Asn Ala Asp Asn Phe Asp Phe Gln Ser Pro Phe Ala Val Leu Ser
165 170 175

Asp Asp Glu Thr Ser Gln His Phe Thr Thr Tyr Leu Ile Ser Pro Ala
180 185 190

Glu His Pro Thr Ile Cys Thr Phe Thr Pro Gln Lys Gly Gly Lys Pro
195 200 205

Ala Gln Leu Ile Ile Trp Ala Leu Ser Glu Gly Lys Ile Thr Lys Lys
210 215 220

Ile Ala Ser Lys Thr Phe Phe Lys Ala Asp Ser Cys Gln Leu Lys Trp
225 230 235 240

Asn Pro Leu Gly Asn Ala Ile Leu Cys Leu Ala Ile Thr Asp Phe Asp
245 250 255

Ser Ser Asn Lys Ser Tyr Tyr Gly Glu Asn Thr Leu Tyr Leu Leu Ser
260 265 270

Phe Gln Gly Val Asn Gly Thr Leu Gly Gly Asn Ser Val Arg Val Ser
275 280 285

Leu Thr Thr Gly Pro Val His Asp Phe Thr Trp Ser Pro Thr Ser Arg
290 295 300

Gln Phe Gly Val Ile Ala Gly Tyr Met Pro Ala Thr Ile Ser Phe Phe
305 310 315 320

Asp Leu Arg Gly Asn Val Val His Ser Leu Pro Gln Gln Ala Lys Asn
325 330 335

Thr Met Leu Phe Ser Pro Ser Gly His Tyr Ile Leu Ile Ala Gly Phe
340 345 350

Gly Asn Leu Gln Gly Ser Val Glu Ile Leu Asp Arg Leu Asp Lys Phe
355 360 365

Lys Cys Val Ser Lys Phe Asp Ala Thr Asn Thr Ser Val Cys Lys Trp
370 375 380

Ser Pro Gly Gly Glu Phe Ile Met Thr Ala Thr Thr Ser Pro Arg Leu
385 390 395 400

Arg Val Asp Asn Gly Val Lys Ile Trp His Val Ser Gly Ser Leu Val
405 410 415

Phe Val Lys Glu Phe Lys Glu Leu Leu Lys Val Asp Trp Arg Ser Pro
420 425 430

Cys Asn Tyr Lys Thr Leu Glu Asn Lys Asp Glu Ala Phe Phe Glu Asn
435 440 445

His Ile Ile Asn Asn Trp Glu Pro Ser Pro Asp Ser Thr Thr Ser Ser
450 455 460

Leu Asp Pro Lys Ile Ser Asn Lys Ser Glu Leu Gln Ile His Ser Ser
465 470 475 480

Val Gln Glu Tyr Ile Ser Gln His Pro Ser Arg Glu Ala Ser Ser Asn
485 490 495

Gly Asn Gly Ser Lys Ala Lys Ala Gly Gly Ala Tyr Lys Pro Pro His
500 505 510

Ala Arg Arg Thr Gly Gly Gly Arg Ile Val Pro Gly Val Pro Pro Gly
515 520 525

Ala Ala Lys Lys Thr Ile Pro Gly Leu Val Pro Gly Met Ser Ala Asn
530 535 540

FIG. 1. Amino acid sequence of the protein.

570/762

Lys Asp Ala Asn Thr Lys Asn Arg Arg Arg Arg Ala Asn Lys Lys Ser
545 550 555 560

Ser Glu Thr Ser Pro Asp Ser Thr Pro Ala Pro Ser Ala Pro Ala Ser
565 570 575

Thr Asn Ala Pro Thr Asn Asn Lys Glu Thr Ser Pro Glu Glu Lys Lys
580 585 590

Ile Arg Ser Leu Leu Lys Lys Leu Arg Ala Ile Glu Thr Leu Lys Glu
595 600 605

Arg Gln Ala Val Gly Asp Lys Leu Glu Asp Thr Gln Val Leu Lys Ile
610 615 620

Gln Thr Glu Glu Lys Val Leu Lys Asp Leu Glu Lys Leu Gly Trp Lys
625 630 635 640

Asp Glu

<210> 239

<211> 450

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (450)

<400> 239

atg tca gcc acc aga gcc aat aaa gat att ttc aca cta ttc gac aag 48
Met Ser Ala Thr Arg Ala Asn Lys Asp Ile Phe Thr Leu Phe Asp Lys
1 5 10 15

aag ggt caa ggc gcc att gcc aag gat tcc ttg gga gat tac ctg agg 96
 Lys Gly Gln Gly Ala Ile Ala Lys Asp Ser Leu Gly Asp Tyr Leu Arg
 20 25 30

gca att ggc tac aac ccc acc aac cag glu gta cag gac alc ala aac 144
 Ala Ile Gly Tyr Asn Pro Thr Asn Gln Leu Val Gln Asp Ile Ile Asn
 35 40 45

ggg gat tgg agc ttg cga gac gcc tcc agc ttg acg ctg gac cag att 192
 Ala Asp Ser Ser Leu Arg Asp Ala Ser Ser Leu Thr Leu Asp Gln Ile
 50 55 60

aca ggc cta att gaa gtc aac gaa aag gaa ttg gat gca act acc aag 240
 Thr Gly Leu Ile Glu Val Asn Glu Lys Glu Leu Asp Ala Thr Thr Lys
 65 70 75 80

gca aag aca gaa gac ttc gtc aag gca ttc cag gtc ttc gac aag gaa 288
 Ala Lys Thr Glu Asp Phe Val Lys Ala Phe Gln Val Phe Asp Lys Glu
 85 90 95

agt acc ggc aag gta tcc gtt ggt gac tta agg tac aag cta act ggc 326
 Ser Thr Gly Lys Val Ser Val Gly Asp Leu Arg Tyr Met Leu Thr Gly
 100 105 110

ttg ggt gaa aag tta acc gac ggt gaa gta gac gag ctg ttg aag ggt 364
 Leu Gly Glu Lys Leu Thr Asp Ala Glu Val Asp Glu Leu Leu Lys Gly
 115 120 125

gtt gaa gtg gac agc aac gga gaa att gac tac aag aag ttc atc gaa 402
 Val Glu Val Asp Ser Asn Gly Glu Ile Asp Tyr Lys Lys Phe Ile Glu
 130 135 140

gat gtt ttg aga caa tga 450
 Asp Val Leu Arg Gln
 145

<210> 240

<211> 149

<212> PRT

<213> Saccharomyces cerevisiae

<430> 240

Met Ser Ala Thr Arg Ala Asn Lys Asp Ile Phe Thr Leu His Asp Lys
 1 5 10 15

Lys Gly Gln Gly Ala Ile Ala Lys Asp Ser Leu Gly Asp Tyr Leu Arg
 20 25 30

Ala Ile Gly Tyr Asn Pro Thr Asn Gln Leu Val Gln Asp Ile Ile Asn
 35 40 45

Ala Asp Ser Ser Leu Arg Asp Ala Ser Ser Leu Thr Leu Asp Gln Ile
 50 55 60

Thr Gly Leu Ile Glu Val Asn Glu Lys Glu Leu Asp Ala Thr Thr Lys
 65 70 75 80

Ala Lys Thr Glu Asp Phe Val Lys Ala Phe Gln Val Phe Asp Lys Glu
 85 90 95

Ser Thr Gly Lys Val Ser Val Gly Asp Leu Arg Tyr Met Leu Thr Gly
 100 105 110

Leu Gly Glu Lys Leu Thr Asp Ala Glu Val Asp Glu Leu Leu Lys Gly
 115 120 125

Val Glu Val Asp Ser Asn Gly Glu Ile Asp Tyr Lys Lys Phe Ile Glu
 130 135 140

Asp Val Leu Arg Gln
 145

Seq. ID: 1 (1782 bp) (1782 bp) (1782 bp)

<210> 241
 <211> 1782
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1782)

<400> 241
 atg caa cca att gtt aaa gag att att gta gat cct tac aaa aga cta 48
 Met Tyr Ser Thr Val Lys Glu Ile Ile Val Asp Pro Tyr Lys Arg Leu
 1 5 10 15
 aaa tgg ggt ttt att cca gta aag cgg cag gtg gaa gac ctg cca gat 96
 Lys Trp Gly Phe Ile Pro Val Tyr Arg Gln Val Glu Asp Leu Pro Asp
 20 25 30
 gac tta aat tca aca gaa att gtc acc atc tcc acc agt atc cag agt 144
 Asp Leu Asn Ser Thr Glu Ile Val Thr Ile Ser Asn Ser Ile Gln Ser
 35 40 45
 cat gaa acc gct gaa aat ttc atc atg acc aca agt gaa aaa gat aca 192
 His Glu Thr Ala Glu Asn Phe Ile Thr Thr Thr Ser Glu Lys Asp Gln
 50 55 60
 cta cat ttt gag acc agt agc tat agt gaa cat aaa ccc aat ctg acc 240
 Leu His Phe Glu Thr Ser Ser Tyr Ser Glu His Lys Asp Asn Val Asn
 65 70 75 80
 gtt act aga agt tat gaa tat aga gat gaa gcc gat agg cca tgg tgg 288
 Val Thr Arg Ser Tyr Glu Tyr Arg Asp Glu Ala Asp Arg Pro Trp Trp
 85 90 95
 aga ttt ttc gat gaa caa gag tat cgg atc aat gaa aag gaa aga tct 336
 Arg Phe Phe Asp Glu Glu Glu Tyr Arg Ile Asn Glu Lys Glu Arg Ser
 100 105 110
 cac aat aaa tgg tat agt tgg ttc aaa cag ggt acc tct ttc aaa gaa 384
 His Asn Lys Trp Tyr Ser Trp Phe Lys Gln Gly Thr Ser Phe Lys Glu

115	120	125	
aaa aaa tta tta att aaa ttg gat gtc ctt tta gcc ttt tat tct tgt			432
Lys Lys Leu Leu Ile Lys Leu Asp Val Leu Leu Ala Phe Tyr Ser Cys			
130	135	140	
att gct tat tgg gtg aaa tat ctg gat acg gtt aat ata aac aac gct			480
Ile Ala Tyr Trp Val Lys Tyr Leu Asp Thr Val Asn Ile Asn Asn Ala			
145	150	155	160
tac gtt tgg gga atg aag gaa gat tta ggc ttt caa ggt aat gat tgg			528
Tyr Val Ser Gly Met Lys Glu Asp Leu Gly Phe Gln Gly Asn Asp Leu			
165	170	175	
gtg cat act caa gta atg tac aca gct ggt aat att ata ttt caa ttg			576
Val His Thr Gln Val Met Tyr Thr Val Gly Asn Ile Ile Phe Gln Leu			
180	185	190	
cca ttt ttg att tac ctg aac aag ctg cca tta aac tat gta tta cca			624
Pro Phe Leu Ile Tyr Leu Asn Lys Leu Pro Leu Asp Tyr Val Leu Pro			
195	200	205	
agc ctg gac tta tgt tgg tgg ctt tta acc gtt ggt gct gca tat gtc			672
Ser Leu Asp Leu Cys Trp Ser Leu Leu Thr Val Gly Ala Ala Tyr Val			
210	215	220	
aat tct gta cca cac ttg aaa gca att agg ttt ttc att ggg gct ttt			720
Asn Ser Val Pro His Leu Lys Ala Ile Arg Phe Phe Ile Gly Ala Phe			
225	230	235	240
gaa gcg cca agt tat ttg gca tac caa tat ttg ttt ggt tcc ttt taa			768
Glu Ala Pro Ser Tyr Leu Ala Tyr Gln Tyr Leu Phe Gly Ser Phe Tyr			
245	250	255	
aca cat gat gaa atg gtg cgt cgt tct gct ttt tac tat ttg ggc cag			816
Lys His Asp Glu Met Val Arg Arg Ser Ala Phe Tyr Tyr Leu Gly Gln			
260	265	270	
tat atc ggt att cta tcc gct ggt ggg atc cag tca gcc gta tat tca			864
Tyr Ile Gly Ile Leu Ser Ala Gly Gly Ile Cln Ser Ala Val Tyr Ser			
275	280	285	

Seq. ID NO: 1

tcg tta aat ggt gta aat ggt tta gag gga tgg aga tgg aac ttt att	912
Ser Leu Asn Gly Val Asn Gly Leu Glu Gly Trp Arg Trp Asn Phe Ile	
290 295 300	
att gac gct att gtg tot gtc gta gtg ggc ctt att gga ttt tac tcc	960
Ile Asp Ala Ile Val Ser Val Val Val Gly Leu Ile Gly Phe Tyr Ser	
305 310 315 320	
ctg cca ggt gac cca tac aac tgt tac tot att ttc tta act gat gat	1008
Leu Pro Gly Asp Pro Tyr Asn Cys Tyr Ser Ile Phe Leu Thr Asp Asp	
325 330 335	
gaa att agg tgg ggg agg aaa aga tta aaa gaa aac caa aca ggt aaa	1056
Gln Ile Arg Leu Ala Arg Cys Arg Leu Lys Glu Asn Gln Thr Gly Lys	
340 345 350	
agt gat ttt gaa aca aaa gta ttc gat att aaa ctg tgg aac aca att	1104
Ser Asp Phe Glu Thr Lys Val Phe Asp Ile Lys Leu Trp Lys Thr Ile	
355 360 365	
ttc agt gat tgg aaa ata tac att tta act tta tgg aat att ttc tgt	1152
Phe Ser Asp Trp Lys Ile Tyr Ile Leu Thr Leu Trp Asn Ile Phe Cys	
370 375 380	
tgg aat gac gct aat gtt tca tot ggg gca tac cta cta tgg ttg aaa	1200
Trp Asn Asp Ser Asn Val Ser Ser Gly Ala Tyr Leu Leu Trp Leu Lys	
385 390 395 400	
tct tgg aaa aga tac tot att cct aag ctg aat cag tta tcc atg att	1248
Ser Leu Lys Arg Tyr Ser Ile Pro Lys Leu Asn Gln Leu Ser Met Ile	
405 410 415	
act ccg ggt tta ggt atg gtt tat ttg atg ctt act ggt att att gca	1296
Thr Pro Gly Leu Gly Met Val Tyr Leu Met Leu Thr Gly Ile Ile Ala	
420 425 430	
gat aaa tta cac tct cgt tgg ttt ggg att att ttc act cag gtt ttc	1344
Asp Lys Leu His Ser Arg Trp Phe Ala Ile Ile Phe Thr Gln Val Phe	
435 440 445	
aat atc att ggt aac tcc ata tta gcc gct tgg gac gtc gca gaa gga	1392
Asn Ile Ile Gly Asn Ser Ile Leu Ala Ala Trp Asp Val Ala Glu Gly	

450	455	460	
gca aaa tgg ttt gca ttt atg ctg caa tgt ttt ggt tgg gct atg gct	1440		
Ala Lys Trp Phe Ala Phe Met Leu Gln Cys Phe Gly Trp Ala Met Ala			
465	470	475	480
oct gtt tta cac tot tgg caa aac gat att tgt cgc cga gat gct caa	1488		
Pro Val Leu Tyr Ser Trp Gln Asn Asp Ile Cys Arg Arg Asp Ala Gln			
485	490	495	
act aga gct att act tta gtt aca atg aat att atg gct caa tca tot	1536		
Thr Arg Ala Ile Thr Leu Val Thr Met Asn Ile Met Ala Gln Ser Ser			
500	505	510	
acc gca tgg ata agt gtt ctg gtt tgg aaa aca gaa gaa gct ccc agg	1584		
Thr Ala Trp Ile Ser Val Leu Val Trp Lys Thr Glu Glu Ala Pro Arg			
515	520	525	
tat ata aag ggg ttt act ttc act gca tgt tot gct ttt tgt ctg tcc	1632		
Tyr Leu Lys Gly Phe Thr Phe Thr Ala Cys Ser Ala Phe Cys Leu Ser			
530	535	540	
act tgg act tat gtt gta ctc tac ttc tat aaa cgt gat gaa agg aac	1680		
Ile Trp Thr Phe Val Val Leu Tyr Phe Tyr Lys Arg Asp Glu Arg Asn			
545	550	555	560
aat gcc aag aag aac ggt att gtg ctt tat aac tot aaa cat ggt gtc	1728		
Asn Ala Lys Lys Asn Gly Ile Val Leu Tyr Asn Ser Lys His Gly Val			
565	570	575	
gaa aag cca aag tca aaa gac gtt gaa acc tta tca gta tot gat gaa	1776		
Glu Lys Pro Thr Ser Lys Asp Val Glu Thr Leu Ser Val Ser Asp Glu			
580	585	590	
aaa taa	1782		
Lys			

<210> 342

<211> 593

<213> PRT

<213> Saccharomyces cerevisiae

<400> 243

Met Tyr Ser Ile Val Lys Glu Ile Ile Val Asp Pro Tyr Lys Arg Leu

1 5 10 15

Lys Trp Gly Phe Ile Pro Val Lys Arg Gln Val Glu Asp Leu Pro Asp

20 25 30

Asp Leu Asn Ser Thr Glu Ile Val Thr Ile Ser Asn Ser Ile Glu Ser

35 40 45

His Glu Thr Ala Glu Asn Phe Ile Thr Thr Thr Ser Glu Lys Asp Glu

50 55 60

Leu His Phe Glu Thr Ser Ser Tyr Ser Glu His Lys Asp Asn Val Asn

65 70 75 80

Val Thr Arg Ser Tyr Glu Tyr Arg Asp Glu Ala Asp Arg Pro Trp Trp

85 90 95

Arg Phe Phe Asp Glu Gln Glu Tyr Arg Ile Asn Glu Lys Glu Arg Ser

100 105 110

His Asn Lys Trp Tyr Ser Trp Phe Lys Gln Gly Thr Ser Phe Lys Glu

115 120 125

Lys Lys Leu Leu Ile Lys Leu Asp Val Leu Leu Ala Phe Tyr Ser Cys

130 135 140

Ile Ala Tyr Trp Val Lys Tyr Leu Asp Thr Val Asn Ile Asn Asn Ala

145 150 155 160

Tyr Val Ser Gly Met Lys Glu Asp Leu Gly Phe Gln Gly Asn Asp Leu
165 170 175

Val His Thr Gln Val Met Tyr Thr Val Gly Asn Ile Ile Phe Gln Leu
180 185 190

Pro Phe Leu Ile Tyr Leu Asn Lys Leu Pro Leu Asn Tyr Val Leu Pro
195 200 205

Ser Leu Asp Leu Cys Trp Ser Leu Leu Thr Val Gly Ala Ala Tyr Val
210 215 220

Asn Ser Val Pro His Leu Lys Ala Ile Arg Phe Phe Ile Gly Ala Phe
225 230 235 240

Glu Ala Pro Ser Tyr Leu Ala Tyr Gln Tyr Leu Phe Gly Ser Phe Tyr
245 250 255

Lys His Asp Glu Met Val Arg Arg Ser Ala Phe Tyr Tyr Leu Gly Gln
260 265 270

Tyr Ile Gly Ile Leu Ser Ala Gly Gly Ile Gln Ser Ala Val Tyr Ser
275 280 285

Ser Leu Asn Gly Val Asn Gly Leu Glu Gly Trp Arg Trp Asn Phe Ile
290 295 300

Ile Asp Ala Ile Val Ser Val Val Val Gly Leu Ile Gly Phe Tyr Ser
305 310 315 320

Leu Pro Gly Asp Pro Tyr Asn Cys Tyr Ser Ile Phe Leu Thr Asp Asp
 325 330 335

Glu Ile Arg Leu Ala Arg Lys Arg Leu Lys Glu Asn Gln Thr Gly Lys
 340 345 350

Ser Asp Phe Glu Thr Lys Val Phe Asp Ile Lys Leu Trp Lys Thr Ile
 355 360 365

Phe Ser Asp Trp Lys Ile Tyr Ile Leu Thr Leu Trp Asn Ile Phe Cys
 370 375 380

Trp Asn Asp Ser Asn Val Ser Ser Gly Ala Tyr Leu Leu Trp Leu Lys
 385 390 395 400

Ser Leu Lys Arg Tyr Ser Ile Pro Lys Leu Asn Gln Leu Ser Met Ile
 405 410 415

Thr Pro Gly Leu Gly Met Val Tyr Leu Met Leu Thr Gly Ile Ile Ala
 420 425 430

Asp Lys Leu His Ser Arg Trp Phe Ala Ile Ile Phe Thr Gln Val Phe
 435 440 445

Asn Ile Ile Gly Asn Ser Ile Leu Ala Ala Trp Asp Val Ala Glu Gly
 450 455 460

Ala Lys Trp Phe Ala Phe Met Leu Gln Cys Phe Gly Trp Ala Met Ala
 465 470 475 480

Pro Val Leu Tyr Ser Trp Gln Asn Asp Ile Cys Arg Arg Asp Ala Gln
 485 490 495

Thr Arg Ala Ile Thr Leu Val Thr Met Asn Ile Met Ala Glr Ser Ser
 500 505 510

Thr Ala Trp Ile Ser Val Leu Val Trp Lys Thr Glu Glu Ala Pro Arg
 515 520 525

Tyr Leu Lys Gly Phe Thr Phe Thr Ala Cys Ser Ala Phe Cys Leu Ser
 530 535 540

Ile Trp Thr Phe Val Val Leu Tyr Phe Tyr Lys Arg Asp Glu Arg Asn
 545 550 555 560

Asn Ala Lys Lys Asn Gly Ile Val Leu Tyr Asn Ser Lys His Gly Val
 565 570 575

Glu Lys Pro Thr Ser Lys Asp Val Glu Thr Leu Ser Val Ser Asp Glu
 580 585 590

Lys

<210> 243

<211> 1041

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1041)

<400> 243

atg aag gag tgg cac att tgc tct tat ttg cta agc att gca ccc cta

Met Lys Ala Ser His Ile Cys Ser Tyr Leu Leu Ser Ile Ala Pro Leu
1 5 10 15

gtg gtg tcc cat gga gta cac cat aat cga gat cat ggc cac gag gca 96
Val Val Ser His Gly Val His His Asn Arg Asp His Gly His Glu Ala
20 25 30

aac cat gag tcc aag caa agt ttc ttg att tlg aay caa gaa tcc att 144
Asn His Glu Ser Lys Gln Ser Phe Leu Ile Leu Lys Gln Gln Ser Ile
35 40 45

ttt tac tat ata gtt tgc ttt ctg cag aac caa ctc ttt gtc ctg gga 102
Phe Tyr Ser Leu Val Cys Phe Leu Glu Asn His Leu Phe Val Leu Gly
50 55 60

ccc cgt tac aat gag att gtg gct atc cta atc ata caa cll atg cgg 240
 Pro Arg Tyr Asn Ala Ile Val Ala Ile Leu Ile Ile Gln Leu Met Pro
 65 70 75 80

tgt ctt ttc gta ctg ttt gtl ctt gaa ctg cgc aag aac gat cgt gcc 238
Cys Leu Phe Val Leu Phe Val Pro Gly Asu Arg Lys Asn Asp Arg Ala
55 90 95

agg tgg aca ctg tcc tta cta gtt taa ttt tct cta gga aca ctc ctg 336
Ser Leu Thr Leu Ser Leu Val Ser Phe Ser Leu Gly Thr Leu Leu
100 105 110

ggg gat att tta tta cac gtg ata cct gaa agt ctc agc ggc gta act 304
Gly Asp Ile Leu Leu His Val Ile Pro Gln Ser Leu Ser Gly Val Thr
115 120 125

gat gtd aca arg gtt gga gga gcc ata ttt cgg ggg ttt ata agc ttc 402
asp val thr met val gly gly ala ile phe leu gly phe ile ser phe
130 135 140

ttg act ctg gat aaa aag atg cgt att ctg tca ggg aag tcc aac gat 480
Leu Thr Leu Asp Lys Thr Met Arg Ile Leu Ser Gly Thr Ser Asn Asp
145 150 155 160

gag ggc agc ata caa tct cat tcc cat agt cat act cca caa caa act 520
 Asp Gly Ser Ile His Ser His Ser His Ser His Thr Pro Gln Gln Thr
 165 170 175

gca gag aag aau gag ggc tta aac atg tct gag tat ctg aat gtc ata	576
Ala Gln Lys Lys Ala Gly Phe Asn Met Ser Ala Tyr Leu Asn Val Ile	
180 185 190	
taa ggc att gct cat cac atc acg gah ggc ata gag ctg gct acg tca	624
Ser Gly Ile Ala His His Ile Thr Asp Gly Ile Ala Leu Ala Thr Ser	
195 200 205	
ttc tat agt tcc aca caa gtt ggc ata atg acc agc ata gct gtc act	672
Phe Tyr Ser Ser Thr Gln Val Gly Ile Met Thr Ser Ile Ala Val Thr	
210 215 220	
ttc cat gag aac cct cat gag cta ggt gac ttc gcc att ctg ctt tcc	720
Phe His Glu Ile Pro Phe Glu Leu Gly Asp Phe Ala Ile Leu Leu Ser	
225 230 235 240	
agt ggg ttt acg ctg cca caa ggc ata aga gcc caa gag gtg aca gac	768
Ser Gly Phe Thr Phe Pro Gln Ala Ile Arg Ala Gln Ala Val Thr Ala	
245 250 255	
ttc gcc gcc gtc gtt gga acg tcc atc ggc tgc tgg atg aac gaa atc	816
Phe Gly Ala Val Val Gly Thr Ser Phe Gly Cys Trp Met Asn Glu Ile	
260 265 270	
ggg aac aac agc cat aaa gca acg tct tca tcc gag aac gca tct gaa	864
Gly Asn Asn Ser His Lys Ala Thr Ser Ser Ser Ala Asn Ala Ser Glu	
275 280 285	
ctt atg ctg cag ttc acg gag ggc ggc ctg ata tac ata gcc act act	912
Leu Met Leu Pro Phe Thr Ala Gly Gly Leu Ile Tyr Ile Ala Thr Thr	
290 295 300	
agg gtt gla cag cag atc tta cat agc tcc gca ccc gat agc aag ctt	960
Ser Val Val Pro Gln Ile Leu His Ser Ser Ala Pro Asp Ser Lys Leu	
305 310 315 320	
cga gag ttt aag aag tgg gcc ttg cag cta gtc ttc att ttt gta gga	1008
Arg Glu Phe Lys Lys Trp Ala Leu Gln Asn Val Phe Ile Phe Val Gly	
325 330 335	
ttt gcc gtt atg gag ctg atg gat gag cat tga	1044

1" 1" 1" 1" 1" 1"

Phe Ala Val Met Ala Leu Met Asp Glu His

340

345

<210> 244

<211> 346

<212> FRT

<213> Saccharomyces cerevisiae

<400> 244

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15

Val Val Ser His Gly Val His His Asn Arg Asp His Gly His Glu Ala

20

25

30

Asn His Glu Ser Lys Gln Ser Phe Leu Ile Leu Lys Gln Glu Ser Ile

35

40

45

Phe Tyr Ser Leu Val Cys Phe Leu Gln Asn His Leu Phe Val Leu Gly

50

55

60

Pro Arg Tyr Asn Ala Ile Val Ala Ile Leu Ile Ile Gln Leu Met Pro

65

70

75

80

Cys Leu Phe Val Leu Phe Val Pro Gly Leu Arg Lys Asn Asp Arg Ala

85

90

95

Ser Leu Thr Leu Ser Leu Leu Val Ser Phe Ser Leu Gly Thr Leu Leu

100

105

110

Gly Asp Ile Leu Leu His Val Ile Pro Glu Ser Leu Ser Gly Val Thr

115

120

125

Asp Val Thr Met Val Gly Gly Ala Ile Phe Leu Gly Phe Ile Ser Phe
120 135 140

Leu Thr Leu Asp Lys Thr Met Arg Ile Leu Ser Gly Thr Ser Asn Asp
145 150 155 160

Asp Gly Ser Ile His Ser His Ser His Ser His Thr Pro Gln Gln Thr
165 170 175

Ala Glu Lys Lys Ala Gly Phe Asn Met Ser Ala Tyr Leu Asn Val Ile
180 185 190

Ser Gly Ile Ala His His Ile Thr Asp Gly Ile Ala Leu Ala Thr Ser
195 200 205

Phe Tyr Ser Ser Thr Gln Val Gly Ala Met Thr Ser Ile Ala Val Thr
210 215 220

Phe His Glu Ile Pro His Glu Leu Gly Asp Phe Ala Ile Leu Leu Ser
225 230 235 240

Ser Gly Phe Thr Phe Pro Gln Ala Ile Arg Ala Gln Ala Val Thr Ala
245 250 255

Phe Gly Ala Val Val Gly Thr Ser Ile Gly Cys Trp Met Asn Glu Ile
260 265 270

Gly Asn Asn Ser His Lys Ala Thr Ser Ser Ser Ala Asn Ala Ser Glu
275 280 285

Leu Met Leu Pro Phe Thr Ala Gly Gly Leu Ile Tyr Ile Ala Thr Thr

230

295

300

Ser Val Val Pro Gln Ile Leu His Ser Ala Pro Asp Ser Lys Leu
305 310 315 320

Arg Glu Phe Lys Lys Trp Ala Leu Gln Leu Val Phe Ile Phe Val Gly
325 330 335

Phe Ala Val Met Ala Leu Met Asp Glu His
340 345

<210> 245

<211> 429

<212> DNA

<213> *Saccharomyces cerevisiae*

<210>

<221> CDS

<222> (1) .. (459)

<400> 245

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Met Asp Met Val Ser Pro Val Leu Asn Leu Gln Ser Ser Ile Leu Gly
1 5 10 15

gag ctc gta ggc att att gga aaa gtg ttc ttt ctc tta ata gaa gag 56
Glu Leu Val Gly Ile Ile Gly Lys Val Phe Phe Leu Leu Ile Glu Glu
20 25 30

att aag tac cag ata atc aca ccc aag att att gtg gat gcc cag ata 144
Ile Lys Tyr Pro Ile Ile Thr Pro Lys Ile Ile Val Asp Ala Gln Ile
35 40 45

tct tct tgg tca tly ttt ttt ttc gct tca atc tgt aat ctc tct gca 192
Ser Ser Trp Ser Leu Phe Phe Phe Ala Ser Ile Cys Asn Leu Ser Ala
50 55 60

Protein Data Bank

aaa ttt cgg gag cca ata gtg asa aca tgg tca ata ata agt ttg atg 240
 Lys Phe Arg Glu Pro Ile Val Thr Thr Ser Ser Ile Ile Ser Leu Met
 65 70 75 80

gaa tgg gaa aaa gat ctt aaa aat gta aat gag tat ttc caa ata atg 288
 Glu Ser Glu Lys Asp Leu Lys Asn Val Asn Glu Tyr Phe Gln Ile Met
 85 90 95

gcc aaa atg ctg ttt ata ttg gaa aat aaa ata gtt gtt tgg ctg ttc 336
 Ala Lys Met Leu Phe Ile Leu Glu Asn Lys Ile Val Val Ser Leu Phe
 100 105 110

gta gta ttt aac aat tcc gtt ctt aac att gta aag tct gag cca tat 384
 Val Val Phe Asn Ile Ser Val Leu Ile Ile Val Lys Ser Glu Pro Tyr
 115 120 125

cca cat gga aaa ggg ctt ttt aaa cct agt tcc tcc ata ttt tag 428
 Ser Tyr Gly Lys Val Leu Phe Lys Pro Ser Ser Ser Ile Phe
 130 135 140

<210> 246

<211> 142

<212> PRT

<213> Saccharomyces cerevisiae

<400> 246

Met Asp Met Val Ser Pro Val Leu Asn Leu Gln Ser Ser Ile Leu Gly
 1 5 10 15

Glu Leu Val Gly Ile Ile Gly Lys Val Phe Phe Leu Leu Ile Glu Glu
 20 25 30

Ile Lys Tyr Pro Ile Ile Thr Pro Lys Ile Ile Val Asp Ala Gln Ile
 35 40 45

Ser Ser Trp Ser Leu Phe Phe Phe Ala Ser Ile Cys Asn Leu Ser Ala
 50 55 60

Lys Phe Arg Glu Pro Ile Val Thr Thr Ser Ser His Ile Ser Leu Met
 65 70 75 80

Glu Ser Glu Lys Asp Leu Lys Asn Val Asn Glu Tyr Phe Gln Ile Met
 85 90 95

Ala Lys Met Leu Phe Ile Leu Glu Asn Lys Ile Val Val Ser Leu Phe
 100 105 110

Val Val Phe Asn Ile Ser Val Leu Ile Ile Val Lys Ser Glu Pro Tyr
 115 120 125

Ser Tyr Gly Lys Val Leu Phe Lys Pro Ser Ser Ser Ile Phe
 130 135 140

<210> 247

<211> 1167

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(1167)

<400> 247

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 Val Lys His Leu His Arg Phe Phe Ser Ser Asp Ala Ser Gly Gly Ile
 1 5 10 15

att ctt atc att gcc gct atc ctg ggc atg att atg gcc aac agc ggc 96
 Ile Leu Ile Ile Ala Ala Phe Leu Ala Met Ile Met Ala Asn Ser Gly
 20 25 30

gca acc agt gga tgg tat cac gac ttt ctg gag aag cag ggt cag ctc 144

Protein Data Bank

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Ala Thr Ser Gly Trp Tyr His Asp Phe Leu Glu Thr Pro Val Gln Leu	
35 40 45	
ccg gtt ggt tca ctc gaa atc aac aaa uuc atg ctg tta tgg ata aat	192
Arg Val Gly Ser Leu Glu Ile Asn Lys Asn Met Leu Leu Trp Ile Asn	
50 55 60	
gac gag ctg atg gag gta ttt ttc ctg tta gtc ggt ctg guu gtt aaa	240
Asp Ala Leu Met Ala Val Phe Phe Leu Leu Val Gly Leu Glu Val Lys	
65 70 75 80	
cgt gaa ctg atg caa gga tgg cta gcc agc tta cgc cag gcc gca ttt	288
Arg Glu Leu Met Gln Gly Ser Leu Ala Ser Leu Arg Glu Ala Ala Phe	
85 90 95	
cca gtt atc gcc gat aat ggt ggg atg att gtg ccg gca tta ctc tat	336
Pro Val Ile Ala Ala Ile Gly Gly Met Ile Val Pro Ala Leu Leu Tyr	
100 105 110	
ctg gct ttt aac tat gcc gat ccg att aac cgc gaa ggg tgg gcc atc	384
Leu Ala Phe Asn Tyr Ala Asp Pro Ile Thr Arg Glu Gly Trp Ala Ile	
115 120 125	
ccg gag gat aat gac att gat ttt gca ctt ggt gta ctg gag ctg ttg	432
Pro Ala Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Leu Ala Leu Leu	
130 135 140	
gga agt cgt gtt ccg tta gag ctg aag atc ttt ttg atg gat ctg gat	480
Gly Ser Arg Val Pro Leu Ala Leu Lys Ile Phe Asn Met Ala Leu Ala	
145 150 155 160	
att atc gac gat ctt ggg gcc atc att atc atc gca ttg ttc tac act	528
Ile Ile Asp Asp Leu Gly Ala Ile Ile Ile Ile Ala Leu Phe Tyr Thr	
165 170 175	
aat gac tta tgg atg gcc ttt ctt ggc gtc gag gat gta gca aat gag	576
Asn Asp Leu Ser Met Ala Ser Leu Gly Val Ala Ala Val Ala Ile Ala	
180 185 190	
gla ctc gag gta ttg aat ctg tgt ggt gca cgc cgc acg ggc gtc ttc	624
Val Leu Ala Val Leu Asn Leu Cys Gly Ala Arg Arg Thr Gly Val Tyr	
195 200 205	

att ctt gtt ggc gtg gtg ttg tgg act ggc gtg ttg aaa tgg ggg gtt	672
Ile Leu Val Gly Val Val Leu Trp Thr Ala Val Leu Lys Ser Gly Val	
210 215 220	
cac gca act ctg ggc ggg gta att gtc ggc ttc ttt att cct ttg aaa	720
His Ala Thr Leu Ala Gly Val Ile Val Gly Phe Phe Ile Pro Leu Lys	
225 230 235 240	
gag aag cat ggg cgt tct cca ggc aag cga ctg gag cat gtg ttg cac	768
Glu Lys His Gly Arg Ser Pro Ala Lys Arg Leu Glu His Val Leu His	
245 250 255	
cag tgg gtg ggc cac ctg att ttg ccg cgg ttt gca ttt gct aat gct	816
Pro Trp Val Ala Tyr Leu Ile Leu Pro Leu Phe Ala Phe Ala Asn Ala	
260 265 270	
ggc gtt cca ctg cca ggc gtc acg ctg gat ggc ttg acc tcc att cag	864
Gly Val Ser Leu Gln Gly Val Thr Leu Asp Gly Leu Thr Ser Ile Leu	
275 280 285	
cca ttg ggc atc atc gct ggc ttg ctg att ggc aac ccg ctg ggg att	912
Pro Leu Gly Ile Ile Ala Gly Leu Leu Ile Gly Lys Pro Leu Gly Ile	
290 295 300	
agt ctg ttc tgc tgg ctg ggc ctg cgt ttg aaa ctg ggc cat ctg cct	960
Ser Leu Phe Cys Trp Leu Ala Leu Arg Leu Lys Leu Ala His Leu Pro	
305 310 315 320	
gag gga aag cct tat cag cca att atg gtg gtg ggg atc ctg tgc ggt	1008
Glu Gly Thr Thr Tyr Gln Gln Ile Met Val Val Gly Ile Leu Cys Gly	
325 330 335	
atc ggt ttt acf atg tct atc ttt att gcc agc ctg gcc ttt ggt agc	1056
Ile Gly Phe Thr Met Ser Ile Phe Ile Ala Ser Leu Ala Phe Gly Ser	
340 345 350	
gta gat cca gaa ctg att aac tgg ggc aaa ctc ggt atc ctg gtc ggt	1104
Val Asp Pro Glu Leu Ile Asn Trp Ala Lys Leu Gly Ile Leu Val Gly	
355 360 365	
tct atc tct tgg ggc gta att gga tac agc tgg tta cgc gtl cgt ttg	1152

Seq. ID: 1 (2,200 nt) (2,200 nt)

Ser Ile Ser Ser Ala Val Ile Gly Tyr Ser Trp Leu Arg Val Arg Leu
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cgt cca tca gtt tga

1157

Arg Pro Ser Val

385

<210> 248

<211> 388

<212> PRT

<213> Escherichia coli

<400> 248

Val Lys His Leu His Arg Phe Phe Ser Ser Asp Ala Ser Gly Gly Ile
 1 5 10 15

Ile Leu Ile Ile Ala Ala Ile Leu Ala Met Ile Met Ala Asn Ser Gly
 20 25 30

Ala Thr Ser Gly Trp Tyr His Asp Phe Leu Glu Thr Pro Val Glu Leu
 35 40 45

Arg Val Gly Ser Leu Glu Ile Asn Lys Asn Met Leu Leu Trp Ile Asp
 50 55 60

Asp Ala Leu Met Ala Val Phe Phe Leu Leu Val Gly Leu Glu Val Lys
 65 70 75 80

Arg Glu Leu Met Gln Gly Ser Leu Ala Ser Leu Arg Gln Ala Ala Phe
 85 90 95

Pro Val Ile Ala Ala Ile Gly Gly Met Ile Val Pro Ala Leu Leu Tyr
 100 105 110

Leu Ala Phe Asn Tyr Ala Asp Pro Ile Thr Arg Glu Gly Trp Ala Ile
115 120 125

Pro Ala Ala Thr Asp Ile Ala Phe Ala Leu Gly Val Leu Ala Leu Leu
130 135 140

Gly Ser Arg Val Pro Leu Ala Leu Lys Ile Phe Leu Met Ala Leu Ala
145 150 155 160

Ile Ile Asp Asp Leu Gly Ala Ile Ile Ile Ile Ala Leu Phe Tyr Thr
165 170 175

Asn Asn Leu Ser Met Ala Ser Leu Gly Val Ala Ala Val Ala Ile Ala
180 185 190

Val Leu Ala Val Leu Asn Leu Cys Gly Ala Arg Arg Thr Gly Val Tyr
195 200 205

Ile Leu Val Gly Val Val Leu Trp Thr Ala Val Leu Lys Ser Gly Val
210 215 220

His Ala Thr Leu Ala Gly Val Ile Val Gly Phe Phe Ile Pro Leu Lys
225 230 235 240

Glu Lys His Gly Arg Ser Pro Ala Lys Arg Leu Glu His Val Leu His
245 250 255

Pro Trp Val Ala Tyr Leu Ile Leu Pro Leu Phe Ala Phe Ala Asn Ala
260 265 270

Gly Val Ser Leu Gln Gly Val Thr Leu Asp Gly Leu Thr Ser Ile Leu

275 280 285

Pro Leu Gly Ile Ile Ala Gly Leu Leu Ala Gly Lys Pro Leu Gly Ile
290 295 300

Ser Leu Phe Cys Trp Leu Ala Leu Arg Leu Lys Leu Ala His Leu Pro
305 310 315 320

Glu Gly Thr Thr Tyr Gln Gln Ile Met Val Val Gly Ile Leu Cys Gly
325 330 335

Ile Gly Phe Thr Met Ser Ile Phe Ile Ala Ser Leu Ala Phe Gly Ser
340 345 350

Val Asp Pro Glu Leu Ile Asn Trp Ala Lys Leu Gly Ile Leu Val Gly
355 360 365

Ser Ile Ser Ser Ala Val Ile Gly Tyr Ser Trp Leu Arg Val Arg Leu
370 375 380

Arg Pro Ser Val
385

<210> 249
<211> 1011
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1011)

<400> 249

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ggc att tac gtc gtt gtt tta gtt ttg ctg gcg att att att ttc cag	96
Gly Ile Tyr Val val leu leu Val Leu Leu Ala Ile Ile Ile Phe Gln	
20 25 30	
gac cca aca ttt tta agt ctg ttg aac tta agt aat att ctc acc cag	144
Asp Pro Thr Phe Leu Ser Leu Leu Asn Leu Ser Asn Ile Leu Thr Gln	
35 40 45	
tca tgg gtg cgt att att atc gcg ctc ggt gtg gca ggg tta att gtc	192
Ser Ser Val Arg Ile Ile Ile Ala Leu Gly Val Ala Gly Leu Ile Val	
50 55 60	
acc cag ggg acc gat ctt tct gct ggt cgt cag gta ggg ctg gcg gca	240
Thr Gln Gly Thr Asp Leu Ser Ala Gly Arg Gln Val Gly Leu Ala Ala	
65 70 75 80	
gtg gtg gct gcg aca tta ttg cag tcc atg gat aac gcc aac aac gtg	288
Val Val Ala Ala Thr Leu Leu Gln Ser Met Asp Asn Ala Asn Lys Val	
85 90 95	
ttc cag gac ctg gcg acg atg cag att gcg ctg gtt att ctg att gtc	336
Phe Pro Gln Met Ala Thr Met Pro Ile Ala Leu Val Ile Leu Ile Val	
100 105 110	
tgt gcc att ggt gcg gtg atc ggt ttg atc aac ggt ctg att atc gct	384
Cys Ala Ile Gly Ala Val Ile Gly Leu Ile Asn Gly Leu Ile Ile Ala	
115 120 125	
tat ctc aac gtg acg cag ttc att acc acg ctc ggc acg atg atc atc	432
Tyr Leu Asn Val Thr Pro Phe Ile Thr Thr Leu Gly Thr Met Ile Ile	
130 135 140	
gtc tac gcc atc aac tgg ctc tat tac gac ttt gtc ggg gcg tgg cca	480
Val Tyr Gly Ile Asn Ser Leu Tyr Tyr Asp Phe Val Gly Ala Ser Pro	
145 150 155 160	
att tct ggt ttt gcc agt ggc ttc tct acc ttt gct cag gcc ttt gtc	528
Ile Ser Gly Phe Asp Ser Gly Phe Ser Thr Phe Ala Gln Gly Phe Val	

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165	170	175	
gag ctg ggg agt ttc cgt ctc tct tac atc acc ttc tac gag ttg att			576
Ala Leu Gly Ser Phe Arg Leu Ser Tyr Ile Thr Phe Tyr Ala Leu Ile			
180	185	190	
gag glg gag ttc gtc tgg gtg ttg tgg acc aaa acc cgc ttc ggt aag			624
Ala Val Ala Phe Val Trp Val Leu Trp Asn Lys Thr Arg Phe Gly Lys			
195	200	205	
aac att ttt gcc att ggc ggt aac cgg gaa gag gca aaa gta tct ggt			672
Asn Ile Phe Ala Ile Gly Gly Asn Pro Glu Ala Ala Lys Val Ser Gly			
210	215	220	
gtc aac gtc ggc ctg aac cly cly atg atc tac gag ttg tct gcc gtg			720
Val Asn Val Gly Leu Asn Leu Leu Met Ile Tyr Ala Leu Ser Gly Val			
225	230	235	240
tcc tac gcc ttt ggc ggg atg tta gaa gcc gga cgt atc gcc tct gcc			768
Phe Tyr Ala Phe Gly Gly Met Leu Glu Ala Gly Arg Ile Gly Ser Ala			
245	250	255	
acc aac aac ctc gcc ttt atg tat gag ctg gat gct atc gag gag tgc			816
Thr Asn Asn Leu Gly Phe Met Tyr Glu Leu Asp Ala Ile Ala Ala Cys			
260	265	270	
ctg gta ggc ggt gta tcc ttc agc gcc ggt gtc gag acg ctg att gcc			864
Val Val Gly Gly Val Ser Phe Ser Gly Gly Val Gly Thr Val Ile Gly			
275	280	285	
gtg gtg acc ggg gta gll att ttt acc gtc atc aac tat gcc ctg acc			912
Val Val Thr Gly Val Ile Ile Phe Thr Val Ala Asn Tyr Gly Leu Thr			
290	295	300	
tat acc gcc gta aac ccu tac tgg cag tac atc atc aaa ggg gag att			960
Tyr Ile Gly Val Asn Pro Tyr Trp Gln Tyr Ile Ile Lys Gly Ala Ile			
305	310	315	320
att atc ttc gcc gta gag ctg gat tca ctg aaa tac gag cgt aag aaa			1008
Ile Ile Phe Ala Val Ala Leu Asp Ser Leu Lys Tyr Ala Arg Lys Lys			
325	330	335	

tga 1311

<210> 250

<211> 336

<212> FRT

<213> Escherichia coli

<400> 250

Met Ser Ala Leu Asn Lys Lys Ser Phe Leu Thr Tyr Leu Lys Glu Gly
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Gly Ile Tyr Val Val Leu Leu Val Leu Leu Ala Ile Ile Phe Gln
20 25 30

Asp Pro Thr Phe Leu Ser Leu Leu Asn Leu Ser Asn Ile Leu Thr Gln
35 40 45

Ser Ser Val Arg Ile Ile Ile Ala Leu Gly Val Ala Gly Leu Ile Val
50 55 60

Thr Gln Gly Thr Asp Leu Ser Ala Gly Arg Gln Val Gly Leu Ala Ala
65 70 75 80

Val Val Ala Ala Thr Leu Leu Gln Ser Met Asp Asn Ala Asn Lys Val
85 90 95

Phe Pro Glu Met Ala Thr Met Pro Ile Ala Leu Val Ile Leu Ile Val
100 105 110

Cys Ala Ile Gly Ala Val Ile Gly Leu Ile Asn Gly Leu Ile Ile Ala
115 120 125

Tyr Leu Asn Val Thr Pro Phe Ile Thr Thr Leu Gly Thr Met Ile Ile
130 135 140

Val Tyr Gly Ile Asn Ser Leu Tyr Tyr Asp Phe Val Gly Ala Ser Pro
145 150 155 160

Ile Ser Gly Phe Asp Ser Gly Phe Ser Thr Phe Ala Gln Gly Phe Val
165 170 175

Ala Leu Gly Ser Phe Arg Leu Ser Tyr Ile Thr Phe Tyr Ala Leu Ile
180 185 190

Ala Val Ala Phe Val Trp Val Leu Trp Asn Lys Thr Arg Phe Gly Lys
195 200 205

Asn Ile Phe Ala Ile Gly Gly Asn Pro Glu Ala Ala Lys Val Ser Gly
210 215 220

Val Asn Val Gly Leu Asn Leu Leu Met Ile Tyr Ala Leu Ser Gly Val
225 230 235 240

Phe Tyr Ala Phe Gly Gly Met Leu Glu Ala Gly Arg Ile Gly Ser Ala
245 250 255

Thr Asn Asn Leu Gly Phe Met Tyr Glu Leu Asp Ala Ile Ala Ala Cys
260 265 270

Val Val Gly Gly Val Ser Phe Ser Gly Gly Val Gly Thr Val Ile Gly
275 280 285

Val Val Thr Gly Val Ile Ile Phe Thr Val Ile Asn Tyr Gly Leu Thr
290 295 300

Tyr Ile Gly Val Asn Pro Tyr Trp Gln Tyr Ule Ile Lys Gly Ala Ile
 305 310 315 320

Ile Ile Phe Ala Val Ala Leu Arg Ser Leu Lys Tyr Ala Arg Lys Lys
 325 330 335

<210> 251
 <211> 1290
 <212> DNA
 <213> Escherichia coli

<220>
 <221> CDS
 <222> (1)..(1293)

<400> 251
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 1 5 10 15

gcc tgg cgc aag aca gac acc atg tgg atg ctg ggc att tac ggc acg 95
 Ala Trp Arg Lys Thr Asp Thr Met Trp Met Leu Gly Leu Tyr Gly Thr
 20 25 30

gca atc ggc ggc ggc ctg ctg ttc ctg cca atc aac gac ggt gtt ggc 144
 Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
 35 40 45

ggt atg atc ccg ctg atc atc atg gct atc ctt ggc ttc ccg atg acg 192
 Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
 50 55 60

llt ttt gct caa cgc ggc ctg act cgc ttc gta ctg tct ggt aaa aac 240
 Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Iys Asn
 65 70 75 80

cgc ggc gaa gac atc acc gag gtt gta gaa gaa cac ttt ggt att ggc 288

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Pro Gly Glu Asp Ile Thr Glu Val Val Glu Glu His Phe Gly Ile Gly	
85 90 95	
gca ggt aaa ctg att acc ctg ctc tac ttc ttc gct atc tac cag atc	336
Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile	
100 105 110	
ctg ctg gtt tat acc ctg gca atc acc aat acc gtt gaa agc ttc atg	384
Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Met	
115 120 125	
tct cac cag ctg ggt atg acg cca cag cag cgt gag att ctg tgg ctg	432
Ser His Gln Leu Gly Met Thr Pro Pro Pro Arg Ala Ile Leu Ser Leu	
130 135 140	
atc ctg atc gtg ggt atg atg acc atc gtt cgc ttc ggt gag cag atg	480
Ile Leu Ile Val Gly Met Met Thr Ile Val Arg Phe Gly Glu Gln Met	
145 150 155 160	
atc gtt aac gag atg agt att ctg gta ttc cag ttt gtt ggc gta ctg	528
Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Gly Val Leu	
165 170 175	
atg ctg ctg gct ctg tac ctg atc cag cag tgg aac ggc gct gca ctg	576
Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu	
180 185 190	
gaa acg ctg tat ctg gac act gca tct gca acc gga aac ggt ctg tgg	624
Glu Thr Leu Ser Leu Asp Thr Ala Ser Ala Thr Gly Asn Gly Leu Trp	
195 200 205	
atg acc ctg tgg ctg gca att cag gta atg gtg ttc tgg ttc aac cgc	672
Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His	
210 215 220	
tct cag atc atc tct tct ttc gca gtt gag aag cgt gaa gag tac ggc	720
Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly	
225 230 235 240	
gct atg gca gaa cag aaa tgc tgc aag atc ctg gca ttc gca cac atc	768
Asp Met Ala Glu Gln Lys Cys Ser Lys Ile Leu Ala Phe Ala His Ile	
245 250 255	

atg atg gtg ctg acc gta atg ttc ttc gtc lle agc tgt gta ctg agc	876
Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser	
260 265 270	
ctg act ccg gca gac ctg gct gcg gct aaa gag cag aac acc tgg aat	864
Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile	
275 280 285	
ctg tct tac ctg gct aac cac ttt aac gca ccg gtt atc gcg tgg atg	912
Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Val Ile Ala Trp Met	
290 295 300	
gct cag att atc gcg att atc gct atc acc aaa tcc ttc ctg ggt cag	960
Ala Pro Ile Ile Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His	
305 310 315 320	
tac ctg ggc gca cgt gaa ggc atc aac ggt atg gtg att aaa tct ctg	1008
Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu	
325 330 335	
cgt ggt aaa ggt aag tct atc gca atc aac aag ctg aac cgt atc act	1056
Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Arg Ile Thr	
340 345 350	
gcg ctg ttc atg ctg gta ccg acc tgg att gtt gcc acc ctg aac ccg	1104
Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro	
355 360 365	
agc atc ctg ggt atg att gaa acc ctg ggc ggt cca atc atc gcg atg	1152
Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met	
370 375 380	
atc ctg ttc ctg atg ccg atg tac gca att cag aaa gta ccg gca atg	1200
Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met	
385 390 395 400	
cgt aag tuc agc ggt cag atc agc aac gta ttc gtt gtc gtg atg ggt	1248
Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Val Met Gly	
405 410 415	
ctg att gca atc tcc gca atc ttc tuc tct ctg ttc agc taa	1290

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Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
 420 425

<210> 252

<211> 429

<212> PRT

<213> Escherichia coli

<400> 252

Met Glu Thr Thr Glu Thr Ser Thr Ile Ala Ser Lys Asp Ser Arg Ser
 1 5 10 15

Ala Trp Arg Lys Thr Asp Thr Met Trp Met Leu Gly Leu Tyr Gly Thr
 20 25 30

Ala Ile Gly Ala Gly Val Leu Phe Leu Pro Ile Asn Ala Gly Val Gly
 35 40 45

Gly Met Ile Pro Leu Ile Ile Met Ala Ile Leu Ala Phe Pro Met Thr
 50 55 60

Phe Phe Ala His Arg Gly Leu Thr Arg Phe Val Leu Ser Gly Lys Asn
 65 70 75 80

Pro Gly Glu Asp Glu Thr Glu Val Val Glu Glu His Phe Gly Ile Gly
 85 90 95

Ala Gly Lys Leu Ile Thr Leu Leu Tyr Phe Phe Ala Ile Tyr Pro Ile
 100 105 110

Leu Leu Val Tyr Ser Val Ala Ile Thr Asn Thr Val Glu Ser Phe Met
 115 120 125

Ser His Gln Leu Gly Met Thr Pro Pro Pro Arg Ala Ile Leu Ser Leu
130 135 140

Ile Leu Ile Val Gly Met Met Thr Ile Val Arg Phe Gly Glu Gln Met
145 150 155 160

Ile Val Lys Ala Met Ser Ile Leu Val Phe Pro Phe Val Gly Val Leu
165 170 175

Met Leu Leu Ala Leu Tyr Leu Ile Pro Gln Trp Asn Gly Ala Ala Leu
180 185 190

Glu Thr Leu Ser Leu Asp Thr Ala Ser Ala Thr Gly Asn Gly Leu Trp
195 200 205

Met Thr Leu Trp Leu Ala Ile Pro Val Met Val Phe Ser Phe Asn His
210 215 220

Ser Pro Ile Ile Ser Ser Phe Ala Val Ala Lys Arg Glu Glu Tyr Gly
225 230 235 240

Asp Met Ala Glu Gln Lys Cys Ser Tyr Ile Leu Ala Phe Ala His Ile
245 250 255

Met Met Val Leu Thr Val Met Phe Phe Val Phe Ser Cys Val Leu Ser
260 265 270

Leu Thr Pro Ala Asp Leu Ala Ala Ala Lys Glu Gln Asn Ile Ser Ile
275 280 285

Leu Ser Tyr Leu Ala Asn His Phe Asn Ala Pro Val Ile Ala Trp Met

290 295 300

Ala Pro Ile Ile Ala Ile Ile Ala Ile Thr Lys Ser Phe Leu Gly His
305 310 315 320

Tyr Leu Gly Ala Arg Glu Gly Phe Asn Gly Met Val Ile Lys Ser Leu
325 330 335

Arg Gly Lys Gly Lys Ser Ile Glu Ile Asn Lys Leu Asn Arg Ile Thr
340 345 350

Ala Leu Phe Met Leu Val Thr Thr Trp Ile Val Ala Thr Leu Asn Pro
355 360 365

Ser Ile Leu Gly Met Ile Glu Thr Leu Gly Gly Pro Ile Ile Ala Met
370 375 380

Ile Leu Phe Leu Met Pro Met Tyr Ala Ile Gln Lys Val Pro Ala Met
385 390 395 400

Arg Lys Tyr Ser Gly His Ile Ser Asn Val Phe Val Val Val Met Gly
405 410 415

Leu Ile Ala Ile Ser Ala Ile Phe Tyr Ser Leu Phe Ser
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<210> 253

<211> 219

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(219)

<400> 253

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1			5					10					15			

cgc	tat	atc	act	gac	acg	aca	aaa	gag	cgt	tat	cac	cag	tgt	cag	aac	96
Arg	Tyr	Ile	Thr	Asp	Thr	Thr	Lys	Glu	Arg	Tyr	His	Gln	Cys	Gln	Asn	
			20					25					30			

gtg	aat	tgc	agg	gcc	acg	ttc	atc	act	tat	gag	tgc	gta	cag	cga	tac	144
Val	Asn	Cys	Ser	Ala	Thr	Phe	Ile	Thr	Tyr	Glu	Ser	Val	Gln	Arg	Tyr	
	35							40					45			

att	gtg	aag	cgg	gga	gaa	gtc	caa	gtc	gta	agg	cgg	cac	cgg	tty	cgg	192
Ile	Val	Lys	Pro	Gly	Gln	Val	His	Val	Val	Arg	Pro	His	Pro	Leu	Pro	
	50						55					60				

tca	ggg	cag	caa	att	atg	tgg	atg	caa								219
Ser	Gly	Gln	Gln	Ile	Met	Trp	Met									
65						70										

<310> 254

<311> 73

<312> PRT

<313> Escherichia coli

<400> 254

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1				5					10					15	

Arg	Tyr	Ile	Thr	Asp	Thr	Thr	Lys	Glu	Arg	Tyr	His	Gln	Cys	Gln	Asn
			20					25					30		

Val	Asn	Cys	Ser	Ala	Thr	Phe	Ile	Thr	Tyr	Glu	Ser	Val	Gln	Arg	Tyr
	35							40					45		

Ile Val Lys Pro Gly Glu Val His Val Val Arg Pro His Pro Leu Pro
 50 55 60

Ser Gly Gln Gln Ile Met Trp Met
 65 70

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<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(2391)

<400> 255

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 Met Ala Ile Asn Asn Thr Gly Ser Arg Arg Leu Leu Val Thr Leu Thr
 1 5 10 15

gac att ttt gca gag att tgc ggg ctg tat cta ctc att ggc gca ggc 96
 Ala Leu Phe Ala Ala Leu Cys Gly Leu Tyr Leu Leu Ile Gly Gly Gly
 20 25 30

tgg ctg gtc gag att ggc ggc tcc tgg tac tac cct atc gct ggc ctc 144
 Trp Leu Val Ala Ile Gly Gly Ser Trp Tyr Tyr Pro Ile Ala Gly Leu
 35 40 45

gtg atg ctc ggc gtc gcc tgg atg ctg tgg cgc agt aac cgc gcc gag 192
 Val Met Leu Gly Val Ala Trp Met Leu Trp Arg Ser Lys Arg Ala Ala
 50 55 60

ctt tgg cca tac gca gcc ctg ctg ctc ggc acc atg att tgg ggc gtc 240
 Leu Trp Leu Tyr Ala Ala Leu Leu Leu Gly Thr Met Ile Trp Gly Val
 65 70 75 80

tgg gaa gtt ggt ttc gac ttc tgg gag ctg act cag cgc agc gac att 288

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Trp	Glu	Val	Gly	Phe	Asp	Phe	Trp	Ala	Leu	Thr	Pro	Arg	Ser	Asp	Ile	
			85					90					95			
ctg	gtc	ttc	tto	ggc	atc	tgg	ctg	acc	ctg	cag	ttt	gtc	tac	cgt	cgc	336
Leu	Val	Phe	Phe	Gly	Ile	Trp	Leu	Ile	Leu	Pro	Phe	Val	Trp	Arg	Arg	
			100				105					110				
ctg	gtc	att	cct	ggc	agg	ggc	gca	gtt	gcc	gca	ctg	gag	gtc	gca	ctg	384
Leu	Val	Ile	Pro	Ala	Ser	Gly	Ala	Val	Ala	Ala	Leu	Val	Val	Ala	Leu	
		115					120				125					
ctg	att	agg	ggc	ggc	atc	ctg	acc	tgg	ggc	gga	ttt	acc	gat	cag	cag	432
Leu	Ile	Ser	Gly	Gly	Ile	Leu	Thr	Trp	Ala	Gly	Phe	Asn	Asp	Pro	Gln	
	130				135				140							
gag	atc	aac	ggc	acc	tta	agg	gcc	cac	gcc	aca	cct	gct	gaa	gct	atc	480
Glu	Ile	Asn	Gly	Thr	Leu	Ser	Ala	Asp	Ala	Thr	Pro	Ala	Glu	Ala	Ile	
145			150				155				160					
tcc	ccc	gta	gcc	gat	cag	gac	tgg	cct	gac	tat	ggt	cgt	aac	cag	gac	528
Ser	Pro	Val	Ala	Asp	Gln	Asp	Trp	Pro	Ala	Tyr	Gly	Arg	Asn	Gln	Gln	
			165				170				175					
ggc	caa	cgc	ttt	tgg	cag	ctg	aaa	cnn	att	aac	gcc	gat	aac	gtc	cct	576
Gly	Gln	Arg	Phe	Ser	Phe	Leu	Lys	Gln	Ile	Asn	Ala	Asp	Asn	Val	His	
	180						185				190					
aat	ctc	aaa	gaa	gcc	tgg	gtg	tto	cgt	act	ggc	gat	gtg	aag	cag	cag	624
Asn	Leu	Lys	Glu	Ala	Trp	Val	Phe	Arg	Thr	Gly	Asp	Val	Lys	Gln	Pro	
	195						200				205					
aac	gat	cag	ggc	gaa	atc	acc	aat	gaa	gtg	acc	cag	att	aaa	gtg	ggc	672
Asn	Asp	Pro	Gly	Glu	Ile	Thr	Asn	Glu	Val	Thr	Pro	Ile	Lys	Val	Gly	
	210					215					220					
gac	acc	cct	tac	ctg	tgt	acc	gct	cac	cag	cgc	ctg	ttt	gag	ctt	gat	720
Asp	Thr	Leu	Tyr	Leu	Cys	Thr	Ala	His	Gln	Arg	Leu	Phe	Ala	Leu	Asp	
225			230				235				240					
gcc	gcc	agg	ggc	aaa	gag	aaa	tgg	cac	tac	gat	cct	gag	ctg	aaa	acc	768
Ala	Ala	Ser	Gly	Lys	Glu	Lys	Trp	His	Tyr	Asp	Pro	Glu	Leu	Lys	Thr	
			245				250				255					

aac gag tct ttc cag caa qta acc tgc cgt ggt gtc tct tat cct gaa	816
Asn Glu Ser Phe Gln His Val Thr Cys Arg Gly Val Ser Tyr His Glu	
260 265 270	
gcc aaa gca gaa acc gct tgg cgg gaa gtg atg gag gat tgc cgg cgt	864
Ala Lys Ala Glu Thr Ala Ser Pro Glu Val Met Ala Asp Cys Pro Arg	
275 280 285	
cgt atc att ctt cgg gtc aac gat ggt cgt ctg att gag att aac gct	912
Arg Ile Ile Leu Pro Val Asn Asp Gly Arg Leu Ile Ala Ile Asn Ala	
290 295 300	
gaa aac ggc aaa ctg tgc gaa acc ttc gcc aat aaa ggc gtg ctg aat	960
Glu Asn Gly Lys Leu Cys Glu Thr Phe Ala Asn Lys Gly Val Leu Asn	
305 310 315 320	
ctg caa agc aat atg cca gac acc aaa cgg ggt ctg tat gaa cgg cct	1008
Leu Gln Ser Asn Met Pro Asp Thr Lys Pro Gly Leu Tyr Glu Pro Thr	
325 330 335	
tgg cca cgg att atc acc gat aaa acc atc gtg atg gcc ggt tca ctt	1056
Ser Pro Pro Ile Ile Thr Asp Lys Thr Ile Val Met Ala Gly Ser Val	
340 345 350	
acc gat aac ttc tca acc cgg gaa cgg tct ggc gtg atc cgt ggt ttt	1104
Thr Asp Asn Phe Ser Thr Arg Glu Thr Ser Gly Val Ile Arg Gly Phe	
355 360 365	
gat gtc aac acc ggt gag ctg ctg tgg gct ttt gat ccc ggc gag aac	1152
Asp Val Asn Thr Gly Glu Leu Leu Trp Ala Phe Asp Pro Gly Ala Lys	
370 375 380	
gat cgg aac gca atc cgg tct gac gaa cac acc ttt acc ttt aac tgg	1200
Asp Pro Asn Ala Ile Pro Ser Asp Glu His Thr Phe Thr Phe Asn Ser	
385 390 395 400	
cca aac tcc tgg gca cca gag gcc tat gac gcg aag ctg gat ctg gtc	1248
Pro Asn Ser Trp Ala Pro Ala Ala Tyr Asp Ala Lys Leu Asp Leu Val	
405 410 415	
tat ctg cgg atg ggc gtg acc acg cgg gat atc tgg ggc ggt aac cgc	1296

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Tyr	Leu	Pro	Met	Gly	Val	Thr	Thr	Pro	Asp	Ile	Trp	Gly	Gly	Asn	Arg	
			420					425					430			
aca	ccg	gaa	cag	gaa	cgt	tat	gou	aga	tug	att	ctg	gog	ctg	aat	goc	1344
Thr	Pro	Gln	Gln	Glu	Arg	Tyr	Ala	Ser	Ser	Tle	Leu	Ala	Leu	Asn	Ala	
			435				440					445				
act	acc	ggg	aaa	ctg	gog	tgg	agc	tac	cag	acc	gtt	cac	cac	gac	ctg	1392
Thr	Thr	Gly	Lys	Leu	Ala	Trp	Ser	Tyr	Gln	Thr	Val	Fis	His	Asp	Leu	
			450				455				460					
tgg	gac	atg	gat	ctt	ccg	gca	cag	ccg	acg	ctg	gog	gac	atc	acc	gtt	1440
Trp	Asp	Met	Asp	Leu	Pro	Ala	Gln	Pro	Thr	Leu	Ala	Asp	Ile	Thr	Val	
			465			470				475				480		
aat	ggc	cag	aaa	gtg	cca	gtt	att	tac	gct	ccg	gog	aaa	acc	ggc	aac	1488
Asn	Gly	Gln	Lys	Val	Pro	Val	Ile	Tyr	Ala	Pro	Ala	Lys	Thr	Gly	Asn	
			485					490					495			
att	ttt	gtg	ctc	gat	cgt	cgt	aat	ggc	gaa	ctg	gtg	gtt	ccg	gca	ccg	1536
Ile	Phe	Val	Leu	Asp	Arg	Arg	Asn	Gly	Glu	Leu	Val	Val	Pro	Ala	Pro	
			500					505					510			
gaa	aaa	ccg	gtt	ccc	caa	ggt	gca	gog	aaa	ggc	gat	tac	gta	acc	cca	1584
Glu	Lys	Pro	Val	Pro	Gln	Gly	Ala	Ala	Lys	Gly	Asp	Tyr	Val	Thr	Pro	
			515				520				525					
act	caa	ccg	ttt	tct	gaa	ctg	agc	ttc	cgt	ccg	acg	caa	gat	ttg	agc	1632
Thr	Gln	Pro	Phe	Ser	Glu	Leu	Ser	Phe	Arg	Pro	Thr	Lys	Asp	Leu	Ser	
			530				535				540					
ggc	gag	gat	atg	tgg	gga	gcc	acc	atg	ttt	gac	caa	ctg	gtg	tgc	cgc	1680
Gly	Ala	Asp	Met	Trp	Gly	Ala	Thr	Met	Phe	Asp	Gln	Leu	Val	Cys	Arg	
			545			550				555			560			
gtg	atg	ttc	cac	cag	atg	cgc	tat	gaa	ggc	att	ttc	acc	ccg	cca	tct	1728
Val	Met	Phe	His	Gln	Met	Arg	Tyr	Glu	Gly	Ile	Phe	Thr	Pro	Pro	Ser	
			565					570				575				
gaa	cag	ggt	acg	ctg	gtc	ttc	ccg	ggt	aac	ctg	ggg	atg	ttc	gaa	tgg	1776
Glu	Gln	Gly	Thr	Leu	Val	Phe	Pro	Gly	Asn	Leu	Gly	Met	Phe	Glu	Trp	
			580					585				590				

ggc gag att leu gll gat cca aat cgt gaa gtg gog att gcc aac cca	1824
Gly Gly Ile Ser Val Asp Pro Asn Arg Glu Val Ala Ile Ala Asn Pro	
595 600 605	
atg gca ctg cag ttt gtt tgg aaa cly atc cgg cgt ggt cct ggc aac	1872
Met Ala Leu Pro Phe Val Ser Lys Leu Ile Pro Arg Gly Pro Gly Asn	
610 615 620	
cag atg gag cag cag aaa gat gcc aaa ggc acg ggt acg gaa tcc ggc	1920
Pro Met Glu Gln Pro Lys Asp Ala Lys Gly Thr Gly Thr Glu Ser Gly	
625 630 635 640	
att cag cca cag tac ggt gta cag tat ggt gtc acg ctc aac cag ttc	1968
Ile Gln Pro Gln Tyr Gly Val Pro Tyr Gly Val Thr Leu Asn Pro Phe	
645 650 655	
ctc tca cca ttt ggt ctg cca tgt aaa cag cca gca lgg ggt tat atc	2016
Leu Ser Pro Phe Gly Leu Pro Cys Lys Gln Pro Ala Trp Gly Tyr Ile	
660 665 670	
tgg gag ctg gat ctg aaa act aat gaa gtg gtg tgg aag aaa cgt att	2064
Ser Ala Leu Asp Leu Lys Thr Asn Glu Val Val Trp Lys Lys Arg Ile	
675 680 685	
ggt acg cag cag gac agt atg cgg ttc cag atg cag gtt cag gly cag	2112
Gly Thr Pro Gln Asp Ser Met Pro Phe Pro Met Pro Val Pro Val Pro	
690 695 700	
ttc aat atg ggt atg cag atg ctg ggc ggg cca atc tcc acg gag ggt	2160
Phe Asn Met Gly Met Pro Met Leu Gly Gly Pro Ile Ser Thr Ala Gly	
705 710 715 720	
aac ctg ctg ttt atc gcc gct acg gca gat aac tac ctg cgc gct tac	2208
Asn Val Leu Phe Ile Ala Ala Thr Ala Asp Asn Tyr Leu Arg Ala Tyr	
725 730 735	
aac atg agc aac ggt gaa aaa ctg tgg cag ggt cgt tta cca gag ggt	2256
Asn Met Ser Asn Gly Glu Lys Leu Trp Gln Gly Arg Leu Pro Ala Gly	
740 745 750	
ggt cag gct aag cca atg acc tat gaa gtg aat ggt aag cag tat gtg	2304

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Gly Gln Ala Thr Pro Met Thr Tyr Glu Val Asn Gly Lys Gln Tyr Val
 755 760 765

gtg atc tcc gca ggc ggt cac ggt Leu ttt ggt acg aag atg ggc gac 2352
 Val Ile Ser Ala Gly Gly His Gly Ser Phe Gly Thr Lys Met Gly Asp
 770 775 780

tat atc gtg gct tat gcg ctg ccg gat gat gtg aag taa 2391
 Tyr Ile Val Ala Tyr Ala Leu Pro Asp Asp Val Lys
 785 790 795

<210> 256

<211> 796

<212> PRT

<213> Escherichia coli

<400> 256

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Ala Leu Phe Ala Ala Leu Cys Gly Leu Tyr Leu Leu Ile Gly Gly Gly
 20 25 30

Trp Leu Val Ala Ile Gly Gly Ser Trp Tyr Tyr Pro Ile Ala Gly Leu
 35 40 45

Val Met Leu Gly Val Ala Trp Met Leu Trp Arg Ser Cys Arg Ala Ala
 50 55 60

Leu Trp Leu Tyr Ala Ala Leu Leu Leu Gly Thr Met Ile Trp Gly Val
 65 70 75 80

Trp Glu Val Gly Phe Asp Phe Trp Ala Leu Thr Pro Arg Ser Asp Ile
 85 90 95

Leu Val Phe Phe Gly Ile Trp Leu Ile Leu Pro Phe Val Trp Arg Arg
100 105 110

Leu Val Ile Pro Ala Ser Gly Ala Val Ala Ala Leu Val Val Ala Leu
115 120 125

Leu Ile Ser Gly Gly Ile Leu Thr Trp Ala Gly Phe Asn Asp Pro Gln
130 135 140

Glu Ile Asn Gly Thr Leu Ser Ala Asp Ala Thr Pro Ala Glu Ala Ile
145 150 155 160

Ser Pro Val Ala Asp Gln Asp Trp Pro Ala Tyr Gly Arg Asn Gln Glu
165 170 175

Gly Gln Arg Phe Ser Pro Leu Lys Gln Ile Asn Ala Asp Asn Val His
180 185 190

Asn Leu Lys Glu Ala Trp Val Phe Arg Thr Gly Asp Val Lys Gln Pro
195 200 205

Asn Asp Pro Gly Glu Ile Thr Asn Glu Val Thr Pro Ile Lys Val Gly
210 215 220

Asp Thr Leu Tyr Leu Cys Thr Ala His Gln Arg Leu Phe Ala Leu Asp
225 230 235 240

Ala Ala Ser Gly Lys Glu Lys Trp His Tyr Asp Pro Glu Leu Lys Thr
245 250 255

Asn Glu Ser Phe Gln His Val Thr Cys Arg Gly Val Ser Tyr His Glu

260	265	270
Ala Lys Ala Glu Thr Ala Ser Pro Glu Val Met Ala Asp Cys Pro Arg		
275	280	285
Arg Ile Ile Leu Pro Val Asn Asp Gly Arg Leu Ile Ala Ile Asn Ala		
290	295	300
Glu Asn Gly Lys Leu Cys Glu Thr Phe Ala Asn Lys Gly Val Leu Asn		
305	310	315
320		
Leu Gln Ser Asn Met Pro Asp Thr Lys Pro Gly Leu Tyr Glu Pro Thr		
325	330	335
Ser Pro Pro Ile Ile Thr Asp Lys Thr Ile Val Met Ala Gly Ser Val		
340	345	350
Thr Asp Asn Phe Ser Thr Arg Glu Thr Ser Gly Val Ile Arg Gly Phe		
355	360	365
Asp Val Asn Thr Gly Glu Leu Leu Trp Ala Phe Asp Pro Gly Ala Lys		
370	375	380
Asp Pro Asn Ala Ile Pro Ser Asp Glu His Thr Phe Thr Phe Asn Ser		
385	390	395
400		
Pro Asn Ser Trp Ala Pro Ala Ala Tyr Asp Ala Lys Leu Asp Leu Val		
405	410	415
Tyr Leu Pro Met Gly Val Thr Thr Pro Asp Ile Trp Gly Gly Asn Arg		
420	425	430

Thr Pro Glu Gln Glu Arg Tyr Ala Ser Ser Ile Leu Ala Leu Asn Ala
435 440 445

Thr Thr Gly Lys Leu Ala Trp Ser Tyr Gln Thr Val His His Asp Leu
450 455 460

Trp Asp Met Asp Leu Pro Ala Gln Pro Thr Leu Ala Asp Ile Thr Val
465 470 475 480

Asn Gly Gln Lys Val Pro Val Ile Tyr Ala Pro Ala Lys Thr Gly Asn
485 490 495

Ile Phe Val Leu Asp Arg Arg Asn Gly Gln Leu Val Val Pro Ala Pro
500 505 510

Glu Lys Pro Val Pro Gln Gly Ala Ala Lys Gly Asp Tyr Val Thr Pro
515 520 525

Thr Gln Pro Phe Ser Glu Leu Ser Phe Arg Pro Thr Lys Asp Leu Ser
530 535 540

Gly Ala Asp Met Trp Gly Ala Thr Met Phe Asp Gln Leu Val Cys Arg
545 550 555 560

Val Met Phe His Gln Met Arg Tyr Glu Gly Ile Phe Thr Pro Pro Ser
565 570 575

Glu Gln Gly Thr Leu Val Phe Pro Gly Asn Leu Gly Met Phe Glu Trp
580 585 590

Gly Gly Ile Ser Val Asp Pro Asn Arg Glu Val Ala Ile Ala Asn Pro

605

Gly Gln Ala Thr Pro Met Thr Tyr Gln Val Asn Gly Lys Gln Tyr Val
755 760 765

Val Ile Ser Ala Gly Gly His Gly Ser Phe Gly Thr Lys Met Gly Asp
 770 775 780

Tyr Ile Val Ala Tyr Ala Leu Pro Asp Asp Val Tyr
 785 790 795

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 Met Ser Thr Ser Asp Ser Ile Val Ser Ser Gln Thr Lys Gln Ser Ser
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 tgg cgt aaa tca gat acc aca tgg aag ttc ggc ttg ttt ggt aag gca 96
 Trp Arg Lys Ser Asp Thr Thr Trp Thr Leu Gly Leu Phe Gly Thr Ala
 20 25 30
 atc ggc gcc cag gtg ctg ttc ttc cct atc cgc gca ggt ttt ggc gga 144
 Ile Gly Ala Gly Val Leu Phe Phe Pro Ile Arg Ala Gly Phe Gly Gly
 35 40 45
 ctg atc cag att ctg ctg atg ttg gta ttg gca tac ccc atc gag att 192
 Leu Ile Pro Ile Leu Leu Met Leu Val Leu Ala Tyr Pro Ile Ala Phe
 50 55 60
 tat tgc cac agg gag ctg gag cgt ctg tgt ctc tct ggc tct aac cct 240
 Tyr Cys His Arg Ala Leu Ala Arg Leu Cys Leu Ser Gly Ser Asn Pro
 65 70 75 80
 tcc ggc aac att aag gaa aag gtg gaa gag cat ttt ggt aaa act gcc 288
 Ser Gly Asn Ile Thr Glu Thr Val Glu Glu His Phe Gly Lys Thr Gly

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	85	90	95	
ggc gtc gtt atc acg ttc ctg tac ttc ttc gcg att tgc cca ctg ctg				336
Gly Val Val Ile Thr Phe Leu Tyr Phe Phe Ala Ile Cys Pro Leu Leu				
	100	105	110	
tgg att tat ggc gtt act att acc aat acc ttt atg acg ttc tgg gaa				384
Trp Ile Tyr Gly Val Thr Ile Thr Asn Thr Phe Met Thr Phe Trp Glu				
	115	120	125	
aac cag ctg ggc ttt gca ccc ctg aat cgc ggc ttt gtg gcg ctg ttc				432
Asn Gln Leu Gly Phe Ala Pro Leu Asn Arg Gly Phe Val Ala Leu Phe				
	130	135	140	
ctg ttg ctg ctg atg gct ttc gtc atc tgg ttt ggt aag gac ctg atg				480
Leu Leu Leu Leu Met Ala Phe Val Ile Trp Phe Gly Lys Asp Leu Met				
	145	150	155	160
gll aac gtc atg agc tac ctg gta tgg ccc ttt atc gcc agc ctg gtc				528
Val Lys Val Met Ser Tyr Leu Val Trp Pro Phe Ile Ala Ser Leu Val				
	165	170	175	
ctg att tat ttg tgg ctg atc cct tac tgg aac tct gcc gtt atc gac				576
Leu Ile Ser Leu Ser Leu Ile Pro Tyr Trp Asn Ser Ala Val Ile Asp				
	180	185	190	
cag gtc gac ctg ggt ccc ctg tgg tta acc ggt cat gac ggt atc ctg				624
Gln Val Asp Leu Gly Ser Leu Ser Leu Thr Gly His Asp Gly Ile Leu				
	195	200	205	
atc acc gtc tgg ctg ggg att tcc atc atg att ttc tcc ttt aac ttc				672
Ile Thr Val Trp Leu Gly Ile Ser Ile Met Val Phe Ser Phe Asn Phe				
	210	215	220	
tgg cca atc gtc tct tcc ttc gtg gtt tct aag cgt gaa gag tat gag				720
Ser Pro Ile Val Ser Ser Phe Val Val Ser Lys Arg Glu Glu Tyr Glu				
	225	230	235	240
aaa gac ttc ggt cgc gac ttc acc gaa cgt aaa tgt tcc caa atc att				768
Lys Asp Phe Gly Arg Asp Phe Thr Gln Arg Lys Cys Ser Gln Ile Ile				
	245	250	255	

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tct cgt gcc agc atg ctg atg gtt gca gtc gtc atg ttc ttt gcc ttt	816
Ser Arg Ala Ser Met Leu Met Val Ala Val Val Met Phe Phe Ala Phe	
260 265 270	
agg tgc ctg ttt act ctg tct ccg gcc aac atg gag gaa gcc aaa gag	864
Ser Cys Leu Phe Thr Leu Ser Pro Ala Asn Met Ala Glu Ala Lys Ala	
275 280 285	
cag aac att cca gtg ctt tct tat ctg gct aac cag ttt gag tcc atg	912
Gln Asn Ile Pro Val Leu Ser Tyr Leu Ala Asn His Phe Ala Ser Met	
290 295 300	
acc ggt acc aaa acc acg ttc gag att acc ctg gaa tat gag gct tcc	960
Thr Gly Thr Lys Thr Thr Phe Ala Ile Thr Leu Glu Tyr Ala Ala Ser	
305 310 315 320	
atc atc gca ctg gtc gct atc ttc aaa tct ttc ttc ggt cag tat ctg	1008
Ile Ile Ala Leu Val Ala Ile Phe Lys Ser Phe Phe Gly His Tyr Leu	
325 330 335	
gga acc ctg gaa ggt ctg aat ggc ctg gtc ctg aag ttt ggt tat aaa	1056
Gly Thr Leu Glu Gly Leu Asn Gly Leu Val Leu Lys Phe Gly Tyr Lys	
340 345 350	
ggc gcc aac aac aac gtg tgc ctg ggt aac ctg aac act atc agc atg	1104
Gly Asp Lys Thr Lys Val Ser Ileu Gly Lys Leu Asn Thr Ile Ser Met	
355 360 365	
atc ttc atc atg ggc tcc aac tgg gtt gtt gcc tac gcc aac ccg aac	1152
Ile Phe Ile Met Gly Ser Thr Trp Val Val Ala Tyr Ala Asn Pro Asn	
370 375 380	
ata ctt gac ctg att gaa gcc atg ggc gca ccg att atc gca tcc ctg	1200
Ile Leu Asp Leu Ile Glu Ala Met Gly Ala Pro Ile Ile Ala Ser Leu	
385 390 395 400	
ctg tgc ctg ttg ccg atg tat gcc atc cgt aaa gag ccg tct ctg gag	1248
Leu Cys Leu Leu Pro Met Tyr Ala Ile Arg Lys Ala Pro Ser Leu Ala	
405 410 415	
aaa tac cgt ggt cgt ctg gat aac gtg ttt gtt acc gtg att ggt ctg	1296
Lys Tyr Arg Gly Arg Leu Asp Asn Val Phe Val Thr Val Ile Gly Leu	

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420	425	430	
ctg acc atc ctg aac atc gta tac aaa ctg ttt taa			1332
Leu Thr Ile Leu Asn Ile Val Tyr Lys Leu Phe			
435	440		
<210>	258		
<211>	443		
<212>	PRT		
<213>	Escherichia coli		
<400>	258		
Met Ser Thr Ser Asp Ser Ile Val Ser Ser Gln Thr Lys Gln Ser Ser			
1	5	10	15
Trp Arg Lys Ser Asp Thr Thr Trp Thr Leu Gly Leu Phe Gly Thr Ala			
	20	25	30
Ile Gly Ala Gly Val Leu Phe Phe Pro Ile Arg Ala Gly Phe Gly Gly			
	35	40	45
Leu Ile Pro Ile Leu Leu Met Leu Val Leu Ala Tyr Pro Ile Ala Phe			
	50	55	60
Tyr Cys His Arg Ala Leu Ala Arg Leu Cys Leu Ser Gly Ser Asn Pro			
65	70	75	80
Ser Gly Asn Ile Thr Glu Thr Val Glu Glu His Phe Gly Lys Thr Gly			
	85	90	95
Gly Val Val Ile Thr Phe Leu Tyr Phe Phe Ala Ile Cys Pro Leu Leu			
	100	105	110

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Trp Ile Tyr Gly Val Thr Ile Thr Asn Thr Phe Met Thr Phe Trp Glu
115 120 125

Asn Gln Leu Gly Phe Ala Pro Leu Asn Arg Gly Phe Val Ala Leu Phe
130 135 140

Leu Leu Leu Leu Met Ala Phe Val Ile Trp Phe Gly Lys Asp Leu Met
145 150 155 160

Val Lys Val Met Ser Tyr Leu Val Trp Pro Phe Ile Ala Ser Leu Val
165 170 175

Leu Ile Ser Leu Ser Leu Ile Pro Tyr Trp Asn Ser Ala Val Ile Asp
180 185 190

Gln Val Asp Leu Gly Ser Leu Ser Leu Thr Gly His Asp Gly Ile Leu
195 200 205

Ile Thr Val Trp Leu Gly Ile Ser Ile Met Val Phe Ser Phe Asn Phe
210 215 220

Ser Pro Ile Val Ser Ser Phe Val Val Ser Lys Arg Glu Glu Tyr Glu
225 230 235 240

Lys Asp Phe Gly Arg Asp Phe Thr Glu Arg Lys Cys Ser Gln Ile Ile
245 250 255

Ser Arg Ala Ser Met Leu Met Val Ala Val Val Met Phe Phe Ala Phe
260 265 270

Ser Cys Leu Phe Thr Leu Ser Pro Ala Asn Met Ala Gln Ala Lys Ala
275 280 285

Gln Asn Ile Pro Val Leu Ser Tyr Leu Ala Asn His Phe Ala Ser Met
290 295 300

Thr Gly Thr Lys Thr Thr Phe Ala Ile Thr Leu Glu Tyr Ala Ala Ser
305 310 315 320

Ile Ile Ala Leu Val Ala Ile Phe Cys Ser Phe Phe Gly His Tyr Leu
325 330 335

Gly Thr Leu Gln Gly Leu Asn Gly Ser Val Leu Lys Phe Gly Tyr Lys
340 345 350

Gly Asp Lys Thr Lys Val Ser Leu Gly Lys Leu Asn Thr Ile Ser Met
355 360 365

Ile Phe Ile Met Gly Ser Thr Trp Val Val Ala Tyr Ala Asn Pro Asn
370 375 380

Ile Leu Asp Leu Ile Glu Ala Met Gly Ala Pro Thr Ile Ala Ser Leu
385 390 395 400

Leu Cys Leu Leu Pro Met Tyr Ala Ile Arg Lys Ala Pro Ser Leu Ala
405 410 415

Lys Tyr Arg Gly Arg Leu Asp Asn Val Phe Val Thr Val Ile Gly Leu
420 425 430

Leu Thr Ile Leu Asn Ile Val Tyr Lys Leu Phe
435 440

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 <211> 2049
 <212> DNA
 <213> Escherichia coli

<220>
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 1 5 10 15
 gca ggc cag acc ttc gct gta gaa gal atc aag cgt gct gat caa att 96
 Ala Gly Gln Thr Phe Ala Val Glu Asp Ile Thr Arg Ala Asp Gln Ile
 20 25 30
 ccc gta ltu aag gaa gag acg cag cat ccc aag gta agt gag cgc gta 144
 Pro Val Leu Lys Glu Glu Thr Gln His Ala Thr Val Ser Glu Arg Val
 35 40 45
 acg tog cgc ttc acc cgt tct cat tat cgc cag ltu gac ctg gat cag 192
 Thr Ser Arg Phe Thr Arg Ser His Tyr Arg Gln Phe Asp Leu Asp Gln
 50 55 60
 gca ttt tog gcc aaa atc ttt gaa cgc tac ctg aat ctg ctg gat tac 240
 Ala Phe Ser Ala Lys Ile Phe Asp Arg Tyr Leu Asn Leu Leu Asp Tyr
 65 70 75 80
 agc cac aac gcy cly ctg gca agc gat gtt gaa cag ttc ggc aaa aag 288
 Ser His Asn Val Leu Leu Ala Ser Asp Val Glu Gln Phe Ala Lys Lys
 85 90 95
 aaa acc gag cta ggc gat gaa ctg cgt ltu ggc aaa ctg gac gtt ttc 336
 Lys Thr Glu Leu Gly Asp Gln Leu Arg Ser Gly Lys Don Asp Val Phe
 100 105 110
 tac gat ctg tac aat ctg gag caa aag cgc cgt ttt gag cgt ltu cag 384
 Tyr Asp Leu Tyr Asn Leu Ala Gln Lys Arg Arg Phe Gln Arg Tyr Gln
 115 120 125

tac gct ttg tgg gta ctg gaa aag ccc atg gat ttc acc ggc aac gac	432
Tyr Ala Leu Ser Val Leu Glu Lys Pro Met Asp Phe Thr Gly Asn Asp	
130 135 140	
act tat aac ctt gac cgc agc aaa gag ccc tgg ccg aag aac gag gct	480
Thr Tyr Asn Leu Asp Arg Ser Lys Ala Pro Trp Pro Lys Asn Glu Ala	
145 150 155 160	
gag ttg aac gag ctg tgg gac agt aaa gtc aaa ttc gac gag tta agc	528
Glu Leu Asn Ala Leu Trp Asp Ser Lys Val Lys Phe Asp Glu Leu Ser	
165 170 175	
ctg aag ctg aca gga aaa acg gat aaa gaa att cgt gaa acc ctg act	576
Leu Lys Leu Thr Gly Lys Thr Asp Lys Glu Ile Arg Glu Thr Leu Thr	
180 185 190	
cgc cgc tac aaa ttt gcc att cgt cgt ctg gag caa acc aac agc gaa	624
Arg Arg Tyr Lys Phe Ala Ile Arg Asp Leu Ala Cln Thr Asn Ser Glu	
195 200 205	
gat gtt ttc tgg ctg gaa atg acg gag ttt gag cgt gaa atc gac ccg	672
Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile Asp Pro	
210 215 220	
cat acc aac tac ctt tcc ccg cgt aat acc gaa cag ttc aac acb gaa	720
His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Glu Phe Asn Thr Glu	
225 230 235 240	
atg agt ttg tgg ctg gaa ggt att ggc gca gtg ctg caa atg gat gat	768
Met Ser Leu Ser Leu Glu Gly Ile Gly Ala Val Leu Glu Met Asp Asp	
245 250 255	
gac tac acc gtt atc aat tgg atg gtg gca ggt ggt ccg gca gcg aag	816
Asp Tyr Thr Val Ile Asn Ser Met Val Ala Gly Gly Pro Ala Ala Lys	
260 265 270	
agt aaa gct atc agc gtt ggt gac aaa att gtc ggt gtt ggt cuu uu	864
Ser Lys Ala Ile Ser Val Gly Asp Lys Phe Val Gly Val Gly Cln Thr	
275 280 285	
ggc aag ccg atg gtt gac gtg att ggc tgg cgt ctt gat gat gtg gtt	912

Gly Lys Pro Met Val Asp Val Ile Gly Trp Arg Leu Asp Asp Val Val	
290 295 300	
gca tta att aaa ggg ccg aag cgc aat aaa gtt cgt ctg gaa att tta	960
Ala Leu Ile Lys Gly Pro Lys Gly Ser Lys Val Arg Leu Glu Ile Leu	
305 310 315 320	
oct gct ggt aaa ggg acc aag acc cgt act gta aag ttg acc cgt gaa	1008
Pro Ala Gly Lys Gly Thr Lys Thr Arg Thr Val Thr Leu Thr Arg Glu	
325 330 335	
cgt att cgt ctg gaa gac cgc gcg gtt aaa atg tcg ctg aag acc gtc	1056
Arg Ile Arg Leu Glu Asp Arg Ala Val Lys Met Ser Val Lys Thr Val	
340 345 350	
ggt aaa gag aaa gtc ggc gtg ctg gat att ccg ggc ttc tat gtg ggc	1104
Gly Lys Glu Lys Val Gly Val Leu Asp Ile Pro Gly Phe Tyr Val Gly	
355 360 365	
ctg acc gac gal gtc aaa gtg caa ctg cag aaa ctg gaa aaa cag aac	1152
Leu Thr Asp Asp Val Lys Val Gln Leu Gln Lys Leu Glu Lys Gln Asn	
370 375 380	
glu agc agc gtc atc atc gac ctg cgt acc aat ggc cgt ggg gcg tta	1200
Val Ser Ser Val Ile Ile Asp Leu Arg Ser Asn Gly Gly Gly Ala Leu	
385 390 395 400	
act gaa gcc gta tcg ctg tcc ggt ctg ttt att cct gcg ggt ccc att	1248
Thr Glu Ala Val Ser Leu Ser Gly Leu Phe Ile Pro Ala Gly Pro Ile	
405 410 415	
gtc cag gtc cgc gat aac aac ggc aag gtt cgt gaa gat agc gat acc	1296
Val Gln Val Arg Asp Asn Asn Gly Lys Val Arg Glu Asp Ser Asp Thr	
420 425 430	
gac gga cag gtt ttc tat aaa ggc ccg ctg gtg gtg ctg gtt gac cgc	1344
Asp Gly Gln Val Phe Tyr Lys Gly Pro Leu Val Val Leu Val Asp Arg	
435 440 445	
ttc agt gct tcg gct tca gaa atc ttt gcc gcg gca atg cag gat tac	1392
Phe Ser Ala Ser Ala Ser Gln Ile Phe Ala Ala Ala Met Gln Asp Tyr	
450 455 460	

cgt cgt gcg ctg gtt gtg ggt gaa cgg acg ttt ggt aaa ggc acc gtt	1440
Gly Arg Ala Leu Val Val Gly Glu Pro Thr Phe Gly Lys Gly Thr Val	
465 470 475 480	
cag caa tac cgt tca ttg aac cgt att tac gat cag atg tta cgt cct	1488
Gln Gln Tyr Arg Ser Leu Asn Arg Ile Tyr Asp Gln Met Leu Arg Pro	
485 490 495	
gaa tgg cca gcg ctg ggt tct gtg cag aac acg atc cag aaa ttc tat	1536
Glu Trp Pro Ala Leu Gly Ser Val Gln Tyr Thr Ile Gln Lys Phe Tyr	
500 505 510	
cgc gtt aac ggc ggc agt acg caa cgt aaa ggc gta acg cca gac atc	1584
Arg Val Asn Gly Gly Ser Thr Gln Arg Lys Gly Val Thr Pro Asp Ile	
515 520 525	
atc atg cgg acg ggt aat gaa gaa acg gaa acg ggt gag aaa ttc gaa	1632
Ile Met Pro Thr Gly Asn Glu Glu Thr Glu Thr Gly Glu Lys Phe Glu	
530 535 540	
gat aac gcg ctg cgg tgg gat agc att gat gcc gcg aat tat gtg aaa	1680
Asp Asn Ala Leu Pro Trp Asp Ser Ile Asp Ala Ala Thr Tyr Val Tyr	
545 550 555 560	
tca gga gat tta acg gcc tct gaa cgg gag ctg ctg aag gaa cat aat	1728
Ser Gly Asp Leu Thr Ala Phe Glu Pro Glu Leu Leu Lys Glu His Asn	
565 570 575	
gcg cgt atc gcg aaa gat cct gag tta cgg aac atc atg aag gat atc	1776
Ala Arg Ile Ala Lys Asp Pro Glu Phe Gln Asn Ile Met Lys Asp Ile	
580 585 590	
gcg cgc ttc aac gct atg aag gac aag cgc aat atc gtt tct ctg aat	1824
Ala Arg Phe Asn Ala Met Lys Asp Lys Arg Asn Ile Val Ser Leu Asn	
595 600 605	
tac gct gtg cgt gag aaa gag aat aat gaa gat gat gcg acg cgt ctg	1872
Tyr Ala Val Arg Glu Lys Glu Asn Asn Glu Asp Asp Ala Thr Arg Leu	
610 615 620	
gcg cgt ttg aac gaa cgc ttt aaa cgc gaa ggt aaa cgg gag lly aag	1920

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Ala Arg Leu Asn Glu Arg Phe Lys Arg Glu Gly Lys Pro Glu Leu Lys
 625 630 635 640

 aaa ctg qat qat cta cgg aaa gat tac cag gaa cgg gat cct tat ctg 1938
 Lys Leu Asp Asp Leu Pro Lys Asp Tyr Gln Glu Pro Asp Pro Tyr Leu
 645 650 655

 gat gag aag ggg aat atc gca ctc gat ctg ggg aag ctt gaa aaa gcc 2016
 Asp Glu Thr Val Asn Ile Ala Leu Asp Leu Ala Lys Leu Glu Lys Ala
 660 665 670

 aga ccc ggg gaa cca ccc gct ccc gtc aag taa 2049
 Arg Pro Ala Glu Gln Pro Ala Pro Val Lys
 675 680

 <210> 260
 <211> 682
 <212> PRT
 <213> Escherichia coli

 <400> 260

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 20 25 30

 Pro Val Leu Lys Glu Glu Thr Gln His Ala Thr Val Ser Glu Arg Val
 35 40 45

 Thr Ser Arg Phe Thr Arg Ser His Tyr Arg Gln Phe Asp Leu Asp Gln
 50 55 60

 Ala Phe Ser Ala Lys Ile Phe Asp Arg Tyr Leu Asn Leu Leu Asp Tyr
 65 70 75 80

Ser His Asn Val Leu Leu Ala Ser Asp Val Glu Gln Phe Ala Lys Lys
85 90 95

Lys Thr Glu Leu Gly Asp Glu Leu Arg Ser Gly Lys Leu Asp Val Phe
100 105 110

Tyr Asp Leu Tyr Asn Leu Ala Gln Lys Arg Arg Phe Glu Arg Tyr Gln
115 120 125

Tyr Ala Leu Ser Val Leu Glu Lys Pro Met Asp Phe Thr Gly Asn Asp
130 135 140

Thr Tyr Asn Leu Asp Arg Ser Lys Ala Pro Trp Pro Lys Asn Glu Ala
145 150 155 160

Glu Leu Asn Ala Leu Trp Asp Ser Lys Val Lys Phe Asp Glu Leu Ser
165 170 175

Leu Lys Leu Thr Gly Lys Thr Asp Lys Glu Ile Arg Glu Thr Leu Thr
180 185 190

Arg Arg Tyr Lys Phe Ala Ile Arg Arg Leu Ala Gln Thr Asn Ser Cln
195 200 205

Asp Val Phe Ser Leu Ala Met Thr Ala Phe Ala Arg Glu Ile Asp Pro
210 215 220

His Thr Asn Tyr Leu Ser Pro Arg Asn Thr Glu Gln Phe Asn Thr Glu
225 230 235 240

Met Ser Leu Ser Leu Glu Gly Ile Cln Ala Val Leu Gln Met Asp Asp

	245		250		255
Asp Tyr Thr Val Ile Asn Ser Met Val Ala Gly Gly Pro Ala Ala Lys					
	260		265		270
Ser Lys Ala Ile Ser Val Gly Asp Pys Ile Val Gly Val Gly Gln Thr					
	275		280		285
Gly Lys Pro Met Val Asp Val Ile Gly Ser Arg Leu Asp Asp Val Val					
	290		295		300
Ala Leu Ile Lys Gly Pro Pys Gly Ser Lys Val Arg Leu Glu Ile Leu					
	305		310		315
Pro Ala Gly Lys Gly Thr Lys Thr Arg Thr Val Thr Leu Thr Arg Glu					
	325		330		335
Arg Ile Arg Leu Glu Asp Arg Ala Val Lys Met Ser Val Lys Thr Val					
	340		345		350
Gly Lys Glu Lys Val Gly Val Leu Asp Ile Pro Gly Phe Tyr Val Gly					
	355		360		365
Leu Thr Asp Asp Val Lys Val Gln Leu Gln Lys Leu Glu Lys Gln Asn					
	370		375		380
Val Ser Ser Val Ile Ile Asp Leu Arg Ser Asn Gly Gly Gly Ala Leu					
	385		390		395
Thr Gln Ala Val Ser Leu Ser Gly Leu Phe Ile Pro Ala Gly Pro Ile					
	405		410		415

Val Gln Val Arg Asp Asn Asn Gly Lys Val Arg Glu Asp Ser Asp Thr
420 425 430

Asp Gly Gln Val Phe Tyr Lys Gly Pro Leu Val Val Leu Val Asp Arg
435 440 445

Phe Ser Ala Ser Ala Ser Glu Ile Phe Ala Ala Ala Met Gln Asp Tyr
450 455 460

Gly Arg Ala Leu Val Val Gly Glu Pro Thr Phe Gly Lys Gly Thr Val
465 470 475 480

Gln Gln Tyr Arg Ser Leu Asn Arg Ile Tyr Asp Gln Met Leu Arg Pro
485 490 495

Glu Trp Pro Ala Leu Gly Ser Val Gln Tyr Thr Ile Gln Lys Phe Tyr
500 505 510

Arg Val Asn Gly Gly Ser Thr Gln Arg Lys Gly Val Thr Pro Asp Ile
515 520 525

Ile Met Pro Thr Gly Asn Glu Glu Thr Glu Thr Gly Glu Lys Phe Glu
530 535 540

Asp Asn Ala Leu Pro Trp Asp Ser Ile Asp Ala Ala Thr Tyr Val Lys
545 550 555 560

Ser Gly Asp Leu Thr Ala Phe Glu Pro Glu Leu Leu Lys Glu His Asn
565 570 575

Ala Arg Ile Ala Lys Asp Pro Glu Phe Gln Asn Ile Met Lys Asp Ile

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580

585

590

Ala Arg Phe Asn Ala Met Lys Asp Lys Arg Asn Ile Val Ser Leu Asn
595 600 605

Tyr Ala Val Arg Glu Lys Glu Asn Asn Glu Asp Asp Ala Thr Arg Leu
610 615 620

Ala Arg Leu Asn Glu Arg Phe Lys Arg Glu Gly Lys Pro Glu Leu Lys
625 630 635 640

Lys Leu Asp Asp Leu Pro Lys Asp Tyr Gln Glu Pro Asp Pro Tyr Leu
645 650 655

Asp Gln Thr Val Asp Ile Ala Leu Asp Leu Ala Lys Leu Glu Lys Ala
660 665 670

Arg Pro Ala Glu Gln Pro Ala Pro Val Lys
675 680

<210> 261
<211> 1551
<212> DNA
<213> Escherichia coli

<220>
<221> CDS
<222> (1)..(1551)

<400> 261
ttg ttc atg gca act tat atg act ttt tca tta aag caa tca ggg aga 48
Leu Phe Met Ala Thr Tyr Met Thr Phe Ser Leu Lys Gln Ser Gly Arg
1 5 10 15

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gca atg agt aaa cac gac acc gac act cca gat caa cac gcc gcg aaa	96
Ala Met Ser Lys His Asp Thr Asp Thr Ser Asp Gln His Ala Ala Lys	
20 25 30	
cgc cgc tgg ctt aat gcc cac gaa gag ggg tat cac aaa gcg atg ggc	144
Arg Arg Trp Leu Asn Ala His Gln Gln Gly Tyr His Lys Ala Met Gly	
35 40 45	
aat cgc cag gtg cag atg atc gcc att ggc gcc gcg att gcc acc gcc	192
Asn Arg Gln Val Gln Met Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly	
50 55 60	
ttg tll tta ggt gca gga gcc cga ctg caa atg gcg ggg ccc gca ctg	240
Leu Phe Leu Gly Ala Gly Ala Arg Leu Gln Met Ala Gly Pro Ala Leu	
65 70 75 80	
gca ctg gtt tat tta att tgt gcc ttg ttt tgg ttt ttt att ctg cgt	288
Ala Leu Val Tyr Leu Ile Cys Gly Leu Phe Ser Phe Phe Ile Leu Arg	
85 90 95	
gca tcy ggt gag ctg gtg cta cac cgc cct cac agt gcc agt ttt gtt	336
Ala Leu Gly Glu Leu Val Leu His Arg Pro Ser Ser Gly Ser Phe Val	
100 105 110	
tct tat gcc cgt gag ttt ttg ggt gag aaa gcc got tat gtt got gcc	384
Ser Tyr Ala Arg Gln Phe Leu Gly Glu Lys Ala Ala Tyr Val Ala Gly	
115 120 125	
tgg atg tac ttc atc aac tgg gcc atg acc ggg att gtt gat att acc	432
Trp Met Tyr Phe Ile Asn Trp Ala Met Thr Gly Ile Val Asp Ile Thr	
130 135 140	
gcc gtc gct ctg tct atg cat tac tgg ggt gcc ttt gcc gcc gtg cgc	480
Ala Val Ala Leu Tyr Met His Tyr Trp Gly Ala Phe Gly Gly Val Pro	
145 150 155 160	
cag tgg gtc ttt gcg ctc gct gca ctt acc atc gtt gcc acc atg aat	528
Gln Trp Val Phe Ala Leu Ala Ala Leu Thr Ile Val Gly Thr Met Asn	
165 170 175	
atg atc ggt gtg aaa tgg ttt gcg gag atg gag ttc tgg ttt gcg ctt	576
Met Ile Gly Val Lys Trp Phe Ala Glu Met Glu Phe Trp Phe Ala Leu	

180	185	190	
att aaa gtg ctc gcc att gtg acc ttc ttg gtc gtg ggt aca gtg ttc			624
Ile Lys Val Leu Ala Ile Val Thr Phe Leu Val Val Gly Thr Val Phe			
195	200	205	
ctc ggt agt ggt cag ccg ctg gat ggc aac acc act ggc ttt cat tta			672
Leu Gly Ser Gly Gln Pro Leu Asp Gly Asn Thr Thr Gly Phe His Leu			
210	215	220	
atc acc gat aat ggc ggc ttc ttc ccc ccc ggt ttg ctg acc gag ctg			720
Ile Thr Asp Asn Gly Gly Phe Phe Pro His Gly Leu Leu Pro Ala Leu			
225	230	235	240
gtg ttg att cag ggc gla gbg ltt gct ttt gcc tcc att gaa atg gtg			768
Val Leu Ile Gln Gly Val Val Phe Ala Phe Ala Ser Ile Glu Met Val			
245	250	255	
ggt aca gct gcc gga gaa tgt aaa gat ccg cag acc atg gtg cct aaa			816
Gly Thr Ala Ala Gly Glu Cys Lys Asp Pro Gln Thr Met Val Pro Lys			
260	265	270	
gcc att aac agt gtg att tgg cgt att ggc ctg ttt tac gtc ggc tcc			864
Ala Ile Asn Ser Val Ile Trp Arg Ile Gly Leu Phe Tyr Val Gly Ser			
275	280	285	
gtg gtg ttg ctg gtt atg tta ttg ccg tgg agc gcg tat cag ccg ggg			912
Val Val Leu Leu Val Met Leu Leu Pro Trp Ser Ala Tyr Gln Ala Gly			
290	295	300	
caa agc ccg ltc gbg aag ttt ttc tct aaa ctg ggt gtg caa tat atc			960
Gln Ser Pro Phe Val Thr Phe Phe Ser Lys Leu Gly Val Pro Tyr Ile			
305	310	315	320
ggc agc att atg aac att gtg gtg ctg acc gct gcc ctc tcc agc ctg			1008
Gly Ser Ile Met Asn Ile Val Val Leu Thr Ala Ala Leu Ser Ser Leu			
325	330	335	
aat tca ggt ctg tac tgc acc gga cgt att ctg ccg tca atg gcg atg			1056
Asn Ser Gly Leu Tyr Cys Thr Gly Arg Ile Leu Arg Ser Met Ala Met			
340	345	350	

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ggc ggt tcc gcc ccg agt ttt atg gcg aaa atg agt cgt cag cat gtg	1104
Gly Gly Ser Ala Pro Ser Phe Met Ala Lys Met Ser Arg Gln His Val	
355 360 365	
ccg tat gcc ggg atc ctg gcg aca cta gtt gtg tat gtc gtc gcc gta	1152
Pro Tyr Ala Gly Ile Leu Ala Thr Leu Val Val Tyr Val Val Gly Val	
370 375 380	
ttc ctc aac tat ctg gtg ccg tcg cgc gta ttt gag att gtg ttg aac	1200
Phe Leu Asn Tyr Leu Val Pro Ser Arg Val Phe Glu Ile Val Leu Asn	
385 390 395 400	
ttc gcg tcg ctg gga atc atc gct tca tcg ccg ttt atc atc gtg tgc	1248
Phe Ala Ser Leu Gly Ile Ile Ala Ser Trp Ala Phe Ile Ile Val Cys	
405 410 415	
cag atg cgc ctg cgt aac gcg att aaa gaa gcc aac gcc gcc gat gtc	1296
Gln Met Arg Leu Arg Lys Ala Ile Lys Glu Gly Lys Ala Ala Asp Val	
420 425 430	
agt ttt aaa ctg cct gcc gcg ccc ttc act tcc tgg ctg aca tta ctg	1344
Ser Phe Lys Leu Pro Gly Ala Pro Phe Thr Ser Trp Leu Thr Leu Leu	
435 440 445	
ttt tta ctg agt gcc att gcg ctg atg gcg ttc gat tac ccg aac gcc	1392
Phe Leu Leu Ser Val Leu Val Leu Met Ala Phe Asp Tyr Pro Asn Gly	
450 455 460	
act tac act atc gcg gcc ctg ccg att atc ggt att ttg ctg gtt ata	1440
Thr Tyr Thr Ile Ala Ala Leu Pro Ile Ile Gly Ile Leu Leu Val Ile	
465 470 475 480	
ggc tgg ttt ggt gtg cgc aaa cgc gtt gct gaa att caa agc act gcg	1488
Gly Trp Phe Gly Val Arg Lys Arg Val Ala Glu Ile His Ser Thr Ala	
485 490 495	
cca gtc gtc gag gaa gat gaa gaa aaa ccg gaa att gtg ttt aag cct	1536
Pro Val Val Glu Glu Asp Glu Glu Lys Gln Glu Ile Val Phe Lys Pro	
500 505 510	
gaa acg gcg agt taa	1551
Glu Thr Ala Ser	

515

<210> 262

<211> 516

<212> PRT

<213> Escherichia coli

<400> 262

Leu Phe Met Ala Thr Tyr Met Thr Phe Ser Leu Lys Gln Ser Gly Arg
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Ala Met Ser Lys His Asp Thr Asp Thr Ser Asp Gln His Ala Ala Lys
20 25 30

Arg Arg Trp Leu Asn Ala His Glu Glu Gly Tyr His Lys Ala Met Gly
35 40 45

Asn Arg Gln Val Gln Met Ile Ala Ile Gly Gly Ala Ile Gly Thr Gly
50 55 60

Leu Phe Leu Gly Ala Gly Ala Arg Leu Gln Met Ala Gly Pro Ala Leu
65 70 75 80

Ala Leu Val Tyr Leu Ile Cys Gly Leu Phe Ser Phe Phe Ile Leu Arg
85 90 95

Ala Leu Gly Glu Leu Val Leu His Arg Pro Ser Ser Gly Ser Phe Val
100 105 110

Ser Tyr Ala Arg Glu Phe Leu Gly Glu Lys Ala Ala Tyr Val Ala Gly
115 120 125

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Trp Met Tyr Phe Ile Asn Trp Ala Met Thr Gly Ile Val Asp Ile Thr
130 135 140

Ala Val Ala Leu Tyr Met His Tyr Trp Gly Ala Phe Gly Gly Val Pro
145 150 155 160

Gln Trp Val Phe Ala Leu Ala Ala Leu Thr Ile Val Gly Thr Met Asn
165 170 175

Met Ile Gly Val Lys Trp Phe Ala Gln Met Gln Phe Trp Phe Ala Leu
180 185 190

Ile Lys Val Leu Ala Ile Val Thr Phe Leu Val Val Gly Thr Val Phe
195 200 205

Leu Gly Ser Gly Gln Pro Leu Asp Gly Asn Thr Thr Gly Phe His Leu
210 215 220

Ile Thr Asp Asn Gly Gly Phe Phe Pro His Gly Leu Leu Pro Ala Leu
225 230 235 240

Val Leu Ile Gln Gly Val Val Phe Ala Phe Ala Ser Ile Gln Met Val
245 250 255

Gly Thr Ala Ala Gly Gln Cys Lys Asp Pro Gln Thr Met Val Pro Lys
260 265 270

Ala Ile Asn Ser Val Ile Trp Arg Ile Gly Leu Phe Tyr Val Gly Ser
275 280 285

Val Val Leu Leu Val Met Leu Leu Pro Trp Ser Ala Tyr Gln Ala Gly
290 295 300

Gln Ser Pro Phe Val Thr Phe Phe Ser Lys Leu Gly Val Pro Tyr Ile
305 310 315 320

Gly Ser Ile Met Asn Ile Val Val Leu Thr Ala Ala Leu Ser Ser Leu
325 330 335

Asn Ser Gly Leu Tyr Cys Thr Gly Arg Ile Leu Arg Ser Met Ala Met
340 345 350

Gly Gly Ser Ala Pro Ser Phe Met Ala Lys Met Ser Arg Gln His Val
355 360 365

Pro Tyr Ala Gly Ile Leu Ala Thr Leu Val Val Tyr Val Val Gly Val
370 375 380

Phe Leu Asn Tyr Leu Val Pro Ser Arg Val Phe Glu Ile Val Leu Asn
385 390 395 400

Phe Ala Ser Leu Gly Ile Ile Ala Ser Trp Ala Phe Ile Ile Val Cys
405 410 415

Gln Met Arg Leu Arg Lys Ala Ile Lys Glu Gly Lys Ala Ala Asp Val
420 425 430

Ser Phe Lys Leu Pro Gly Ala Pro Phe Thr Ser Trp Leu Thr Leu Leu
435 440 445

Phe Leu Leu Ser Val Leu Val Leu Met Ala Phe Asp Tyr Pro Asn Gly
450 455 460

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Thr Tyr Thr Ile Ala Ala Leu Pro Ile Ile Gly Ile Leu Leu Val Ile
 465 470 475 480

Gly Trp Phe Gly Val Arg Lys Arg Val Ala Glu Ile His Ser Thr Ala
 485 490 495

Pro Val Val Glu Glu Asp Glu Glu Lys Gln Glu Ile Val Phe Lys Pro
 500 505 510

Glu Thr Ala Ser
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<210> 263

<211> 681

<212> DNA

<213> Escherichia coli

<320>

<321> CDS

<322> (1)..(681)

<400> 263

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 1 5 10 15

tgg ctg aag aac gat att att cgc ggt aat ttt caa ccc gat gaa aaa 96
 Trp Leu Lys Asn Asp Ile Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys
 20 25 30

tta cga atg agt ttg ctg aca tgg cgt tat gaa ctt ggc gtt ggg ccc 144
 Leu Arg Met Ser Leu Leu Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro
 35 40 45

tta cgg gaa gct ctt tgg caa ctg gtc gcg gaa cgg ctg gtc aag gtc 192
 Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val
 50 55 60

gtg aat cca aaa ggg tat cgg gtg gcg tct atg tca gag cag gag ctg	240
Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln Glu Leu	
65 70 75 80	
ctc gat att ttc gac gcc cgc gcc aat atg caa gcg atg tta gtc aqt	288
Leu Asp Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Ser	
85 90 95	
ctg gcg att gcc cgc ggt gcc gat gag tgg gag gca gac gtt ctc gca	336
Leu Ala Ile Ala Arg Gly Gly Asp Glu Trp Glu Ala Asp Val Leu Ala	
100 105 110	
caa gcg cat ctg ctg agt aag ctt gag gcc tgt gac gcc agc gag aaa	384
Lys Ala His Leu Leu Ser Lys Leu Glu Ala Cys Asp Ala Ser Glu Lys	
115 120 125	
atg ctt gat gag tgg gat ctg cgt cat cag gcg ttt cat acg gca att	432
Met Leu Asp Glu Trp Asp Leu Arg His Glu Ala Phe His Thr Ala Ile	
130 135 140	
gtg gcg gcc tgc ggt tct cac tat ttg ctg caa atg cgt gaa cgg ttg	480
Val Ala Gly Cys Gly Ser His Tyr Leu Leu Glu Met Arg Glu Arg Leu	
145 150 155 160	
ttt gat ctg gcg gcg cgt tat cga ttt atc tgg ctg cgg cga acg gtg	528
Phe Asp Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val	
165 170 175	
ctt tcc gtg gaa atg ctg gag gat aaa cac gat cag cac cag acc ctg	576
Leu Ser Val Glu Met Leu Glu Asp Pys His Asp Glu His Glu Thr Leu	
180 185 190	
act gcg gcg gta ctg gcg cga gat acc gcg cgc gcc agt gag tta atg	624
Thr Ala Ala Val Leu Ala Arg Asp Thr Ala Arg Ala Ser Glu Leu Met	
195 200 205	
cgc cag cat tta ctg acg cca att ccc att atc cag cag gcg atg gct	672
Arg Gln His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala Met Ala	
210 215 220	
ggc aat caa	681

Gly Asn

225

<210> 264

<211> 226

<212> FRT

<213> Escherichia coli

<400> 264

Met Ile Arg Ser His Thr Met Thr Ala Thr Ser Leu Asp Gly Tyr Arg
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Trp Leu Lys Asn Asp Ile Ile Arg Gly Asn Phe Gln Pro Asp Glu Lys
20 25 30

Leu Arg Met Ser Leu Leu Thr Ser Arg Tyr Ala Leu Gly Val Gly Pro
35 40 45

Leu Arg Glu Ala Leu Ser Gln Leu Val Ala Glu Arg Leu Val Thr Val
50 55 60

Val Asn Gln Lys Gly Tyr Arg Val Ala Ser Met Ser Glu Gln Glu Leu
65 70 75 80

Leu Asp Ile Phe Asp Ala Arg Ala Asn Met Glu Ala Met Leu Val Ser
85 90 95

Leu Ala Ile Ala Arg Gly Gly Asp Glu Trp Glu Ala Asp Val Leu Ala
100 105 110

Lys Ala His Leu Leu Ser Lys Leu Glu Ala Cys Asp Ala Ser Glu Lys
115 120 125

Met Leu Asp Glu Trp Asp Leu Arg His Gln Ala Phe His Thr Ala Ile
 130 135 140

Val Ala Gly Cys Gly Ser His Tyr Leu Leu Gln Met Arg Glu Arg Leu
 145 150 155 160

Phe Asp Leu Ala Ala Arg Tyr Arg Phe Ile Trp Leu Arg Arg Thr Val
 165 170 175

Leu Ser Val Glu Met Leu Glu Asp Lys His Asp Gln His Gln Thr Leu
 180 185 190

Thr Ala Ala Val Leu Ala Arg Asp Thr Ala Arg Ala Ser Glu Leu Met
 195 200 205

Arg Gln His Leu Leu Thr Pro Ile Pro Ile Ile Gln Gln Ala Met Ala
 210 215 220

Gly Asn
 225

<210> 265
 <211> 1152
 <212> DNA
 <213> Escherichia coli

<220>
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 <222> (1)..(1152)

<400> 265
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1	5	10	15	
ggg ggt gtt ggg gct tta acc gat gag gtg aac cgc cgt ggt tat cag	96			
Gly Ala Val Gly Ala Leu Thr Asp Glu Val Lys Arg Arg Gly Tyr Gln				
20	25	30		
aag gag ctg atc gtc acc gat aac acg ctg gtg caa tgc ggc gtg gtg	144			
Lys Ala Leu Ile Val Thr Asp Lys Thr Leu Val Gln Cys Gly Val Val				
35	40	45		
ggg aaa gtg acc gat aag atg gat gct gca ggg ctg gca tgg ggg att	192			
Ala Lys Val Thr Asp Lys Met Asp Ala Ala Gly Leu Ala Trp Ala Ile				
50	55	60		
tac gac ggc gta gtg ccc aac cca aca att act gtc gtc aac gaa ggg	240			
Tyr Asp Gly Val Val Pro Asn Pro Thr Ile Thr Val Val Lys Gln Gly				
65	70	75	80	
ctc ggt gta ttc cag aat agc ggc gcc gat tac ctg atc gct att ggt	288			
Leu Gly Val Phe Gln Asn Ser Gly Ala Asp Tyr Leu Ile Ala Ile Gly				
85	90	95		
ggg ggt tct cca cag gat act tct aaa ggg att ggc att atc agc aac	336			
Gly Gly Ser Pro Gln Asp Thr Cys Lys Ala Ile Gly Ile Ile Ser Asn				
100	105	110		
aac ccg gag ttt gcc gat gtg cgt agc ctg gaa ggg ctt tcc cag acc	384			
Asn Pro Glu Phe Ala Asp Val Arg Ser Leu Glu Gly Leu Ser Pro Thr				
115	120	125		
aat aaa ccc agt gta ccg atc ctg gca att cct acc acc gca cct acc	432			
Asn Lys Pro Ser Val Pro Ile Leu Ala Ile Pro Thr Thr Ala Gly Thr				
130	135	140		
ggg gca gaa gtg acc att aac tac gtg atc act gac gaa gag aac cgg	480			
Ala Ala Glu Val Thr Ile Asn Tyr Val Ile Thr Asp Glu Glu Lys Arg				
145	150	155	160	
cgc aag ttt gtt tgc gtt gat ccg cat gat aac ccg cag gtg ggg ttt	528			
Arg Lys Phe Val Cys Val Asp Pro His Asp Ile Pro Gln Val Ala Phe				
165	170	175		

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att gac gct gac atg atg gat ggt atg cct cca gag ctg aaa gct gcg	576
Ile Asp Ala Asp Met Met Asp Gly Met Pro Pro Ala Leu Lys Ala Ala	
130 135 140	
acg ggt gtc gat gcg ctg acc cat gct att gag ggg tat att acc cgt	624
Thr Gly Val Asp Ala Leu Thr His Ala Ile Glu Gly Tyr Ile Thr Arg	
195 200 205	
ggc gcg tgg gcg cta acc gat gca ctg cac att aaa gcg att gaa atc	672
Gly Ala Trp Ala Leu Thr Asp Ala Leu His Ile Lys Ala Ile Glu Ile	
210 215 220	
att gct ggg gcg ctg cga gga tog gtt gct ggt gat aag gat gcc gga	720
Ile Ala Gly Ala Leu Arg Gly Ser Val Ala Gly Asp Lys Asp Ala Gly	
225 230 235 240	
gaa gaa atg gcg ctg ggg cag tat gtt gcg ggt atg ggc ttc tog aat	768
Glu Glu Met Ala Leu Gly Glu Tyr Val Ala Gly Met Gly Phe Ser Asn	
245 250 255	
gtt ggg tta ggg ttg atg cat ggt atg gcg cct cca ctg ggc gcg ttt	816
Val Gly Leu Gly Leu Val His Gly Met Ala His Pro Leu Gly Ala Phe	
260 265 270	
tat aac act cca cac ggt gtt gcg aac gcc atc ctg tta ccg cat gtc	864
Tyr Asn Thr Pro His Gly Val Ala Asn Ala Ile Leu Leu Pro His Val	
275 280 285	
atg cgt tat aac gct gac ttt acc ggt gag aag tac cgc gat atc gcg	912
Met Arg Tyr Asn Ala Asp Phe Thr Gly Glu Lys Tyr Arg Asp Ile Ala	
290 295 300	
cgc gtt atg ggc gtg aaa gtg gaa ggt atg agc ctg gaa gag gcg cgt	960
Arg Val Met Gly Val Lys Val Glu Gly Met Ser Leu Glu Glu Ala Arg	
305 310 315 320	
aat gcc gct gtt gaa gcg ctg ttt gct ctg aac cgt gat gtc ggt att	1008
Asn Ala Ala Val Glu Ala Val Phe Ala Leu Asn Arg Asp Val Gly Ile	
325 330 335	
ccg cca cat ttg cgt gat gtt ggt gta cgc aag gaa gac att ccg gca	1056
Pro Pro His Leu Arg Asp Val Gly Val Arg Lys Glu Asp Ile Pro Ala	

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340	345	350	
ctg gcg cag gcg gca ctg gat gat gtc tgt acc ggt ggc aac ccg cgt			1134
Leu Ala Gln Ala Ala Leu Asp Asp Val Cys Thr Gly Gly Asn Pro Arg			
355	360	365	
gaa gca acg ctt gag gat att cta gag ctt tac cat acc gcc tcg taa			1152
Glu Ala Thr Leu Glu Asp Ile Val Glu Leu Tyr His Thr Ala Trp			
370	375	380	
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Gly Ala Val Gly Ala Leu Thr Asp Gly Val Lys Arg Arg Gly Tyr Gln			
20	25	30	
Lys Ala Leu Ile Val Thr Asp Lys Thr Leu Val Gln Cys Gly Val Val			
35	40	45	
Ala Lys Val Thr Asp Lys Met Asp Ala Ala Gly Leu Ala Trp Ala Ile			
50	55	60	
Tyr Asp Gly Val Val Pro Asn Pro Thr Ile Thr Val Val Lys Glu Gly			
65	70	75	80
Leu Gly Val Phe Gln Asn Ser Gly Ala Asp Tyr Leu Ile Ala Ile Gly			
85	90	95	

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Gly Gly Ser Pro Gln Asp Thr Cys Lys Ala Ile Gly Ile Ile Ser Asn
100 105 110

Asn Pro Glu Phe Ala Asp Val Arg Ser Leu Glu Gly Leu Ser Pro Thr
115 120 125

Asn Lys Pro Ser Val Pro Ile Leu Ala Ile Pro Thr Thr Ala Gly Thr
130 135 140

Ala Ala Glu Val Thr Ile Asn Tyr Val Ile Thr Asp Glu Glu Lys Arg
145 150 155 160

Arg Lys Phe Val Cys Val Asp Pro His Asp Ile Pro Gln Val Ala Phe
165 170 175

Ile Asp Ala Asp Met Met Asp Gly Met Pro Pro Ala Leu Lys Ala Ala
180 185 190

Thr Glu Val Asp Ala Leu Thr His Ala Ile Glu Gly Tyr Ile Thr Arg
195 200 205

Gly Ala Trp Ala Leu Thr Asp Ala Leu His Ile Lys Ala Ile Glu Ile
210 215 220

Ile Ala Gly Ala Leu Arg Gly Ser Val Ala Gly Asp Lys Asp Ala Gly
225 230 235 240

Glu Glu Met Ala Leu Gly Gln Tyr Val Ala Gly Met Gly Phe Ser Asn
245 250 255

Val Gly Leu Gly Leu Val His Gly Met Ala His Pro Leu Gly Ala Phe
260 265 270

Tyr Asn Thr Pro His Gly Val Ala Asn Ala CLe Leu Leu Pro His Val
 275 280 285

Met Arg Tyr Asn Ala Asp Phe Thr Gly Glu Lys Tyr Arg Asp Ile Ala
 290 295 300

Arg Val Met Gly Val Lys Val Glu Gly Met Ser Leu Glu Glu Ala Arg
 305 310 315 320

Asn Ala Ala Val Glu Ala Val Phe Ala Leu Asn Arg Asp Val Gly Ile
 325 330 335

Pro Pro His Leu Arg Asp Val Gly Val Arg Lys Glu Asp Ile Pro Ala
 340 345 350

Leu Ala Glu Ala Ala Leu Asp Asp Val Cys Thr Gly Gly Asn Pro Arg
 355 360 365

Glu Ala Thr Leu Glu Asp Ile Val CLe Leu Tyr His Thr Ala Thr
 370 375 380

<210> 267

<211> 1197

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1) .. (1197)

<400> 267

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6440762

Met	Asn	Tyr	Arg	Tyr	Arg	Ala	Met	Thr	Gln	Asp	Gly	Gln	Lys	Leu	Gln				
1				5					10						15				
ggg	atc	att	gat	gct	aac	gac	gaa	cgt	cag	gca	cca	ctg	egg	ctg	cgt				95
Gly	Ile	Ile	Asp	Ala	Asn	Asp	Glu	Arg	Gln	Ala	Arg	Leu	Arg	Leu	Arg				
			20					25					30						
gaa	gaa	ggg	ctt	ttc	ctg	ctg	gat	att	cgc	ccc	caa	aaa	agt	tgc	gga				144
Glu	Glu	Gly	Leu	Phe	Leu	Leu	Asp	Ile	Arg	Pro	Gln	Lys	Ser	Ser	Gly				
			35				40						45						
gta	aaa	aca	cgt	cgc	cag	agg	atc	agc	cat	agt	gaa	ctg	acg	ctt	ttc				192
Val	Lys	Thr	Arg	Arg	Pro	Arg	Ile	Ser	His	Ser	Gln	Leu	Thr	Leu	Phe				
	50					55					60								
acc	egg	cag	ttg	gca	acc	tta	agc	gca	ggg	gca	tta	ccc	ctg	gaa	gag				240
Thr	Arg	Gln	Leu	Ala	Thr	Leu	Ser	Ala	Ala	Ala	Leu	Pro	Leu	Glu	Glu				
65				70					75					80					
agc	ctt	gac	gta	atc	ggg	caa	caa	agc	agt	aat	aaa	cga	ctg	ggg	gac				288
Ser	Leu	Ala	Val	Ile	Gly	Gln	Gln	Ser	Ser	Asn	Lys	Arg	Leu	Gly	Asp				
			85					90					95						
gtg	tta	aat	cag	gta	cgc	agc	gac	atc	ctt	gaa	ggg	cat	ccc	ctt	tcc				336
Val	Leu	Asn	Gln	Val	Arg	Ser	Ala	Ile	Leu	Glu	Gly	His	Pro	Leu	Ser				
			100					105					110						
gat	gca	tta	cag	cat	ttt	ccc	acg	ctt	ttc	gat	cag	ctc	tat	cgt	acc				384
Asp	Ala	Leu	Gln	His	Phe	Pro	Thr	Leu	Phe	Asp	Ser	Leu	Tyr	Arg	Thr				
		115				120						125							
ctg	gta	aaa	ggg	ggc	gaa	aag	agc	ggg	ctg	ctg	gac	ccg	gtg	ttg	gaa				432
Leu	Val	Lys	Ala	Gly	Glu	Lys	Ser	Gly	Leu	Leu	Ala	Pro	Val	Leu	Glu				
	130					135					140								
aag	ctg	gct	gat	tac	aat	gaa	aac	egg	cag	aaa	atc	cgc	agc	aag	ctc				480
Lys	Leu	Ala	Asp	Tyr	Asn	Glu	Asn	Arg	Gln	Lys	Ile	Arg	Ser	Lys	Leu				
145					150				155					160					
att	cag	tca	ctg	atc	tac	ccc	tgt	atg	ctc	act	acg	gtg	gag	att	ggg				528
Ile	Gln	Ser	Leu	Ile	Tyr	Pro	Cys	Met	Leu	Thr	Thr	Val	Ala	Ile	Gly				
			165					170						175					

gtc gtc att att ctc ctc act gct gtc gtg ccc aaa att acc gaa cag	576
val val ile ile leu leu thr ala val val pro lys ile thr glu gln	
180 185 190	
ttc gtg cat atg aag cag caa ctg cgg ctg agt acn cgc att ctt tta	624
phe val his met lys gln gln leu pro leu ser thr arg ile leu leu	
195 200 205	
ggc ctg agc gac acg ttg caa cgt acc ggc cgg acc tta tta ggc acc	672
gly leu ser asp thr leu gln arg thr gly pro thr leu leu ala thr	
210 215 220	
gtg ttt att gtc gct gta ggt ttc tgg ctc tgg tta aaa cgc ggc aat	720
val phe ile val ala val gly phe trp leu trp leu lys arg gly asn	
225 230 235 240	
aac cgc cac cgt ttt cat gcc atg ttg ctg cgc gtt ggc ctc atc ggc	768
asn arg his arg phe his ala met leu leu arg val ala leu ile gly	
245 250 255	
cgc ctg att tgc gcc att aac agc gca cgc tat ctc cgc act tta agt	816
pro leu ile cys ala ile asn ser ala arg tyr leu arg thr leu ser	
260 265 270	
att ttg caa tcc agc ggc gtc cct ctg ctg gat ggg atg aat ttg tcc	864
ile leu gln ser ser gly val pro leu leu asp gly met asn leu ser	
275 280 285	
acc gaa agc ctc aac aac ctc gaa att cgc cag cgt ctg gca aat ggc	912
thr glu ser leu asn asn leu glu ile arg gln arg leu ala asn ala	
290 295 300	
gca gag aac gtt cgc cag ggt aac agc att cat ctt tgc ctg gaa caa	960
ala glu asn val arg gln gly asn ser ile his leu ser leu glu gln	
305 310 315 320	
acc gca att ttc cgg cgg atg atg ctc tac atg gtg gcc tct ggc gaa	1008
thr ala ile phe pro pro met met leu tyr met val ala ser gly glu	
325 330 335	
aaa agc ggg cag ctc ggc acc tta atg gtc aga gcc gca gat aac cag	1056

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Lys Ser Gly Gln Leu Gly Thr Leu Met Val Arg Ala Ala Asp Asn Gln
 340 345 350

Gag acg ctc caa caa aat cgg atc gcc tta acg ctc tcc atc ttc gag 1164
 Glu Thr Leu Gln Gln Asn Arg ile Ala Leu Thr Leu Ser ile Phe Glu
 355 360 365

cca gca ctc att att acg atg gca ctg atc gtc cgg ttt att gtc gtg 1152
 Pro Ala Leu ile ile Thr Met Ala leu ile Val Leu Phe ile Val Val
 370 375 380

cag gta ctc caa cct ctt ctt caa ctt aac tca atg att aat taa 1197
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 385 390 395

<210> 268

<211> 398

<212> PRT

<213> Escherichia coli

<400> 268

Met Asn Tyr Arg Tyr Arg Ala Met Thr Gln Asp Gly Gln Lys Leu Gln
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Gly ile ile Asp Ala Asn Asp Glu Arg Gln Ala Arg Leu Arg leu Arg
 20 25 30

Glu Glu Gly Leu Phe leu Leu Asp ile Arg Pro Gln Lys Ser Ser Gly
 35 40 45

Val Lys Thr Arg Arg Pro Arg ile Ser His Ser Glu Leu Thr Leu Phe
 50 55 60

Thr Arg Gln Leu Ala Thr Leu Ser Ala Ala Ala Leu Pro Leu Glu Glu
 65 70 75 80

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Ser Leu Ala Val Ile Gly Gln Gln Ser Ser Asn Pys Arg Leu Gly Asp
85 90 95

Val Leu Asn Gln Val Arg Ser Ala Ile Leu Glu Gly His Pro Leu Ser
100 105 110

Asp Ala Leu Gln His Phe Pro Thr Leu Phe Asp Ser Leu Tyr Arg Thr
115 120 125

Leu Val Lys Ala Gly Glu Lys Ser Cys Leu Leu Ala Pro Val Leu Glu
130 135 140

Lys Leu Ala Asp Tyr Asn Glu Asn Arg Gln Lys Ile Arg Ser Lys Leu
145 150 155 160

Ile Gln Ser Leu Ile Tyr Pro Cys Met Leu Thr Thr Val Ala Ile Gly
165 170 175

Val Val Ile Ile Leu Leu Thr Ala Val Val Pro Lys Ile Thr Glu Gln
180 185 190

Phe Val His Met Lys Gln Gln Asn Pro Leu Ser Thr Arg Ile Leu Leu
195 200 205

Gly Leu Ser Asp Thr Leu Gln Arg Thr Gly Pro Thr Leu Leu Ala Thr
210 215 220

Val Phe Ile Val Ala Val Gly Phe Trp Leu Trp Leu Lys Arg Gly Asn
225 230 235 240

Asn Arg His Arg Phe His Ala Met Leu Leu Arg Val Ala Leu Ile Gly

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245

250

255

Pro Leu Ile Cys Ala Ile Asn Ser Ala Arg Tyr Leu Arg Thr Leu Ser
260 265 270

Ile Leu Gln Ser Ser Gly Val Pro Leu Leu Asp Gly Met Asn Leu Ser
275 280 285

Thr Glu Ser Leu Asn Asn Leu Glu Ile Arg Gln Arg Leu Ala Asn Ala
290 295 300

Ala Glu Asn Val Arg Gln Gly Asn Ser Ile His Leu Ser Leu Glu Gln
305 310 315 320

Thr Ala Ile Phe Pro Pro Met Met Leu Tyr Met Val Ala Ser Gly Glu
325 330 335

Lys Ser Gly Gln Leu Gly Thr Leu Met Val Arg Ala Ala Asp Asn Gln
340 345 350

Glu Thr Leu Gln Gln Asn Arg Ile Ala Leu Thr Leu Ser Ile Phe Glu
355 360 365

Pro Ala Leu Ile Ile Thr Met Ala Leu Ile Val Leu Phe Ile Val Val
370 375 380

Ser Val Leu Gln Pro Leu Leu Gln Leu Asn Ser Met Ile Asn
385 390 395

<210> 269

<211> 660

<212> DNA

649762

<213> Escherichia coli

42202

<221> CDS

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3 5 10 15

acc cat aag ctg ctg cgt aat acc tat ttt ctg ctg agt ctg acg ctg 96
Thr His Lys Val Leu Arg Asn Thr Tyr Phe Leu Leu Ser Leu Thr Leu
20 35 30

gac ttt tog gcg att acc gca act ggc agt acg gtg ctg atg ctg cca 144
Ala Phe Ser Ala Ile Thr Ala Thr Ala Ser Thr Val Leu Met Leu Pro
35 40 45

tat cag ggt ctg att ctg acg ctg gtg ggt atg tat ggt ttg atg ttc 192
 Ser Pro Gly Leu Ile Leu Thr Leu Val Gly Met Tyr Gly Leu Met Phe
 50 55 60

ctg acc tat caa acg gcg aat aag cag acc ggg att atc tcc gca ttc 240
 leu thr tyr lys thr ala asn lys pro thr gly ile ile ser ala phe
 65 70 75 80

gac ttt acc ggt ttt ctg ggt tat atc ctc gga cct att ctg aac acc 288
Ala Phe Thr Gly Phe Leu Gly Tyr Phe Leu Gly Pro Ile Leu Asn Thr
85 90 95

tat ctg tct gcc gga atg ggt gac gta atc gct atg gca ctg ggc gga 335
Tyr Leu Ser Ala Gly Met Gly Asp Val Ile Ala Met Ala Leu Gly Gly
103 105 110

acg gag tta gtg ttc ttc tgc tgc tct gca tat gtg ctg acc acc cgc 384
Thr Ala Leu Val Phe Phe Cys Cys Ser Ala Tyr Val Leu Thr Thr Arg
115 120 125

aaa gat atg tgg ttc ctc ggc ggt atg ctg atg gag ggt att gtg gtg 432
Lys Asp Met Ser Phe Leu Gly Gly Met Leu Met Ala Gly Ile Val Val

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130	135	140	
gtg ctg att ggt atg gtt ggg aat atc ttc ctg cag cgg cct gct ctg			483
Val Leu Ile Gly Met Val Ala Asn Ile Phe Leu Glu Leu Pro Ala Leu			
145	150	155	160
cat ctg ggg atc agc ggg gtc ttc att ctg atc tcc tct ggc gct atc			528
His Leu Ala Ile Ser Ala Val Phe Ile Leu Ile Ser Ser Gly Ala Ile			
	165	170	175
ttg ttt gaa acc agc aac atc att cat ggc ggt gag acg aac tat att			576
Leu Phe Glu Thr Ser Asn Ile Ile His Gly Gly Glu Thr Asn Tyr Ile			
	180	185	190
cgt gcc acg gtt agc ctg tat gtt tgg ctg tac aac atc ttc gtc agc			624
Arg Ala Thr Val Ser Leu Tyr Val Ser Leu Tyr Asn Ile Phe Val Ser			
	195	200	205
ctg ctg agc att ctg ggc ttc gct agc cgg gat taa			660
Leu Leu Ser Ile Leu Gly Phe Ala Ser Arg Asp			
210	215		
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<211> 219			
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Thr His Lys Val Leu Arg Asn Thr Tyr Phe Leu Leu Ser Leu Thr Leu			
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Ala Phe Ser Ala Ile Thr Ala Thr Ala Ser Thr Val Leu Met Leu Pro			
35	40	45	

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Ser Pro Gly Leu Ile Leu Thr Leu Val Gly Met Tyr Gly Leu Met Phe
50 55 60

Leu Thr Tyr Lys Thr Ala Asn Tyr Pro Thr Gly Ile Ile Ser Ala Phe
65 70 75 80

Ala Phe Thr Gly Phe Leu Gly Tyr Ile Leu Gly Pro Ile Leu Asn Thr
85 90 95

Tyr Leu Ser Ala Gly Met Gly Asp Val Ile Ala Met Ala Leu Gly Gly
100 105 110

Thr Ala Leu Val Phe Phe Cys Cys Ser Ala Tyr Val Leu Thr Thr Arg
115 120 125

Lys Asp Met Ser Phe Leu Gly Gly Met Leu Met Ala Gly Ile Val Val
130 135 140

Val Leu Ile Gly Met Val Ala Asn Ile Phe Leu Gln Leu Pro Ala Leu
145 150 155 160

His Leu Ala Ile Ser Ala Val Phe Ile Leu Ile Ser Ser Gly Ala Ile
165 170 175

Leu Phe Glu Thr Ser Asn Ile Ile His Gly Gly Glu Thr Asn Tyr Ile
180 185 190

Arg Ala Thr Val Ser Leu Tyr Val Ser Leu Tyr Asn Ile Phe Val Ser
195 200 205

Leu Leu Ser Ile Leu Gly Phe Ala Ser Arg Asp
210 215

<210> 271
<211> 1290
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1)..(1290)

<400> 271
atg tcc aac aag ctg ttc agg tta gat gca ggc tac caa caa tac gac
48
Met Ser Asn Lys Leu Phe Arg Leu Asp Ala Gly Tyr Gln Gln Tyr Asp
1 5 10 15

tgg ggt aaa atc ggc tct tct tca gct gtc gct caa ttt gct gcc cat
96
Trp Gly Lys Ile Gly Ser Ser Ser Ala Val Ala Gln Phe Ala Ala His
20 25 30

tct gac ccc tct gtt caa att gaa caa gat aaa caa tat gca gag tta
144
Ser Asp Pro Ser val Gln ile Glu Gln Asp Lys Pro Tyr Ala Glu Leu
35 40 45

tgg atg ggt acc cac agc aag atg cct tcc tac aac cat gag tct aag
192
Trp Met Gly Thr His Ser Lys Met Pro Ser Tyr Asn His Glu Ser Lys
50 55 60

gaa tcc ctg aga gat atc atc tcc aag aac ccc tct gcc atg tta ggt
240
Glu Ser Leu Arg Asp Ile Ile Ser Lys Asn Pro Ser Ala Met Leu Gly
65 70 75 80

aag gac att att gat aag ttc cac gcc aca aat gaa tly ccc ttc ctt
288
Lys Asp ile ile Asp Lys Phe His Ala Thr Asn Glu Leu Pro Phe Leu
85 90 95

653/762

ttc aaa gtl ttg tcc att gaa aaa glt tgg tct att caa gca cat ccc
336

Phe Lys Val Leu Ser Ile Glu Lys Val Leu Ser Ile Gln Ala His Pro
100 105 110

gac aaa gcc ttg ggt aaa ata ttg cac gct caa gat cct aag aac tat
384

Asp Lys Ala Leu Gly Lys Ile Leu His Ala Gln Asp Pro Lys Asn Tyr
115 120 125

cct gat gat aat cac aaa cct gaa atg gcc atc gct gtg act gac ttt
432

Pro Asp Asp Asn His Lys Pro Glu Met Ala Ile Ala Val Thr Asp Phe
130 135 140

gaa ggt ttc tgc ggg ttc aaa cct ttg caa gag att gca gat gaa ttg
480

Glu Gly Phe Cys Gly Phe Lys Pro Leu Gln Glu Ile Ala Asp Glu Leu
145 150 155 160

aaa cgt att cct gaa tta cgc aac att gtt ggt gaa gaa act tcc agg
528

Lys Arg Ile Pro Glu Leu Arg Asn Ile Val Gly Glu Glu Thr Ser Arg
165 170 175

aat ttt att gag aac att caa cct tct gct cag aac ggt tcc caa gaa
576

Asn Phe Ile Glu Asn Ile Gln Pro Ser Ala Gln Lys Gly Ser Pro Glu
180 185 190

gat gag caa aac aaa aag cta ttg caa gct ctc ttc agc agg gtc atg
624

Asp Glu Gln Asn Lys Lys Leu Leu Gln Ala Val Phe Ser Arg Val Met
195 200 205

aac gct tgg gat gac aaa atc aag att caa gct cgc tcc ttg gtc gaa
672

Asn Ala Ser Asp Asp Lys Ile Lys Ile Gln Ala Arg Ser Leu Val Glu
210 215 220

aga tca aag aat tct cca tca gac ttt aac aaa cct gat tta cca gaa
720

654/762

Arg Ser Lys Asn Ser Pro Ser Asp Phe Asn Lys Pro Asp Leu Pro Glu
 225 230 235 240

tta att caa aga atg aat aaa caa ttc cct gat gac gtg ggt tgg ttt
 768

Leu Ile Gln Arg Leu Asn Lys Gln Phe Pro Asp Asp Val Gly Leu Thr
 245 250 255

tgt gga tgt tta ttg ttg aat cac tgc aga ttg aat gct ggt gaa ggc
 816

Cys Gly Cys Leu Leu Leu Asn His Cys Arg Leu Asn Ala Gly Glu Ala
 260 265 270

atc ttt tta aga gct aag gat cct cac gcc tat ata agc ggt gat atc
 864

Ile Phe Leu Arg Ala Lys Asp Pro His Ala Tyr Ile Ser Gly Asp Ile
 275 280 285

atg gaa tgt atg gct gct tct gac aac gta gtt aga gcc ggc ttc act
 912

Met Glu Cys Met Ala Ala Ser Asp Asn Val Val Arg Ala Gly Phe Thr
 290 295 300

cca aaa ttc aag gat gtt aaa aac ttg gtc tcc atg tta acc tat aca
 960

Pro Lys Phe Lys Asp Val Lys Asn Leu Val Ser Met Leu Thr Tyr Thr
 305 310 315 320

tat gat cct gtg gaa aag caa aaa atg cag cct tta aag ttc gac agg
 1038

Tyr Asp Pro Val Glu Lys Gln Lys Met Gln Pro Leu Lys Phe Asp Arg
 325 330 335

tcc tct ggt aac ggt aag tca gtt tta tat uac cct cca atc gaa gaa
 1056

Ser Ser Gly Asn Gly Lys Ser Val Leu Tyr Asn Pro Pro Ile Glu Glu
 340 345 350

ttt gct gta ttg gag act act ttt gat gag aaa ctt ggt caa agg cat
 1104

Phe Ala Val Leu Glu Thr Thr Phe Asp Glu Lys Leu Gly Gln Arg His
 355 360 365

ttt gaa ggt gtt gat ggt cca agt atc tta atc act aca aaa ggt aat
1152

Phe Glu Gly Val Asp Gly Pro Ser Ile Leu Ile Thr Thr Lys Gly Asn
370 375 380

ggt tac att aaa gca gat ggc caa aaa ttg aaa gct gaa ccc ggt ttt
1200

Gly Tyr Ile Lys Ala Asp Gly Gln Lys Leu Lys Ala Glu Pro Gly Phe
385 390 395 400

gtc ttt ttc atc gct cca cac ttg cct gtt gat ttg gaa gct gaa gat
1248

Val Phe Phe Ile Ala Pro His Leu Pro Val Asp Leu Glu Ala Glu Asp
405 410 415

gag gag ttt act acc tat aga gcc ttt gtg gaa cca aat tag
1290

Glu Ala Phe Thr Thr Tyr Arg Ala Phe Val Glu Pro Asn
420 425

<210> 372

<211> 429

<212> PRT

<213> *Zodcharymyces cerevisiae*

<400> 272

Met Ser Asn Lys Leu Phe Arg Leu Asp Ala Gly Tyr Gln Gln Tyr Asp
5 10 15

Trp Gly Lys Ile Gly Ser Ser Ser Ala Val Ala Gln Phe Ala Ala His
20 25 30

Ser Asp Pro Ser Val Gln Ile Glu Gln Asp Lys Pro Tyr Ala Glu Leu
35 40 45

Trp Met Gly Thr His Ser Lys Met Pro Ser Tyr Asn His Glu Ser Lys

50	55	60
Glu Ser Leu Arg Asp Ile Ile Ser Lys Asn Pro Ser Ala Met Leu Gly		
65	70	75
		80
Lys Asp Ile Ile Asp Lys Phe His Ala Thr Asn Gln Leu Pro Phe Leu		
	85	90
		95
Phe Lys Val Leu Ser Ile Glu Lys Val Leu Ser Ile Gln Ala His Pro		
100	105	110
Asp Lys Ala Leu Gly Lys Ile Leu His Ala Gln Asp Pro Lys Asn Tyr		
115	120	125
Pro Asp Asp Asn His Lys Pro Glu Met Ala Ile Ala Val Thr Asp Phe		
130	135	140
Glu Gly Phe Cys Gly Phe Lys Pro Leu Gln Glu Ile Ala Asp Glu Leu		
145	150	155
		160
Lys Arg Ile Pro Glu Leu Arg Asn Ile Val Gly Glu Glu Thr Ser Arg		
	165	170
		175
Asn Phe Ile Glu Asn Ile Gln Pro Ser Ala Gln Lys Gly Ser Pro Glu		
180	185	190
Asp Glu Gln Asn Lys Lys Leu Leu Gln Ala Val Phe Ser Arg Val Met		
195	200	205
Asn Ala Ser Asp Asp Lys Ile Lys Ile Gln Ala Arg Ser Leu Val Glu		
210	215	220

Arg Ser Lys Asn Ser Pro Ser Asp Phe Asn Lys Pro Asp Leu Pro Glu
225 230 235 240

Ile Ile Gln Arg Leu Asn Lys Gln Phe Pro Asp Asp Val Gly Leu Phe
245 250 255

Cys Gly Cys Ile Leu Leu Asn His Cys Arg Leu Asn Ala Gly Glu Ala
260 265 270

Ile Phe Leu Arg Ala Lys Asp Pro His Ala Tyr Ile Ser Gly Asp Ile
275 280 285

Met Glu Cys Met Ala Ala Ser Asp Asn Val Val Arg Ala Gly Phe Thr
290 295 300

Pro Lys Phe Lys Asp Val Lys Asn Leu Val Ser Met Leu Thr Tyr Thr
305 310 315 320

Tyr Asp Pro Val Glu Lys Gln Lys Met Gln Pro Leu Lys Phe Asp Arg
325 330 335

Ser Ser Gly Asn Gly Lys Ser Val Leu Tyr Asn Pro Pro Ile Glu Glu
340 345 350

Phe Ala Val Leu Glu Thr Thr Phe Asp Glu Lys Leu Gly Gln Arg His
355 360 365

Phe Glu Gly Val Asp Gly Pro Ser Ile Leu Ile Thr Thr Lys Gly Asn
370 375 380

Gly Tyr Ile Lys Ala Asp Gly Gln Lys Leu Lys Ala Glu Pro Gly Phe

385 390 395 400

Val Phe Phe Ile Ala Pro His Leu Pro Val Asn Leu Glu Ala Glu Asp
 405 410 415

Glu Ala Phe Thr Thr Tyr Arg Ala Phe Val Glu Pro Asn
 420 425

<210> 273

<211> 1539

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1539)

<400> 273

atg gta gca aca ata atg cag acg aca aca act gtg ctg acg aca gtc
 48

Met Val Ala Thr Ile Met Gln Thr Thr Thr Val Leu Thr Thr Val
 1 5 10 15

gcc gca atg tct act acc cta gca tca aat tac ata tct tgg caa gct
 96

Ala Ala Met Ser Thr Thr Leu Ala Ser Asn Tyr Ile Ser Ser Gln Ala
 20 25 30

agt tcc tgg acg agt gta aca aca gta acg aca ata gag aca tca ata
 144

Ser Ser Ser Thr Ser Val Thr Thr Val Thr Thr Ile Ala Thr Ser Ile
 35 40 45

cgc tct aca cgg tct aat cta ctc ttt tct aat gtg gag gct cag cca
 192

Arg Ser Thr Pro Ser Asn Leu Leu Phe Ser Asn Val Ala Ala Gln Pro
 50 55 60

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aaa tca tct tca gca agc aca att ggg ctt tca alc gga ctt acc alc
240

Lys Ser Ser Ser Ala Ser Thr Ile Gly Leu Ser Ile Gly Leu Pro Ile
65 70 75 80

gga ata ttc tct ttc gga lla ctt alc ctt ttg tgt tat ttc tac ctt
280

Gly Ile Phe Cys Phe Gly Leu Leu Ile Leu Leu Cys Tyr Phe Tyr Leu
85 90 95

aaa agg aat tcc gtg tcc att tca aat cca ccc atg tca gct aag att
320

Lys Arg Asn Ser Val Ser Ile Ser Asn Pro Pro Met Ser Ala Thr Ile
100 105 110

cca agg gaa gag gaa tat tgt cgc cgc act aat tgg ttc tca cgg tta
360

Pro Arg Glu Glu Glu Tyr Cys Arg Arg Thr Asn Trp Phe Ser Arg Leu
115 120 125

ttt tgg cag agt aag tgt gag gat cag aat tca tat tct aat cgt gat
400

Phe Trp Gln Ser Lys Cys Glu Asp Gln Asn Ser Tyr Ser Asn Arg Asp
130 135 140

att gag aag tat aac gac acc cag tgg acc tcc ggt gat aac atg tct
440

Ile Glu Lys Tyr Asn Asp Thr Gln Trp Thr Ser Gly Asp Asn Met Ser
145 150 155 160

tca aaa ata cag tcc aaa att tcc aaa ccc ata ata ccc cag cat ata
480

Ser Lys Ile Gln Tyr Lys Ile Ser Lys Pro Ile Ile Pro Gln His Ile
165 170 175

ctg aca cct aag aaa aag gtg aag aac cca tat gct tgg tct ggt aaa
520

Leu Thr Pro Lys Lys Thr Val Lys Asn Pro Tyr Ala Trp Ser Gly Lys
180 185 190

aac att tcc tta gac ccc aaa gtg aac gaa atg gag gaa gag aaa gtt
560

660/762

Asn Ile Ser Leu Asp Pro Lys Val Asn Glu Met Glu Glu Glu Lys Val
 195 200 205

qtg gat gca ttc ctg tat act aaa cca ccg aat att gtc cat att gaa
 672

Val Asp Ala Phe Leu Tyr Thr Lys Pro Pro Asn Ile Val His Ile Glu
 210 215 220

tcg agc atg ccc tgg tat aat gat tta cct tct caa aaa aag gtg tcc
 720

Ser Ser Met Pro Ser Tyr Asn Asp Leu Pro Ser Gln Lys Thr Val Ser
 225 230 235 240

tca aag aaa act gcg tta aaa aag agt gag aaa tgg agt tac gaa tct
 768

Ser Lys Lys Thr Ala Leu Lys Thr Ser Glu Lys Trp Ser Tyr Glu Ser
 245 250 255

cca cta tct cga tgg ttc ttg agg ggt tct aca tac ttt aag gat tat
 816

Pro Leu Ser Arg Trp Phe Leu Arg Gly Ser Thr Tyr Phe Lys Asp Tyr
 260 265 270

ggc tta tca aag acc tct tta aag acc cca cct ggg gct cca cca ctg
 864

Gly Leu Ser Lys Thr Ser Leu Lys Thr Pro Thr Gly Ala Pro Gln Leu
 275 280 285

aag caa atg aaa atg ctc tcc cgg ata agt aag ggt tac ttc aat gag
 912

Lys Gln Met Lys Met Leu Ser Arg Ile Ser Lys Gly Tyr Phe Asn Glu
 290 295 300

tca gat ata atg cct gac gaa cga tgg ccc atc ttg gag tat aat aac
 300

Ser Asp Ile Met Pro Asp Glu Arg Ser Pro Ile Leu Glu Tyr Asn Asn
 305 310 315 320

aag cct ctg gat gca aat gac agt gtg aat aac ttg ggt aat acc aag
 1008

Thr Pro Leu Asp Ala Asn Asp Ser Val Asn Asn Leu Gly Asn Thr Thr
 325 330 335

cca gat tca aaa atc aca tct cat cgc aac aat aac atc gat cta atc
1056

Pro Asp Ser Gln Ile Thr Ser Tyr Arg Asn Asn Asn Ile Asp Leu Ile
340 345 350

acg gca aga ccc ctt tca gtg ata taa ggt act act gca caa caa act
1104

Thr Ala Arg Pro His Ser Val Ile Tyr Gly Thr Thr Ala Gln Gln Thr
355 360 365

ttg gaa acc aac ttc aat gat cat cat gac tgc aat aaa agc act gag
1152

Leu Glu Thr Asn Phe Asn Asp His His Asp Cys Asn Lys Ser Thr Glu
370 375 380

aaa cac gag ttg ata ata ccc acc cca tca aaa cca cta aag aaa agg
1200

Lys His Glu Leu Ile Ile Pro Thr Pro Ser Lys Pro Leu Lys Lys Arg
385 390 395 400

aaa aac agc aga caa agt aaa atc tat cag cat tta caa cat ttg tca
1248

Lys Lys Arg Arg Gln Ser Lys Met Tyr Gln His Leu Glu His Leu Ser
405 410 415

cgt tct aaa cca ttg cag ctt act cca aac tcc aaa tat aat ggg gag
1296

Arg Ser Lys Pro Leu Pro Leu Thr Pro Asn Ser Lys Tyr Asn Gly Gln
420 425 430

gct agc gtc caa tta ggg aag aca tat aca gtc att cag gat taa gag
1344

Ala Ser Val Gln Leu Gly Lys Thr Tyr Thr Val Ile Gln Asp Tyr Glu
435 440 445

cct aga ttg aca gac gaa ata aga atc tcc ctg ggt gaa aaa gtt aaa
1392

Pro Arg Leu Thr Asp Glu Ile Arg Ile Ser Leu Gly Glu Lys Val Lys
450 455 460

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att ctg gcc act cat acc gat gga tgg tgt ctg gta gaa aag tgt aat
1440

Ile Leu Ala Thr His Thr Asp Gly Trp Cys Leu Val Glu Lys Cys Asn
485 470 475 480

aca caa aag ggt tct att cac gtc agt gtt gac gat aaa aga tac ctg
1488

Thr Gln Lys Gly Ser Ile His Val Ser Val Asp Asp Lys Arg Tyr Leu
485 490 495

ast gaa gat aga ggc att gtc cct ggt gac tgt ctg caa gaa tac gac
1536

Asn Glu Asp Arg Gly Ile Val Pro Gly Asp Cys Leu Gln Glu Tyr Asp
500 505 510

aga

1539

<210> 274

<211> 512

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 274

Met Val Ala Thr Ile Met Gln Thr Thr Thr Thr Val Leu Thr Thr Val
1 5 10 15

Ala Ala Met Ser Thr Thr Leu Ala Ser Asn Tyr Ile Ser Ser Gln Ala
20 25 30

Ser Ser Ser Thr Ser Val Thr Thr Val Thr Thr Ile Ala Thr Ser Ile
35 40 45

Arg Ser Thr Pro Ser Asn Leu Leu Phe Ser Asn Val Ala Ala Gln Pro
50 55 60

663/762

Lys Ser Ser Ser Ala Ser Thr Ile Gly Leu Ser Ile Gly Leu Pro Ile
65 70 75 80

Gly Ile Phe Cys Phe Gly Leu Leu Ile Leu Leu Cys Tyr Phe Tyr Leu
85 90 95

Lys Arg Asn Ser Val Ser Ile Ser Asn Pro Pro Met Ser Ala Thr Ile
100 105 110

Pro Arg Glu Glu Gln Tyr Cys Arg Arg Thr Asn Trp Phe Ser Arg Leu
115 120 125

Phe Trp Gln Ser Lys Cys Glu Asp Gln Asn Ser Tyr Ser Asn Arg Asp
130 135 140

Ile Glu Lys Tyr Asn Asp Thr Gln Trp Thr Ser Gly Asp Asn Met Ser
145 150 155 160

Ser Lys Ile Gln Tyr Lys Ile Ser Lys Pro Ile Ile Pro Gln His Ile
165 170 175

Leu Thr Pro Lys Lys Thr Val Lys Asn Pro Tyr Ala Trp Ser Gly Lys
180 185 190

Asn Ile Ser Leu Asp Pro Lys Val Asn Glu Met Glu Gln Glu Lys Val
195 200 205

Val Asp Ala Phe Leu Tyr Thr Lys Pro Pro Asn Ile Val His Ile Glu
210 215 220

Ser Ser Met Pro Ser Tyr Asn Asp Leu Pro Ser Gln Lys Thr Val Ser
225 230 235 240

Ser Lys Lys Thr Ala Leu Lys Thr Ser Glu Lys Trp Ser Tyr Glu Ser
 245 250 255

Pro Leu Ser Arg Trp Phe Leu Arg Gly Ser Thr Tyr Phe Lys Asp Tyr
 260 265 270

Gly Leu Ser Lys Thr Ser Leu Lys Thr Pro Thr Gly Ala Pro Gln Leu
 275 280 285

Lys Gln Met Lys Met Leu Ser Arg Ile Ser Lys Gly Tyr Phe Asn Glu
 290 295 300

Ser Asp Ile Met Pro Asp Glu Arg Ser Pro Ile Leu Glu Tyr Asn Asn
 305 310 315 320

Thr Pro Leu Asp Ala Asn Asp Ser Val Asn Asn Leu Gly Asn Thr Thr
 325 330 335

Pro Asp Ser Gln Ile Thr Ser Tyr Arg Asn Asn Asn Ile Asp Leu Ile
 340 345 350

Thr Ala Arg Pro His Ser Val Ile Tyr Gly Thr Thr Ala Glu Gln Thr
 355 360 365

Leu Glu Thr Asn Phe Asn Asp His His Asp Cys Asn Lys Ser Thr Glu
 370 375 380

Lys His Glu Leu Ile Ile Pro Thr Pro Ser Lys Pro Leu Lys Lys Arg
 385 390 395 400

665/762

Lys Lys Arg Arg Gln Ser Lys Met Tyr Gln His Leu Gln His Leu Ser
 405 410 415

Arg Ser Lys Pro Leu Pro Leu Thr Pro Asn Ser Lys Tyr Asn Gly Gln
 420 425 430

Ala Ser Val Gln Leu Gly Lys Thr Tyr Thr Val Ile Gln Asp Tyr Gln
 435 440 445

Pro Arg Leu Thr Asp Gln Ile Arg Ile Ser Leu Gly Gln Lys Val Tyr
 450 455 460

Ile Leu Ala Thr His Thr Asp Gly Trp Cys Leu Val Gln Lys Cys Asn
 465 470 475 480

Thr Gln Tyr Gly Ser Ile His Val Ser Val Asp Asp Lys Arg Tyr Leu
 485 490 495

Asn Gln Asp Arg Gly Ile Val Pro Gly Asp Cys Leu Gln Gln Tyr Asp
 500 505 510

<210> 275
 <211> 2901
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1) .. (2901)

<400> 275
 atg aat uug ggc ggt guu caa aca ata atg gaa caa ooc gct caa cag
 48
 Met Asn Pro Gly Gly Gln Gln Thr Ile Met Gln Gln Pro Ala Gln Gln

666/762

1	5	10	15
Caa caa caa cag caa caa caa cag cag caa cag caa cag cag gca gca 36			
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Ala 20 25 30			
ggt cct cag cag caa ctc gac caa tta aca caa tca act gcg gaa act 144			
Val Pro Gln Gln Pro Leu Asp Pro Leu Thr Gln Ser Thr Ala Glu Thr 35 40 45			
tgg ctc acc att gct tct ttg gca gaa acc ctt ggt gat ggc gac agg 192			
Trp Leu Ser Ile Ala Ser Leu Ala Glu Thr Leu Gly Asp Gly Asp Arg 50 55 60			
gcc gca atg gca tat gac gcc act tta cag ttc aat ccc tca tct gca 240			
Ala Ala Met Ala Tyr Asp Ala Thr Leu Gln Phe Asn Pro Ser Ser Ala 65 70 75 80			
eag gct tta aca cct ttg gct cac ttg tac cgt tcc aga gac atg ttc 288			
Lys Ala Leu Thr Ser Leu Ala His Leu Tyr Arg Ser Arg Asp Met Phe 85 90 95			
caa aga gct gca gaa tta tat gaa aga gca ctt ttg gta aat ccc gaa 336			
Gln Arg Ala Ala Gln Leu Tyr Glu Arg Ala Leu Leu Val Asn Pro Glu 100 105 110			
cta tca gat ggg tgg gct act tta ggt cat tgt tat ctg atg ctg gat 384			
Leu Ser Asp Val Trp Ala Thr Leu Gly His Cys Tyr Leu Met Leu Asp 115 120 125			
gat ctg caa aga gct tac aat gcc tac caa cag gct ctc tac cac ctc 432			
Asp Leu Gln Arg Ala Tyr Asn Ala Tyr Gln Gln Ala Leu Tyr His Leu 130 135 140			

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agt aat ccc aac gta ccg aaa tta tgg cat gga atc ggc att ctt tat
480

Ser Asn Pro Asn Val Pro Lys Leu Trp His Gly Ile Gly Ile Leu Tyr
145 150 155 160

gac aga tat ggt tgg ctc gac tat gcc gaa gaa gct ttt gcc aaa gtt
528

Asp Arg Tyr Gly Ser Leu Asp Tyr Ala Glu Gln Ala Phe Ala Lys Val
165 170 175

ttg gaa ttg gac cct cat ttt gaa aag gca aac gaa att tac ttc aga
576

Leu Glu Leu Asp Pro His Phe Glu Lys Ala Asn Glu Ile Tyr Phe Arg
180 185 190

cta ggt att att tat aaa cat cag ggt aag tgg tct caa gct ttg gaa
624

Leu Gly Ile Ile Tyr Lys His Gln Gly Lys Trp Ser Gln Ala Leu Glu
195 200 205

tgc ttc aga tac att ctc cct caa cct cct gct ccc ttg cag gag tgg
672

Cys Phe Arg Tyr Ile Leu Pro Gln Pro Pro Ala Pro Leu Gln Glu Trp
210 215 220

gac ata tgg ttt cag ttg ggt agt gtt ttg gag agt atg gga gag tgg
720

Asp Phe Trp Phe Gln Leu Gly Ser Val Leu Glu Ser Met Gly Glu Trp
225 230 235 240

caa ggt gag aag gaa gcc tuc gag cat gtc ttg gct caa aat caa cat
768

Gln Gly Ala Lys Glu Ala Tyr Glu His Val Leu Ala Gln Asn Gln His
245 250 255

cat gcc aaa gta tta caa caa tta ggt tgt ctt tac ggt atg agt aac
816

His Ala Lys Val Leu Gln Gln Leu Gly Cys Leu Tyr Gly Met Ser Asn
260 265 270

gta caa ttt tat gac cct caa aag gca ttg gat tat ctt cta aag tgg
864

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Val Gln Phe Tyr Asp Pro Gln Lys Ala Leu Asp Tyr Leu Leu Lys Ser
 275 280 285

tta gaa gaa gat ccc leu gaa gcc act aca tgg tac cat ctd qgt aga
 312

Leu Glu Ala Asp Pro Ser Asp Ala Thr Thr Trp Tyr His Leu Gly Arg
 290 295 300

gtg caa atg att aga aca gat tat act gcc gaa tat gat gct ttc caa
 360

Val His Met Ile Arg Thr Asp Tyr Thr Ala Ala Tyr Asp Ala Phe Gln
 305 310 315 320

caa gct gtt aat aga gat tca aga aac cct atc ttt tgg tgc tca atc
 1008

Gln Ala Val Asn Arg Asp Ser Arg Asn Pro Ile Phe Trp Cys Ser Ile
 325 330 335

ggt gtt tta tat tac caa att tct caa tac aga gaa gcc tta gac ggc
 1056

Gly Val Leu Tyr Tyr Glu Ile Ser Gln Tyr Arg Asp Ala Leu Asp Ala
 340 345 350

tac aca aga gcc ata aga tta aat ccc tat att agt gaa gtt tgg tac
 1104

Tyr Thr Arg Ala Ile Arg Leu Asn Pro Tyr Ile Ser Gln Val Trp Tyr
 355 360 365

gat cta ggt act ctt tac gaa act tat aac aac caa tta tct gac gcc
 1152

Asp Leu Gly Thr Leu Tyr Glu Thr Cys Asn Asn Gln Leu Ser Asp Ala
 370 375 380

ctt gat ggc tat aag caa gct gca aga ctg gac gta aat aat gtt cac
 1200

Leu Asp Ala Tyr Lys Gln Ala Ala Arg Leu Asp Val Asn Asn Val His
 385 390 395 400

ata aga gaa aga tta gaa gct tta aca aag cag tta gaa aac cca ggc
 1248

Ile Arg Glu Arg Leu Glu Ala Leu Thr Lys Gln Leu Gln Asn Pro Gly
 405 410 415

aat ata aac aaa tag aac ggt gag cca acg aat gac tat cct gcc cca
1296

Asn Ile Asn Lys Ser Asn Gly Ala Pro Thr Asn Ala Ser Pro Ala Pro
420 425 430

cct cct gtg att tta caa cct acc tta caa cct aat gat caa gga aat
1344

Pro Pro Val Ile Leu Gln Pro Thr Leu Gln Pro Asn Asp Gln Gly Asn
435 440 445

cct ttg aac act aga att tca gcc caa cct gcc aat gat aat gat tca
1392

Pro Leu Asn Thr Arg Ile Ser Ala Gln Ser Ala Asn Ala Thr Ala Ser
450 455 460

atg gta caa caa cag cat cct gct caa caa acg cct att aac tat tat
1440

Met Val Gln Gln Gln His Pro Ala Gln Gln Thr Pro Ile Asn Ser Ser
465 470 475 480

gaa aca atg tac agt aat gga gct tcc cct caa tta caa gct caa gct
1488

Ala Thr Met Tyr Ser Asn Gly Ala Ser Pro Gln Leu Gln Ala Gln Ala
485 490 495

caa gct caa gct caa gca caa gct caa gca caa gca caa gct caa gca
1536

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
500 505 510

caa gca caa gca caa gag caa gca caa gca caa gca cag gag caa gca
1584

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
515 520 525

cag gca caa gca caa gca caa gca cat gca caa gag caa gca caa gca
1632

Gln Ala Gln Ala Gln Ala Gln Ala His Ala Gln Ala Gln Ala Gln Ala
530 535 540

670/762

caa gca cag gca caa gca caa gca cag gag cag gca caa caa caa caa
1580

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Gln Gln Gln
545 550 555 560

caa caa cag caa caa caa caa caa caa caa caa caa caa caa caa
1728

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
565 570 575

caa caa caa caa caa caa caa cag cag cag caa tta cag ccc cta cca
1776

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Pro Leu Pro
580 585 590

aga caa cag ctg cag caa aag gga gtt tct ggg caa atg tta aat cct
1824

Arg Gln Gln Leu Gln Gln Lys Gly Val Ser Val Gln Met Leu Asn Pro
595 600 605

caa caa ggg caa cca tat atc cca cag cca acc gtc ata caa gct cac
1872

Gln Gln Gly Gln Pro Tyr Ile Thr Gln Pro Thr Val Ile Gln Ala His
610 615 620

caa ctg caa cca ttt tct cca caa gct atg gaa cat ccg caa agc tct
1920

Gln Leu Gln Pro Phe Ser Thr Cln Ala Met Glu His Pro Gln Ser Ser
625 630 635 640

caa ctg cca cct caa cag caa caa cta caa tct gtt caa cat cca caa
1968

Gln Leu Pro Pro Gln Gln Gln Gln Leu Gln Ser Val Gln His Pro Gln
645 650 655

caa ctt caa ggc cag cct caa gcc caa gct ccc caa cct tta acc cag
2016

Gln Leu Gln Gly Gln Pro Gln Ala Gln Ala Pro Gln Pro Leu Ile Gln
660 665 670

cat aac gtg gaa cag aac gtt tta cct caa aag aga tac atg gaa ggt
2064

671/762

His Asn Val Glu Gln Asn Val Leu Pro Gln Lys Arg Tyr Met Glu Gly
 675 680 685

gca atc cac act tta gta gat gcc gcc gca tcc agl agc acc cac aca
 2112

Ala Ile His Thr Leu Val Asp Ala Ala Val Ser Ser Ser Thr His Thr
 690 695 700

gag aat aac aca aag tct cct cgt caa cca acc cat gcc att cca aag
 2160

Glu Asn Asn Thr Lys Ser Pro Arg Gln Pro Thr His Ala Ile Pro Thr
 705 710 715 720

caa gct ccc gca aca gga ata aag aac gct gaa cca cag gta aag aag
 2208

Gln Ala Pro Ala Thr Gly Ile Thr Asn Ala Glu Pro Gln Val Lys Lys
 725 730 735

caa aag tlg aac tct cca cat tca aac acc aac aca tta gca aat act
 2256

Gln Lys Asn Asn Ser Pro Asn Ser Asn Ile Asn Lys Leu Val Asn Thr
 740 745 750

gct act tcc att gaa gaa aat gca aaa tct gag gtg agc aac caa tcc
 2304

Ala Thr Ser Ile Glu Glu Asn Ala Lys Ser Glu Val Ser Asn Gln Ser
 755 760 765

cca gca gla glg gag tct aat acc aat aat aat tca caa gaa gaa aaa
 2352

Pro Ala Val Val Glu Ser Asn Thr Asn Asn Thr Ser Gln Glu Glu Lys
 770 775 780

cct gta aaa gca aac tca ata cct tca gta att ggc gca cag gaa cct
 2400

Pro Val Lys Ala Asn Ser Ile Pro Ser Val Ile Gly Ala Gln Glu Pro
 785 790 795 800

cca cag gaa gct agt cct gct gaa gaa gct acc aaa gca gct tct gtt
 2448

Pro Gln Glu Ala Ser Pro Ala Gln Glu Ala Thr Lys Ala Ala Ser Val
 805 810 815

tct cct tct acc aaa ccg ctt aat acg gaa cca gag tca tct agt gtc
2496

Ser Pro Ser Thr Lys Pro Leu Asn Thr Glu Pro Glu Ser Ser Ser Val
820 825 830

caa cca act gta tca tca gaa agt tca acc acc aaa gca aat gac caa
2544

Gln Pro Thr Val Ser Ser Glu Ser Ser Thr Thr Lys Ala Asn Asp Gln
835 840 845

agc act gcc gag acc ata gaa ctt tct act gct act gtt cct gca gaa
2592

Ser Thr Ala Glu Thr Ile Glu Leu Ser Thr Ala Thr Val Pro Ala Glu
850 855 860

gca agc cct gta gaa gac gaa gta aga cag cat tct aaa gag gaa aac
2640

Ala Ser Pro Val Glu Asp Glu Val Arg Gln His Ser Lys Glu Glu Asn
865 870 875 880

ggc acc act gaa gca tct gca cct tct act gaa gag cgg gag cca gca
2688

Gly Thr Thr Glu Ala Ser Ala Pro Ser Thr Glu Glu Ala Glu Pro Ala
885 890 895

gct tcc aga gat gct gaa aaa cca cca gat gaa acc gct gct acc acg
2736

Ala Ser Arg Asp Ala Glu Lys Gln Gln Asp Glu Thr Ala Ala Thr Thr
900 905 910

ata act gta atc aaa cct act ttg gaa acc atg gaa acc gtg aaa gag
2784

Ile Thr Val Ile Lys Pro Thr Leu Glu Thr Met Glu Thr Val Lys Glu
915 920 925

gag gcc aaa atg cgt gag gaa gag aaa acc tct cca gaa aaa tcc cca
2832

Glu Ala Lys Met Arg Glu Glu Glu Gln Thr Ser Gln Glu Lys Ser Pro
930 935 940

673/762

cag gag aac aca ctt cca aga gau aat gta gta agg caa gtg gaa gaa
2880

Gln Glu Asn Thr Leu Pro Arg Glu Asn Val Val Arg Gln Val Glu Glu
345 350 355 360

gat gaa aac lac gac gac taa
2901

Asp Gln Asn Tyr Asp Asp
365

<210> 276

<211> 966

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 276

Met Asn Pro Gly Gly Glu Gln Thr Ile Met Glu Gln Pro Ala Gln Gln
1 5 10 15

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Ala Ala
20 25 30

Val Pro Gln Gln Pro Leu Asp Pro Leu Thr Gln Ser Thr Ala Glu Thr
35 40 45

Trp Leu Ser Ile Ala Ser Leu Ala Glu Thr Leu Gly Asp Gly Asp Arg
50 55 60

Ala Ala Met Ala Tyr Asp Ala Thr Leu Gln Phe Asn Pro Ser Ser Ala
65 70 75 80

Lys Ala Leu Thr Ser Leu Ala His Leu Tyr Arg Ser Arg Asp Met Phe
85 90 95

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Gln Arg Ala Ala Glu Leu Tyr Glu Arg Ala Leu Leu Val Asn Pro Gln
 100 105 110

Leu Ser Asp Val Trp Ala Thr Leu Gly His Cys Tyr Leu Met Leu Asp
 115 120 125

Asp Leu Gln Arg Ala Tyr Asn Ala Tyr Gln Gln Ala Leu Tyr His Leu
 130 135 140

Ser Asn Pro Asn Val Pro Lys Leu Trp His Gly Ile Gly Ile Leu Tyr
 145 150 155 160

Asp Arg Tyr Gly Ser Leu Asp Tyr Ala Glu Glu Ala Phe Ala Lys Val
 165 170 175

Leu Glu Leu Asp Pro His Phe Glu Lys Ala Asn Glu Ile Tyr Phe Arg
 180 185 190

Leu Gly Ile Ile Tyr Lys His Gln Gly Lys Trp Ser Gln Ala Leu Glu
 195 200 205

Cys Phe Arg Tyr Ile Leu Pro Gln Pro Pro Ala Pro Leu Gln Glu Trp
 210 215 220

Asp Ile Trp Phe Gln Leu Gly Ser Val Leu Glu Ser Met Gly Glu Trp
 225 230 235 240

Gln Gly Ala Lys Glu Ala Tyr Glu His Val Leu Ala Gln Asn Gln His
 245 250 255

His Ala Lys Val Leu Gln Gln Leu Gly Cys Leu Tyr Gly Met Ser Asn
 260 265 270

Val Gln Phe Tyr Asp Pro Gln Lys Ala Leu Asp Tyr Leu Leu Lys Ser
275 280 285

Leu Glu Ala Asp Pro Ser Asp Ala Thr Thr Trp Tyr His Leu Gly Arg
290 295 300

Val His Met Ile Arg Thr Asp Tyr Thr Ala Ala Tyr Asp Ala Phe Gln
305 310 315 320

Gln Ala Val Asn Arg Asp Ser Arg Asn Pro Ile Phe Trp Cys Ser Ile
325 330 335

Gly Val Leu Tyr Tyr Gln Ile Ser Gln Tyr Arg Asp Ala Leu Asp Ala
340 345 350

Tyr Thr Arg Ala Ile Arg Leu Asn Pro Tyr Ile Ser Glu Val Trp Tyr
355 360 365

Asp Leu Gly Thr Leu Tyr Glu Thr Cys Asn Asn Gln Leu Ser Asp Ala
370 375 380

Leu Asp Ala Tyr Lys Gln Ala Ala Arg Leu Asp Val Asn Asn Val His
385 390 395 400

Ile Arg Glu Arg Leu Glu Ala Leu Thr Lys Gln Leu Glu Asn Pro Gly
405 410 415

Asn Ile Asn Lys Ser Asn Gly Ala Pro Thr Asn Ala Ser Pro Ala Pro
420 425 430

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Pro Pro Val Ile Leu Gln Pro Thr Leu Gln Pro Asn Asp Gln Gly Asn
435 440 445

Pro Leu Asn Thr Arg Ile Ser Ala Gln Ser Ala Asn Ala Thr Ala Ser
450 455 460

Met Val Gln Gln Gln His Pro Ala Gln Gln Thr Pro Ile Asn Ser Ser
465 470 475 480

Ala Thr Met Tyr Ser Asn Gly Ala Ser Pro Gln Leu Gln Ala Gln Ala
485 490 495

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
500 505 510

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala
515 520 525

Gln Ala Gln Ala Gln Ala Gln Ala His Ala Gln Ala Gln Ala Gln Ala
530 535 540

Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Ala Gln Gln Gln
545 550 555 560

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
565 570 575

Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Leu Gln Pro Leu Pro
580 585 590

Arg Gln Gln Leu Gln Gln Lys Gly Val Ser Val Gln Met Leu Asn Pro
595 600 605

Gln Gln Gly Gln Pro Tyr Ile Thr Gln Pro Thr Val Ile Gln Ala His
610 615 620

Gln Leu Gln Pro Phe Ser Thr Gln Ala Met Glu His Pro Gln Ser Ser
625 630 635 640

Gln Leu Pro Pro Gln Gln Gln Gln Leu Gln Ser Val Gln His Pro Gln
645 650 655

Gln Leu Gln Gly Gln Pro Gln Ala Gln Ala Pro Gln Pro Leu Ile Gln
660 665 670

His Asn Val Glu Gln Asn Val Leu Pro Gln Lys Arg Tyr Met Glu Gly
675 680 685

Ala Ile His Thr Leu Val Asp Ala Ala Val Ser Ser Ser Thr His Thr
690 695 700

Glu Asn Asn Thr Lys Ser Pro Arg Gln Pro Thr His Ala Ile Pro Thr
705 710 715 720

Gln Ala Pro Ala Thr Gly Ile Thr Asn Ala Gln Pro Gln Val Lys Lys
725 730 735

Gln Lys Leu Asn Ser Pro Asn Ser Asn Ile Asn Lys Leu Val Asn Thr
740 745 750

Ala Thr Ser Ile Glu Glu Asn Ala Lys Ser Glu Val Ser Asn Gln Ser
755 760 765

Pro Ala Val Val Glu Ser Asn Thr Asn Asn Thr Ser Gln Glu Glu Lys
 770 775 780

Pro Val Lys Ala Asn Ser Ile Pro Ser Val Ile Gly Ala Gln Glu Pro
 785 790 795 800

Pro Gln Glu Ala Ser Pro Ala Glu Gln Ala Thr Lys Ala Ala Ser Val
 805 810 815

Ser Pro Ser Thr Lys Pro Leu Asn Thr Gln Pro Glu Ser Ser Ser Val
 820 825 830

Gln Pro Thr Val Ser Ser Gln Ser Ser Thr Thr Lys Ala Asn Asp Gln
 835 840 845

Ser Thr Ala Glu Thr Ile Glu Leu Ser Thr Ala Thr Val Pro Ala Glu
 850 855 860

Ala Ser Pro Val Glu Asp Glu Val Arg Gln His Ser Lys Glu Glu Asn
 865 870 875 880

Gly Thr Thr Glu Ala Ser Ala Pro Ser Thr Glu Glu Ala Glu Pro Ala
 885 890 895

Ala Ser Arg Asp Ala Glu Lys Gln Gln Asp Glu Thr Ala Ala Thr Thr
 900 905 910

Ile Thr Val Ile Lys Pro Thr Asn Glu Thr Met Glu Thr Val Lys Glu
 915 920 925

Glu Ala Lys Met Arg Glu Glu Glu Gln Thr Ser Gln Glu Lys Ser Pro
 930 935 940

Gln Glu Asn Thr Leu Pro Arg Glu Asn Val Val Arg Gln Val Glu Glu
945 950 955 960

Asp Glu Asn Tyr Asp Asp
965

<210> 377
<211> 600
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> CDS
<222> (1) .. (600)

<400> 377
atg gac aac atc aga gaa aag cta agt aac ttg aag ttg gaa gcc gaa
48
Met Asp Lys Ile Arg Glu Lys Leu Ser Asn Leu Lys Leu Glu Ala Glu
1 5 10 15
tca tgg aag gag aag tac gag gag ttg aaa gag aag aac aag gac ttg
96
Ser Trp Gln Glu Lys Tyr Glu Glu Leu Lys Glu Lys Asn Lys Asp Leu
20 25 30
gag caa gag aac gtc gaa aag gag aat gag atc aag tat tta acc gtc
144
Glu Gln Glu Asn Val Glu Lys Glu Asn Gln Ile Lys Ser Leu Thr Val
35 40 45
aaa aac aag caa ttg gag gat gag atc gag aag ctg gaa gcc gga att
192
Lys Asn Gln Gln Leu Glu Asp Glu Ile Glu Lys Leu Glu Ala Gly Leu
50 55 60

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tct gac tct aag caa aca gaa cag gat aac gtt gaa aua gaa aat cag
240

Ser Asp Ser Lys Gln Thr Gln Gln Asp Asn Val Glu Lys Glu Asn Gln
65 70 75 80

atc aag tcc ttg acg gtg aag aac cac caa ttg gag gaa gag atc gag
288

Ile Lys Ser Leu Thr Val Lys Asn His Gln Leu Glu Glu Glu Ile Glu
65 80 95

aag ttg gaa gca gaa ttg gct gaa tcc aag caa ttg tcc gag gac tct
336

Lys Leu Glu Ala Glu Leu Ala Glu Ser Lys Gln Leu Ser Glu Asp Ser
100 105 110

cac cac ttg cag tcc aac aac gac aat ttc tcc aag aag aac cag caa
384

His His Leu Gln Ser Asn Asn Asp Asn Phe Ser Lys Lys Asn Gln Gln
115 120 125

ttg gaa gaa gac ttg gag gaa agc gat acc aag cta aag gaa acc act
432

Leu Glu Glu Asp Leu Glu Glu Ser Asp Thr Lys Leu Lys Glu Thr Thr
130 135 140

gag aaa ttg aga gag tcc gac ttg aag gca gat caa ttg gaa aga aga
480

Glu Lys Leu Arg Glu Ser Asp Leu Lys Ala Asp Gln Leu Glu Arg Arg
145 150 155 160

gta gct gcc ttg gaa gaa aua aga gaa gaa tgg gaa aga aag aac gag
528

Val Ala Ala Leu Glu Glu Gln Arg Glu Glu Trp Glu Arg Lys Asn Glu
165 170 175

gaa ttg acc gtc aag tac gaa gac gca aag aag gaa ctg gac gaa att
576

Glu Leu Thr Val Lys Tyr Glu Asp Ala Lys Lys Glu Leu Asp Glu Ile
180 185 190

gct gca tct ctg gaa aac ttg tga
600

Ala Ala Ser Leu Glu Asn Leu

195

<210> 278

<211> 199

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 278

Met Asp Lys Ile Arg Glu Lys Leu Ser Asn Leu Lys Leu Glu Ala Glu

1 5 10 15

Ser Thr Gln Glu Lys Tyr Gln Glu Leu Lys Glu Lys Asn Lys Asp Leu

20 25 30

Glu Gln Glu Asn Val Glu Lys Glu Asn Cln Ile Lys Ser Leu Thr Val

35 40 45

Lys Asn Gln Gln Leu Glu Asp Glu Ile Glu Lys Leu Glu Ala Gly Leu

50 55 60

Ser Asp Ser Lys Gln Thr Glu Gln Asp Asn Val Glu Lys Glu Asn Gln

65 70 75 80

Ile Lys Ser Leu Thr Val Lys Asn His Gln Leu Glu Glu Glu Ile Glu

85 90 95

Lys Leu Glu Ala Glu Leu Ala Glu Ser Lys Gln Leu Ser Gln Asp Ser

100 105 110

His His Leu Gln Ser Asn Asn Asp Asn Phe Ser Lys Lys Asn Gln Gln

115 120 125

Leu Glu Glu Asp Leu Glu Glu Ser Asp Thr Lys Leu Lys Glu Thr Thr
 130 135 140

Glu Lys Leu Arg Glu Ser Asp Leu Lys Ala Asp Gln Leu Glu Arg Arg
 145 150 155 160

Val Ala Ala Leu Glu Glu Gln Arg Glu Glu Trp Glu Arg Lys Asn Glu
 165 170 175

Glu Leu Thr Val Lys Tyr Gln Asp Ala Lys Lys Glu Leu Asp Gln Ile
 180 185 190

Ala Ala Ser Leu Glu Asn Leu
 195

<210> 279
 <211> 603
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(603)

<400> 279
 atg gca ggc atc aag ttg acg cat aag ctt tat cag tat tat caa tta
 48
 Met Ala Gly Ile Lys Leu Thr His Lys Leu Tyr Gln Tyr Tyr Gln Leu
 1 5 10 15
 gcc aca agc ttt ttg tat gct gca tta ttg ata cgg tgg ctg ata tta
 96
 Ala Thr Ser Phe Leu Tyr Ala Ala Leu Leu Ile Arg Trp Leu Ile Leu
 20 25 30

683/762

atg cca ctg gta ggg tct cgg ttt tta cgg gga gga atc cag gaa ttc
144

Met Pro Leu Val Gly Ser Arg Phe Leu Pro Gly Gly Ile His Glu Phe
35 40 45

ttg ata tat ttg atg ttt tat tcc agc atc atg gaa gtt att tgg ttg
192

Leu Ile Tyr Leu Met Phe Tyr Ser Ser Ile Met Glu Val Ile Trp Leu
50 55 60

ctt aga ttc cag ggg ttc aaa tat ggt ttg ctt tca aga acg ttt ttg
240

Leu Arg Phe His Gly Phe Lys Tyr Gly Leu Leu Ser Arg Thr Phe Leu
65 70 75 80

aaa gac cta aat ttt atc tac tta gtc agc gtg atc cat ttt tat gac
288

Lys Asp Leu Asn Phe Ile Tyr Leu Val Ser Val Ile His Phe Tyr Asp
85 90 95

gat tat gag cat gca ttg atc ctc aag aat gca tca tat tct agt ttc
336

Asp Tyr Glu His Ala Leu Ile Leu Lys Asn Ala Ser Tyr Ser Ser Phe
100 105 110

att att tcc tta tct tta tca cag gca tat tgc cat tgg tgc aaa cta
360

Ile Ile Ser Leu Ser Leu Ser Glu Ala Tyr Cys His Trp Cys Lys Leu
115 120 125

ttt aaa cgt aag ggc gta aag gaa aga aca ctt gta tgg aag gtt aac
432

Phe Lys Arg Lys Gly Val Lys Glu Arg Thr Leu Val Trp Lys Val Asn
130 135 140

aca ttt gtt aca ttg cca att ctc tac ctg agt gaa ttt gca ttg cta
480

Thr Phe Val Thr Leu Pro Ile Leu Tyr Leu Ser Glu Phe Ala Leu Leu
145 150 155 160

cta tta aat atc cag gtt aag aac tat cat tct acc cgg act ttg gac
528

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Leu Leu Asn Ile Gln Val Lys Asn Tyr His Ser Thr Pro Thr Leu Asp
 165 170 175

ata atc aac agg gty gct Llu cta gca tac ttc cct gta cta cta aca
 576

Ile Ile Asn Arg Val Val Leu Leu Ala Tyr Phe Pro Val Leu Leu Thr
 180 185 190

gca tac aaa aaa cta tta aca aaa tga
 603

Ala Tyr Lys Lys Leu Leu Thr Lys
 195 200

<210> 280
 <211> 200
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 280

Met Ala Gly Ile Lys Leu Thr His Lys Leu Tyr Gln Tyr Tyr Gln Leu
 1 5 10 15

Ala Thr Ser Phe Leu Tyr Ala Ala Leu Leu Ile Arg Arg Leu Ile Leu
 20 25 30

Met Pro Leu Val Gly Ser Arg Phe Leu Pro Gly Gly Ile His Glu Phe
 35 40 45

Leu Ile Tyr Leu Met Phe Tyr Ser Ser Ile Met Gln Val Ile Trp Leu
 50 55 60

Leu Arg Phe His Gly Phe Lys Tyr Gly Leu Leu Ser Arg Thr Phe Leu
 65 70 75 80

Lys Asp Leu Asn Phe Ile Tyr Leu Val Ser Val Ile His Phe Tyr Asp

685/762

85

90

95

Asp Tyr Glu His Ala Leu Ile Leu Lys Asn Ala Ser Tyr Ser Ser Phe
100 105 110

Ile Ile Ser Leu Ser Leu Ser Gln Ala Tyr Cys His Trp Cys Lys Leu
115 120 125

Phe Lys Arg Lys Gly Val Lys Glu Arg Thr Leu Val Trp Lys Val Asn
130 135 140

Thr Phe Val Thr Leu Pro Thr Met Tyr Leu Ser Glu Phe Ala Leu Leu
145 150 155 160

Leu Leu Asn Ile Gln Val Lys Asn Tyr His Ser Thr Pro Thr Leu Asp
165 170 175

Ile Ile Asn Arg Val Val Leu Leu Ala Tyr Phe Pro Val Leu Leu Thr
180 185 190

Ala Tyr Lys Lys Leu Leu Thr Lys
195 200

<210> 281
<211> 447
<212> DNA
<213> *Saccharomyces cerevisiae*

<220>
<221> (DS
<222> (1)..(447)

<400> 281

G8G/762

atg tgt gaa tca tca aat aag act gaa nat gat ata gtc aga ttg tca
48

Met Cys Glu Ser Ser Asn Lys Thr Glu Asn Asp Ile Val Arg Leu Ser
1 5 10 15

caa gct atg gat gtc ctg gct aag ttg atc att tca aag caa aaa gac
96

Gln Ala Met Asp Val Leu Ala Lys Leu Ile Ile Ser Lys Gln Lys Asp
20 25 30

gga tca caa tta caa gtt gag tac gag cat aag ttg aaa gaa tta gag
144

Gly Ser Gln Leu Glu Val Glu Tyr Glu His Lys Leu Lys Glu Leu Glu
35 40 45

aaa ttc att aac cta cta ctg gga ttg cat gaa agc act gtg gga agt
192

Lys Phe Ile Asn Leu Leu Leu Gly Leu His Glu Ser Thr Val Gly Ser
50 55 60

atg atg aat act agt gll ctt gac atg gta ctg cgg aat gga ata gag
240

Met Met Asn Thr Ser Val Leu Asp Met Val Leu Arg Asn Gly Ile Glu
65 70 75 80

atc atg gaa aaa gac gat caa cau tat gcc ctg ata cgg att aaa gcc
288

Ile Met Glu Lys Asp Asp Gln Lys Tyr Ala Leu Ile Pro Ile Lys Ala
85 90 95

aag gaa gag gca gat aaa act aag agc act all cag gga gta acc agc
336

Lys Glu Glu Ala Asp Lys Thr Thr Ser Thr Ile Gln Gly Val Thr Ser
100 105 110

aaa aag agt agt aau aag aaa aaa aat aag ata aaa tgt tca ttt tgt
384

Lys Lys Ser Ser Lys Lys Lys Lys Asn Lys Ile Lys Cys Ser Phe Cys
115 120 125

caa gag gct qgc cac aca agg gca cac tgc ggt ggc aga ctg aca gtt
432

687/762

His Glu Ala Gly His Thr Arg Ala His Cys Gly Ala Arg Leu Thr Val
 130 135 140

ala ser arg ala thr

147

Ile Pro Lys Lys

145

<210> 282

<211> 148

<212> PRT

<213> Saccharomyces cerevisiae

<400> 282

Met Cys Glu Ser Ser Asn Lys Thr Glu Asn Asp Ile Val Arg Leu Ser
 1 5 10 15

Gln Ala Met Asp Val Leu Ala Lys Leu Ile Ile Ser Lys Gln Lys Asp
 20 25 30

Gly Ser Gln Leu Gln Val Glu Tyr Glu His Lys Leu Lys Glu Leu Glu
 35 40 45

Lys Phe Ile Asn Leu Leu Leu Gly Leu His Glu Ser Thr Val Gly Ser
 50 55 60

Met Met Asn Thr Ser Val Leu Asp Met Val Leu Arg Asn Gly Ile Glu
 65 70 75 80

Ile Met Glu Lys Asp Asp Gln Lys Tyr Ala Leu Ile Pro Ile Lys Ala
 85 90 95

Lys Glu Glu Ala Asp Lys Thr Thr Ser Thr Ile Glu Gly Val Thr Ser
 100 105 110

Lys Lys Ser Ser Lys Lys Lys Lys Asn Lys Ile Lys Cys Ser Phe Cys
 115 120 125

His Glu Ala Gly His Thr Arg Ala His Cys Gly Ala Arg Leu Thr Val
 130 135 140

Ile Pro Lys Lys
 145

<210> 263
 <211> 1545
 <212> DNA
 <213> Saccharomyces cerevisiae

<220>
 <221> CDS
 <222> (1)..(1545)

<400> 282
 atg gag gaa caa cgt gaa ata ctg gaa caa ttg aag aaa aat ctg cag
 18
 Met Glu Glu Gln Arg Glu Ile Leu Glu Gln Leu Lys Lys Thr Leu Glu
 1 5 10 15

atg cta aat glu gag cca tct aaa aat aac caa atc gcc aac gaa gaa
 36
 Met Leu Thr Val Glu Pro Ser Lys Asn Asn Gln Ile Ala Asn Glu Glu
 20 25 30

aag gaa aag aaa gaa aat gaa aat tgg tgg tgc atc ctc gag cac aat
 144
 Lys Glu Lys Lys Glu Asn Glu Asn Ser Trp Cys Ile Leu Glu His Asn
 35 40 45

tat gag gat atc gca cag gaa ttc att gat ttc att tac aag aac cct
 192

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Tyr Glu Asp Ile Ala Glu Glu Phe Ile Asp Phe Ile Tyr Lys Asn Pro
 50 55 60

acc aac tac ccc gta gta tca ttt ttc gcc gag ctg lla gat aag cat
 240

Thr Thr Tyr His Val Val Ser Phe Phe Ala Glu Leu Leu Asp Lys His
 65 70 75 80

aac ttc aac tac ttg agc gag aac tcc aat tgg cag gac tcc att gcc
 288

Asn Phe Lys Tyr Leu Ser Glu Lys Ser Asn Trp Glu Asp Ser Ile Gly
 85 90 95

gaa gat ggt ggg aac ttc tac act ata aga aat gga aac aac cta tct
 336

Glu Asp Gly Gly Lys Phe Tyr Thr Ile Arg Asn Gly Thr Asn Leu Ser
 100 105 110

gcc ttt atc ctg gcc aac aac tgg aga gcc gaa aag ggt gtc ggt gtc
 384

Ala Phe Ile Leu Gly Lys Asn Trp Arg Ala Glu Lys Gly Val Gly Val
 115 120 125

att gga tct cat gtc gac gct ttg acg gtc aac ttg aag cct gtc tcc
 432

Ile Gly Ser His Val Asp Ala Leu Thr Val Lys Leu Lys Pro Val Ser
 130 135 140

ttt aac gac aca gcc aac ggt tac gga aga att gct gtt gct ccc tat
 480

Phe Lys Asp Thr Ala Glu Gly Tyr Gly Arg Ile Ala Val Ala Pro Tyr
 145 150 155 160

gga ggt aca ctg aat gaa ttg tgg cta gac aga gac cta ggt att ggt
 528

Gly Gly Thr Leu Asn Glu Leu Trp Leu Asp Arg Asp Leu Gly Ile Gly
 165 170 175

ggt cgc ctt ctt tac aag aag aag gcc act aac gaa att aac agc gcc
 576

Gly Arg Leu Leu Tyr Lys Lys Lys Gly Thr Asn Glu Ile Lys Ser Ala
 180 185 190

ttg qtt gat tdt ada ccd cta cct gtc tqt oga att cct tcd ttg gct
624

Leu Val Asp Ser Thr Pro Leu Pro Val Cys Arg Ile Pro Ser Leu Ala
195 200 205

ccc cat ttc cgt aaa cct gct gaa ggc cca ttt gat caa gag gac caa
672

Pro His Phe Gly Lys Pro Ala Glu Gly Pro Phe Asp Lys Glu Asp Glu
210 215 220

act atc cag gtc atc ggc ttc ccc act cag gat gag gaa ggt act gaa
720

Thr Ile Pro Val Ile Gly Phe Pro Thr Pro Asp Glu Glu Gly Asn Glu
225 230 235 240

cct ccc aag gat gat gaa aag aaa tcc ccc tta tta ggc aaa cac tgc
768

Pro Pro Thr Asp Asp Glu Lys Lys Ser Pro Leu Phe Gly Lys His Cys
245 250 255

atc cac ctg tta agg tac gtt gcc aaa tta gcc ggt gtg gaa gtg tcc
816

Ile His Leu Leu Arg Tyr Val Ala Lys Leu Ala Gly Val Glu Val Ser
260 265 270

gaa ttg att caa atg gat tta gac tta ttc gat gtg caa aag ggt acc
864

Glu Leu Ile Gln Met Asp Leu Asp Leu Phe Asp Val Gln Lys Gly Thr
275 280 285

att gga ggt att ggt aca cac ttc ctt ttt gca cca cgt cta gat gac
912

Ile Gly Gly Ile Gly Lys His Phe Leu Phe Ala Pro Arg Leu Asp Asp
290 295 300

agg ttg tgt agt ttc gca gca atg att gct ttg att tgc tac gat aag
960

Arg Asp Cys Ser Phe Ala Ala Met Ile Ala Leu Ile Cys Tyr Ala Lys
305 310 315 320

gat gtc aat acc gag gaa tca gat tta ttc tct act gtc act ttg tat
1008

Asp Val Asn Thr Glu Glu Ser Asp Leu Phe Ser Thr Val Thr Leu Tyr
325 330 335

gat aat gaa gaa atc gga tgg ttg aca aga caa ggc gca aaa ggt ggc
1056

Asp Asn Glu Glu Ile Gly Ser Leu Thr Arg Gln Gly Ala Lys Gly Gly
340 345 350

ttg ttg gag tca gtg gtg gaa cgc agt cct cct gca ttc act aag aaa
1104

Leu Leu Glu Ser Val Val Glu Arg Ser Ser Ser Ala Phe Thr Lys Lys
355 360 365

ccg gtc gat ttg cat acg gtt tgg gct aat leu atc atc ttg tcc gca
1152

Pro Val Asp Leu His Thr Val Trp Ala Asn Ser Ile Ile Leu Ser Ala
370 375 380

gac gtc aac cac ctc tac aac cca aac ttt cct gaa gtc tat ttg aag
1200

Asp Val Asn His Leu Tyr Asn Pro Asn Phe Pro Glu Val Tyr Leu Lys
385 390 395 400

aat cat ttt cca gtg cct aat gtc gga atc act tta tca ctg gat cct
1248

Asn His Phe Pro Val Pro Asn Val Gly Ile Thr Leu Ser Leu Asp Pro
405 410 415

aac ggt cat atg gcc xca gat gtc gta gga aat gcc cta gta gaa gaa
1296

Asn Gly His Met Ala Thr Asp Val Val Gly Thr Ala Leu Val Glu Glu
420 425 430

tta gca cgc cgc aat gga gac aaa gtg caa tat ttc caa atc aaa aac
1344

Leu Ala Arg Arg Asn Gly Asp Lys Val Gln Tyr Phe Gln Ile Lys Asn
435 440 445

aac tca aga tca ggt ggt act atc ggc cca tca ttg gat tct caa aca
1392

692/762

Asn Ser Arg Ser Gly Gly Thr Ile Gly Pro Ser Leu Ala Ser Gln Thr
 450 455 460

ggc gct cgt acc ata gac ctg gga att gca cag ctg tcc atg cac agc
 1440

Gly Ala Arg Thr Ile Asp Leu Gly Ile Ala Gln Leu Ser Met His Ser
 465 470 475 480

atc aga gct gct aca ggg tcc aag gat gtc gga tta ggt gtt aag ttc
 1488

Ile Arg Ala Ala Thr Gly Ser Lys Asp Val Gly Leu Gly Val Tyr Phe
 485 490 495

ttc aac gga ttt ttc aag cac tgg aga tca gtc tac gat gaa ttc ggc
 1536

Phe Asn Gly Phe Phe Tyr His Trp Arg Ser Val Tyr Asp Glu Phe Gly
 500 505 510

gag ttg tga

1544

Glu Leu

<210> 284
 <211> 514
 <212> PRT
 <213> *Saccharomyces cerevisiae*

<400> 284

Met Glu Glu Gln Arg Glu Ile Leu Glu Gln Leu Lys Lys Thr Leu Gln
 1 5 10 15

Met Leu Thr Val Glu Pro Ser Lys Asn Asn Gln Ile Ala Asn Glu Glu
 20 25 30

Lys Glu Lys Lys Glu Asn Glu Asn Ser Trp Cys Ile Leu Glu His Asn
 35 40 45

Tyr Glu Asp Ile Ala Gln Glu Phe Ile Asp Phe Ile Tyr Lys Asn Pro
50 55 60

Thr Thr Tyr His Val Val Ser Phe Phe Ala Glu Leu Leu Asp Lys His
65 70 75 80

Asn Phe Lys Tyr Leu Ser Glu Lys Ser Asn Trp Gln Asp Ser Ile Gly
85 90 95

Glu Asp Gly Gly Lys Phe Tyr Thr Ile Arg Asn Gly Thr Asn Leu Ser
100 105 110

Ala Phe Ile Leu Gly Lys Asn Trp Arg Ala Glu Lys Gly Val Gly Val
115 120 125

Ile Gly Ser His Val Asp Ala Leu Thr Val Lys Leu Lys Pro Val Ser
130 135 140

Phe Lys Asp Thr Ala Glu Gly Tyr Gly Arg Ile Asn Val Ala Pro Tyr
145 150 155 160

Gly Gly Thr Leu Asn Glu Leu Trp Leu Asp Arg Asp Leu Gly Ile Gly
165 170 175

Gly Arg Leu Leu Tyr Lys Lys Lys Gly Thr Asn Glu Ile Lys Ser Ala
180 185 190

Leu Val Asp Ser Thr Pro Leu Pro Val Cys Arg Ile Pro Ser Leu Ala
195 200 205

Pro His Phe Gly Lys Pro Ala Glu Gly Pro Phe Asp Lys Glu Asp Glu

210	215	220
Thr Ile Pro Val Ile Gly Phe Pro Thr Pro Asp Glu Glu Gly Asn Glu		
225	230	235 240
Pro Pro Thr Asp Asp Glu Lys Lys Ser Pro Leu Phe Gly Lys His Cys		
245	250	255
Ile His Leu Leu Arg Tyr Val Ala Lys Leu Ala Gly Val Glu Val Ser		
260	265	270
Glu Leu Ile Gln Met Asp Leu Asp Leu Phe Asp Val Gln Lys Gly Thr		
275	280	285
Ile Gly Gly Ile Gly Lys His Phe Leu Phe Ala Pro Arg Leu Asp Asp		
290	295	300
Arg Leu Cys Ser Phe Ala Ala Met Ile Ala Leu Ile Cys Tyr Ala Lys		
305	310	315 320
Asp Val Asn Thr Glu Glu Ser Asp Leu Phe Ser Thr Val Thr Leu Tyr		
325	330	335
Asp Asn Glu Glu Ile Gly Ser Leu Thr Arg Gln Gly Ala Lys Gly Gly		
340	345	350
Leu Leu Glu Ser Val Val Glu Arg Ser Ser Ser Ala Phe Thr Lys Lys		
355	360	365
Pro Val Asp Leu His Thr Val Trp Ala Asn Ser Ile Ile Leu Ser Ala		
370	375	380

Asp Val Asn His Leu Tyr Asn Pro Asn Phe Pro Glu Val Tyr Leu Lys
 385 390 395 400

Asn His Phe Pro Val Pro Asn Val Gly Ile Thr Leu Ser Leu Asp Pro
 405 410 415

Asn Gly His Met Ala Thr Asp Val Val Gly Thr Ala Leu Val Glu Glu
 420 425 430

Leu Ala Arg Arg Asn Gly Asp Lys Val Gln Tyr Phe Gln Ile Lys Asn
 435 440 445

Asn Ser Arg Ser Gly Gly Thr Ile Gly Pro Ser Leu Ala Ser Gln Thr
 450 455 460

Gly Ala Arg Thr Ile Asp Leu Gly Ile Ala Gln Leu Ser Met His Ser
 465 470 475 480

Ile Arg Ala Ala Thr Gly Ser Lys Asp Val Gly Leu Gly Val Lys Phe
 485 490 495

Phe Asn Gly Phe Phe Lys His Trp Arg Ser Val Tyr Asp Glu Phe Gly
 500 505 510

Glu Leu

<210> 205

<211> 579

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1) .. (379)

<400> 285

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48

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly Asp Gly

1

5

10

15

gct cgt gcc aag acc tct tta cta tat gta ttt acc tta gga aaa ttc

96

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly Lys Phe

20

25

30

cct gaa caa tat cat ccg acc gtg ttc gag aat tat gtc act gat tgc

144

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr Asp Cys

35

40

45

aga gtt gac gga ata aaa gtg tcc tta acc cta tgg gat acc gag gga

192

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr Ala Gly

50

55

60

caa gag gaa tat gaa cgt tta cgt cca ttc tca tat tca aac gca gat

240

Gln Glu Gln Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys Ala Asp

65

70

75

80

ata ata tta att ggg ttt gct gta gac aat ttt gag tca cta att aac

288

Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu Ile Asn

85

90

95

gca agg acg aaa cgg ggg gat gag gca tta cga tat tgt cct gac gca

336

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro Asp Ala

100

105

110

697/762

cca atc ggt ctt gta gcc ttg aaa aaa gal ccg agg caa gaa gcc cat
384

Pro Ile Val Leu Val Gly Leu Lys Lys Asp Ileu Arg Gln Glu Ala His
115 120 125

ttc aaa gag aat gct acc gac gaa atg gtt ccc att gaa gai gca aaa
432

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp Ala Lys
130 135 140

caa ggt gca agg gcc att ggg gcc aag aaa tac atg gaa tgt agt gca
480

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala
145 150 155 160

ctg act ggt gag ggt gtg gat gat gtc ttt gaa gta gct aca aga acc
528

Ileu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr
165 170 175

agt ttg ctt atg aag aag gaa cca ggg gct aac tgt tgc ata att tta
576

Ser Leu Leu Met Lys Lys Glu Pro Gly Ala Asn Cys Cys Ile Ile Leu
180 185 190

tac

579

<210> 286

<211> 192

<212> FRT

<213> Saccharomyces cerevisiae

<400> 286

Met Ser Glu Lys Ala Val Arg Arg Lys Leu Val Ile Ile Gly Asp Gly
1 5 10 15

Ala Cys Gly Lys Thr Ser Leu Leu Tyr Val Phe Thr Leu Gly Lys Phe
20 25 30

Pro Glu Gln Tyr His Pro Thr Val Phe Glu Asn Tyr Val Thr Asp Cys
35 40 45

Arg Val Asp Gly Ile Lys Val Ser Leu Thr Leu Trp Asp Thr Ala Gly
50 55 60

Gln Glu Glu Tyr Glu Arg Leu Arg Pro Phe Ser Tyr Ser Lys Ala Asp
65 70 75 80

Ile Ile Leu Ile Gly Phe Ala Val Asp Asn Phe Glu Ser Leu Ile Asn
85 90 95

Ala Arg Thr Lys Trp Ala Asp Glu Ala Leu Arg Tyr Cys Pro Asp Ala
100 105 110

Pro Phe Val Leu Val Gly Leu Lys Lys Asp Leu Arg Gln Glu Ala His
115 120 125

Phe Lys Glu Asn Ala Thr Asp Glu Met Val Pro Ile Glu Asp Ala Lys
130 135 140

Gln Val Ala Arg Ala Ile Gly Ala Lys Lys Tyr Met Glu Cys Ser Ala
145 150 155 160

Leu Thr Gly Glu Gly Val Asp Asp Val Phe Glu Val Ala Thr Arg Thr
165 170 175

Ser Leu Leu Met Lys Lys Gln Pro Gly Ala Asn Cys Cys Ile Ile Leu
180 185 190

<210> 287
 <211> 792
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(792)

<400> 287
 atg atc gct acc tcc aga gcc gta aac atg aat aaa gaa tca aaa cac
 48
 Met Ile Ala Thr Ser Arg Ala Val Asn Met Asn Lys Glu Ser Lys His
 1 5 10 15

aag aag gct ctc gcc aaa cca tgc aga gag aga caa act tca gtt aca
 96
 Lys Lys Ala Val Ala Lys Pro Cys Arg Glu Arg Gln Thr Ser Val Thr
 20 25 30

aga gcc atg aga cca gct gta gcc cgt gat cct cgc aga ctt tca acg
 144
 Arg Ala Met Arg Pro Ala Val Ala Arg Asp Pro Arg Arg Leu Ser Thr
 35 40 45

tgg tgg tct cct tct tgg tca cca atg tca gcc cag aga agg ctt tgg
 192
 Ser Ser Ser Pro Ser Ser Ser Pro Met Ser Ala Gln Arg Arg Leu Ser
 50 55 60

agg gaa gaa ata ata aac gaa atg gaa aag gag caa gac gct att gta
 240
 Arg Glu Glu Ile Ile Asn Gln Met Gln Lys Glu Gln Asp Ala Ile Val
 65 70 75 80

gta aga ctt cta cgg gaa att gaa act tta aaa gaa gaa aac tct agg
 288
 Val Arg Leu Leu Arg Glu Ile Glu Thr Leu Lys Glu Glu Asn Ser Arg
 85 90 95

tta aaa aat uaa atg cac cat cgg gtc cgg gct aga agg tgg tct cca
336

Ieu Lys Asn Gln Leu His His Pro Val Pro Ala Arg Arg Ser Ser Pro
100 105 110

ttt ttc gaa ggc gag tct gcc atc cta gat gat gat gac tgc aat tat
384

Phe Phe Glu Gly Glu Ser Ala Ile Leu Asp Asp Asp Asp Cys Asn Tyr
115 120 125

ggc taa acc ctc gac act cca aag cta aag ctc aca gat ggt gca tcc
432

Gly Tyr Thr Leu Asp Thr Pro Lys Leu Lys Leu Thr Asp Gly Ala Ser
130 135 140

aga cac acc gta ctt ccc tta aca ccg aag gac tcc atg acc cac att
480

Arg His Thr Val Leu Pro Leu Thr Pro Lys Asp Ser Met Thr His Ile
145 150 155 160

tcc cat tcc gcc aga agy tca agc cgg aac gct tcc ata tct cac gga
528

Ser His Ser Ala Arg Arg Ser Ser Arg Asn Ala Ser Ile Ser Asn Gly
165 170 175

aca agc atc tca gac acg att ttc ccc att gag act aac acc cac tca
576

Thr Ser Ile Ser Asp Thr Ile Phe Pro Ile Glu Thr Lys Ile His Ser
180 185 190

gca cca aca aca aac aga aac ctt ccg tcc gcc gat ctt cca cat cac
624

Ala Pro Thr Thr Asn Arg Asn Leu Pro Ser Ala Asp Leu Pro His His
195 200 205

act ctt ctt cca cgt tct cta agc ggc att tgg tct agc gat tta acc
672

Thr Leu Leu Pro Arg Ser Leu Ser Gly Ile Ser Ser Ser Asp Leu Thr
210 215 220

gaa tcc ggt gct ctt ctt cat gac agy aga agy cgt tcc tcc aat tac
720

701/762

Glu Ser Gly Ala Leu Leu His Asp Arg Arg Arg Ser Ser Asn Tyr
 225 230 235 240

agt ctc gat ggc tcaaac tct tta aag gct gat ctc atg gca aag aga
 760

Ser Leu Asp Gly Ser Asn Ser Leu Lys Ala Asp Leu Met Ala Lys Arg
 245 250 255

ttc caa act ggt tca ttg aaa tag
 792

Phe Gln Thr Gly Ser Leu Lys
 260

<210> 288
 <211> 263
 <212> PRT
 <213> Saccharomyces cerevisiae

<400> 288

Met Ile Ala Thr Ser Arg Ala Val Asn Met Asn Lys Glu Ser Lys His
 1 5 10 15

Lys Lys Ala Val Ala Lys Pro Cys Arg Glu Arg Gln Thr Ser Val Thr
 20 25 30

Arg Ala Met Arg Pro Ala Val Ala Arg Asp Pro Arg Arg Leu Ser Thr
 35 40 45

Ser Ser Ser Pro Ser Ser Ser Pro Met Ser Ala Gln Arg Arg Leu Ser
 50 55 60

Arg Glu Glu Ile Ile Asn Glu Met Glu Lys Glu Gln Asp Ala Ile Val
 65 70 75 80

Val Arg Leu Leu Arg Glu Ile Gln Thr Leu Lys Glu Glu Asn Ser Arg

85

90

95

Leu Lys Asn Gln Leu His His Pro Val Pro Ala Arg Arg Ser Ser Pro
100 105 110

Phe Phe Glu Gly Gln Ser Ala Ile Leu Asp Asp Asp Asp Cys Asn Tyr
115 120 125

Gly Tyr Thr Leu Asp Thr Pro Lys Leu Lys Leu Thr Asp Gly Ala Ser
130 135 140

Arg His Thr Val Leu Pro Leu Thr Pro Lys Asp Ser Met Thr His Thr
145 150 155 160

Ser His Ser Ala Arg Arg Ser Ser Arg Asn Ala Ser Ile Ser Asn Gly
165 170 175

Thr Ser Ile Ser Asp Thr Ile Phe Pro Ile Gln Thr Lys Ile His Ser
180 185 190

Ala Pro Thr Thr Asn Arg Asn Leu Pro Ser Ala Asp Leu Pro His His
195 200 205

Thr Leu Leu Pro Arg Ser Leu Ser Gly Ile Ser Ser Ser Asp Leu Thr
210 215 220

Glu Ser Gly Ala Leu Leu His Asp Arg Arg Arg Arg Ser Ser Asn Tyr
225 230 235 240

Ser Leu Asp Gly Ser Asn Ser Leu Lys Ala Asp Leu Met Ala Lys Arg
245 250 255

Phe Gln Thr Gly Ser Leu Lys

260

<210> 289

<211> 576

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(576)

<400> 289

atg gct tcc tca agt agc aag cta cag att cat atg tat att aga ccc

48

Met Ala Ser Ser Ser Ser Thr Leu Pro Leu His Met Tyr Ile Arg Pro

1

5

10

15

tta atc att gaa gat tta aag cag att ttg aac ttg gaa agc cca ggt

96

Leu Ile Ile Glu Asp Leu Lys Gln Ile Leu Asn Leu Glu Ser Gln Gly

20

25

30

ttc cca cca aac gaa aga ggt tca gaa gaa att atc agc ttt cgt ttg

144

Phe Pro Pro Asn Glu Arg Ala Ser Glu Glu Ile Ile Ser Phe Arg Leu

35

40

45

atc aat tgt cca gag cta tgt tca ggt ctt ttc atc aga gag atc gag

192

Ile Asn Cys Pro Glu Leu Cys Ser Gly Leu Phe Ile Arg Glu Ile Glu

50

55

60

ggc aaa gaa gtt aaa aag gag aca cta att ggt cat att atg ggt act

240

Gly Lys Glu Val Lys Lys Glu Thr Leu Ile Gly His Ile Met Gly Thr

65

70

75

80

aag ata cct cat gaa tac att act atc gaa agc atg ggc aaa tta caa
288

Lys Ile Pro His Glu Tyr Ile Thr Ile Glu Ser Met Gly Lys Leu Gln
85 90 95

gtg gaa tgg agt aat caa att ggt att cac tct gta gta atc aag cca
336

Val Glu Ser Ser Asn His Ile Gly Ile His Ser Val Val Ile Lys Pro
100 105 110

gaa tac cag aaa aaa aac ctg gct act tta ctc tta act gac tac att
384

Glu Tyr Gln Lys Lys Asn Leu Ala Thr Leu Leu Leu Thr Asp Tyr Ile
115 120 125

cag aaa ttg agt aat cag gaa att ggt aac aaa att gtc ctt att gct
432

Gln Lys Leu Ser Asn Gln Glu Ile Gly Asn Lys Ile Val Leu Ile Ala
130 135 140

caa gag cca ttg ata cca ttt tat gaa aga gtt ggt ttc aag atc atc
480

His Glu Pro Leu Ile Pro Phe Tyr Glu Arg Val Gly Phe Lys Ile Thr
145 150 155 160

gct gag aac acc aat gtt gct aag gac aaa aac ttc gaa gaa cag aaa
528

Ala Glu Asn Thr Asn Val Ala Lys Asp Lys Asn Phe Ala Glu Gln Lys
165 170 175

Lgg atc gat atg gag aga gaa cta att aag gaa gaa tac gac aac tag
576

Trp Ala Asp Met Glu Arg Glu Leu Ile Lys Glu Glu Tyr Asp Asn
180 185 190

<210> 290

<211> 191

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 290

Met Ala Ser Ser Ser Ser Thr Leu Pro Leu His Met Tyr Ile Arg Pro
1 5 10 15

Leu Ile Ile Glu Asp Leu Lys Glu Ile Leu Asn Leu Glu Ser Gln Gly
20 25 30

Phe Pro Pro Asn Glu Arg Ala Ser Glu Glu Ile Ile Ser Phe Arg Leu
35 40 45

Ile Asn Cys Pro Glu Leu Cys Ser Gly Leu Phe Ile Arg Gln Ile Glu
50 55 60

Gly Lys Glu Val Lys Lys Glu Thr Leu Ile Gly His Ile Met Gly Thr
65 70 75 80

Lys Ile Pro His Glu Tyr Ile Thr Ile Glu Ser Met Gly Lys Leu Gln
85 90 95

Val Glu Ser Ser Asn His Ile Gly Ile His Ser Val Val Ile Lys Pro
100 105 110

Gln Tyr Glu Cys Lys Asn Leu Ala Thr Leu Leu Leu Thr Asp Tyr Ile
115 120 125

Gln Lys Leu Ser Asn Gln Glu Ile Gly Asn Lys Ile Val Leu Ile Ala
130 135 140

His Glu Pro Leu Ile Pro Phe Tyr Glu Arg Val Gly Phe Lys Phe Ile
145 150 155 160

Ala Glu Asn Thr Asn Val Ala Lys Asp Lys Asn Phe Ala Glu Gln Lys

165

170

175

Trp Ile Asp Met Glu Arg Glu Leu Ile Lys Glu Glu Tyr Asp Asn

180

185

190

Homologs to YDR101C (ORF368), SEQ. ID No. 17

>GM48929802

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>GM48929802

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Homologs to YBR025C (ORF696), SEQ. No. 31

>BN42370798 DNA: putative GTP-binding protein

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BN42370798 protein: putative GTP-binding protein

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rgficars*

>BN44233997 DNA: Similar to GTP-binding protein

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attgtaaaagaaggagaigtgatgctttccgcttcaacgtaata

>BN44233997 protein: Similar to GTP-binding protein

mslkagivglpnvgkstlfnawvenykaqaunfpctiepvnvgivavpdsrlqvlsklinsqkvvpasiefvdlaglvkgas
qgeglnkflahirevdsilqvvrfeclndivhvngkwdptedidvinlelifcdldqlgkrldrnkgkpkdsqskvkeaaek
salqrigealldgkparvalndickdavlkhclltmkpmiyvanvaetdledpdknefvqqvkaesdlqsgshvrvsaqv
cseltelpder toylnstgvsesglnlratylslgklyltsgeketrawti hagmiapqaasvihsdfekgfiraetvayed
fvsagslaaardkgllrsegkeyivlcegdvmlfrfnv*

>BN46708845 DNA: putative GTP-binding protein

atgcctcogaaagcaaaagcaaaaggatgcaggcccggtggagagggcctattcttgccgcttctcgtctcacctcaagat
cgggaatcgtggggctgccaaacgtggggaagctacactttcaacactcttacgaagcttccagctgagaaacttc
cccttctgtacattgagcctaaccgaggcgcgtgtgaatatcccgacgagagggttcgallggctttgcagttatacaagc
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tgcttccgctaagcccgllgtttacttgattaacatgaatgagagagactaccagaggaagaaaaacaagttctgccca
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tggcaatgaaaccgcagtcacaggcgccagggaataacagacaggagggggaaaacataigtgttcaggatggagat
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>BN46708845 protein: putative GTP-binding protein

mppkakakdagpverpilgrfsshkigivglpnvgkstlntllklsipaenfpctiepnearvnipderfdwlcqlykpkse
ipafcihdiaglvrgahcgqglgnnflshiravdgifhvratedpdiihvddivdpvrdeiteelrkdielkkiedveks
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ggdtmipfsgvferstadmipdeaakyceenklqsalpriiktgsainliyfftagpdevkcwqlnrqskapqaagaihdtf
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>GM50231579 DNA: GTP-binding protein

atgcctccaaaatctgocaaatccaaggaagctccagctgagcgacccatcctcggtcgattctctctcactcctcaaaatt
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atatctttaagttcaacgtttctgggtggggcaagaagtaa

>GM 50231579 protein: GTP-binding protein

mppksakskeapeerpiigrfsshkigivglpnvgkstlntllklaipaenfpctiepnearvnvdpderfewlcqlfkpkse
vsafleihdiaglvrgahqggglgnnflshiravdgifhvratedpdiihvddivdpvrdeiteelrkdielmerkiodieks
mkrsndkqlkiecccqvkallegkdinrgdvkaadieilnsqlltakpvvylvnmtekdqyrknkflpkihawvqeh
ggetiipfscalemiamppdeaakyceenktqsaltkiiktgsainliyfftagpdevkcwqlnrqskapqaagaihdtf
rgficaevmkfedlkelgsesavkaagkykqegktyvvqgdgdiiffkfnvsgggkk*

>GM51934922 DNA: Similar to GTP-binding protein

atggcaagagcagcttgcacatcccttcaattgggtccaggtttagttcatcctctaaagtcaacctcttcacaaatcacact
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gttctgtctgttgcacttctgcagcacgagagaaaggactgttgcagatcgaagggtaaagactacgttgcacaagaagc
agatgtcatgtttcttcgaattcaattttaa

>GM51934822 protein: Similar to GTP-binding protein

maraaenhlhlypelvhpklstltnhtlettrfygihrfssssskiemslkagivgipnvgsstfinavvengkaqaanfp
ctiepnvgivavpdsrlhvsldlskaqrpvasiefvdiaglvkgasqgelqglgnkfshirevdsliqvvrfoedndivhvn
gkvdpksddivnlelvfsldldjekridklkkgkakdsqklkoeaeksalekirealmdgkparsvltldferdavkhldlt
mkpviyvanvaeedladpannnvykdvtnvselqsrivtsaqvaeeltelpveerqeylqalgvscsglgnlratydlg
lryttagetkewtilagmtapqaagvifhsdfekglireatvseyedfvaegslsaarckglfseglodyvwqeadvmlrl
nv

Homologs to YGR121C (ORF1466), SEQ. ID No. 69

>Gim59617924 DNA: putative ammonium transporter AMT1:1

[illegible]

mslpacpaeqlaqlgpnitdasaaasliocgfaavdskfvdtafavdntylfisaylvfemqlgfamlcagsvrakntmni
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gfvypvshwfwspdgwasafkildrfstgvidfagsgvwhmvvggiaglwgaiaqprmgfdhagravalrghsaslv
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e

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[illegible]

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atggctgcacgaagcaccgggggaggaagctgaaggcggagcccaaggaagctccagttcgaaagctcc
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gcgtatcgggtggcgaggccatgggtga

>OS35840251 putative histone H3

atggccccgcacgaagcagacggcgagggaagtcacccggcgggcaaggcgccgagggaagcagctggcgacgaagg
cgggcgcgcaagtcggcccccggcgaacggcgggcggtgaagaagcccccacccgttcaggccggggaacccgtggcgctcc
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cgcccgccgcacatccgtggcgagaggcgtag

>OS40216588 histone H3

atggcccccacaaagcagacggcggaaggaagtcacccgcacgaatgtgcggagggaagctgctggtgatgaagggtg
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gagatccgcacataccagaagagcaccagagctgctaaccgcgaagctcccccctccaggcggtggtgacggagatccg
gcaggacgttaggtctatgttccgttcacgagctctgcgcgtggtgcgcgtgcaggaggctcccgagaccttacctgtggg
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gcacacaggggcgagaaaggccag

>OS41565420 histone H3.3

atggcccgtaaccaagcagacccgctcgttaagtcacagcagggaagggtccacagggaagcagcgttcacaccaaggctg
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>BN42032866 histone H3.3

atggctcgtacgaagcaaacccgcaagaaaatccaccggagggaaaaagctcccagggaagcagctcgcacccaaggc
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gagaacgtgcttaa

>BN42113630 histone H3.3

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gactgacctgcglltccagagccatgcgggtgctgaactccaggaggcgagcgtgaagcataacctgtgggactctttgagg

acaactaacctgtgogccaltcaagccaagcgtgtgaccatcatgcccgaaggacatccagctcgctgcagggatcagag
gagagcgtgtcttaa

>BN12307928 putative GTP-binding protein

atgyckxycaccaagcagacggcaagggaatcaaccggaggcaaggcccccaagggaagcagctagcaacaaaag
cagcgagggaatcagctccagccaccggaggagtgaagaagccgcacagaitcaggccagggaacagtggtcttaa
gagagatcagggaaglacagaagagcacccagctcctgatccgcaagctcccgltccagaggctagttagagagatc
gtcagcatttcaagaacggatctccgttccagagcagcgccgtcgccgctctccagggaagctgcgcagggttaacctgt
cggacgtlltaggatactaattctgtgtcgatccacgccaaagagggtgacgatsatgcctaaggacatacagctcgcca
gaagaatcagagggtgaaagggttag

>BN12421819 putative histone H3

atggctcgtaccgaagcaaacccgctagaaaatccaccggagggaagggtctccgaggaagcagctggcgacgaagcgg
ggcagggaagtcggctccggccaccgggaggagtgaagaagccgcacagattccgtcccggaaccgtcgccctcgtg
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gacttcaagatggatctgagggttccagagcagcgccgtcgccggtttgcaagaggctgctgaggcttaacctgllggtttgtt
cgaagacaccaatctctgtcgatccagccaaaagagltgacgatcatgcccgaaggatatccagctcgctaggagaat
ccgtggtgaaagagcttga

>BN45381195 putative histone H3

atggctcgtaccgaagcaaacccgctagaaaatccaccggagggaagggtctccgaggaagcagctggcgacgaagc
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gagatcagggaagtaaccagaagagcacctgagcttctgatccgtaagcttcccttccagcgtcggctcgtgagatcgtcag
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ccgtggtgaaagagcttga

>BN46364583 histone H3.3

atggctcgtaccgaagcagactgocagggaatcgacaggagggaagggtctccgaggaagcagctggcgacgaagc
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gattcgttaagtaaccagaagagcacctgaggttgatccglaaaacttccctccagcgtcttgttctgtaaatcgctcaggatit
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gagagcgtgtcttag

>BN46422365 putative histone H3

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gagatcagggaagtaaccagaagagcacccgagcttctgatccgcaagctcccttccagcgtcttgttccgtgagatcgtc
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agaatcagaggcgaaagagcttga

>BN47900015 putative histone H3

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agaatccgtggcgaaagagcttga

>BN51269917 putative histone H3

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>OS32404891 histone H3.3

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havlalqeaaeaylvglfedtnlcaihakrvtimpkdiqlarringer*

>OS32795441 putative histone H3

marfkqtarkstggkaprkqlatkaarksapatggvkkphrfrpgtvalreirkyqkstellirkfpqrlvrelaqdfktdlrfqs
savaalqeaaeaylvglfedtnlcaihakrvtimpkdiqlarringer*

>OS34693911 histone H3 protein

marfkqtarkstggkaprkqlatkaarksaptggvkkphrfrpgtvalreirkyqkstellirkfpqrlvrelaqdfktdlrfqs
havlalqeaaeaylvglfedtnlcaihakrvtimpkdiqlarringer*

>OS35840251 putative histone H3

marfkqtarkstggkaprkqlatkaarksapatggvkkphrfrpgtvalreirkyqkstellirkfpqrlvrelaqdfktdlrfqs
savaalqeaaeaylvglfedtnlcaihakrvtimpkdiqlarringer*

>OS40216588 histone H3

marfkqtakkstasnvprkllvmkvarksaptmaglkkphrkpgtvalreirkyqkstellirkfpqrlvrelaqdvrsyvr/q
ssavvalqeaaetylvglfktdnlcviahakrvtimpkdiqlarringer*

>OS41585420 histone H3.3

marfkqtarkstggkprkqlatkaarksapitggvkkphryrpgtvalreirkyqkstellirklpqrlvrelaqdfktdlrfqs
havlalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN42032866 histone H3.3

marfkqtarkstggkprkqlatkaarksapitggvkkphryrpgtvalreirkyqkstellirklpqrlvrelaqdfktdlrfqs
havlalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN42113630 histone H3.3

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havlalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN42307928 putative GTP-binding protein

marfkqtarkstggkprkqlatkaarksapatggvkkphrfrpgtvalreirkyqkstellirklpqrlvrelaqdfktdlrfqs
savaalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN42421819 putative histone H3

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ssavaalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN45384195 putative histone H3

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savaalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN45384583 histone H3.3

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havlalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN46422385 putative histone H3

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savaalqeaaeaylvglfedtnlcaihakrvtmpkdiqlarrirgera*

>BN47900015 putative histone H3

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>BN51269917 putative histone H3

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Homologs to YKL058W (ORF1686), SEQ. ID No. 93

ORF1686-YKL058W

>OS39533967 DNA: transcription factor IIA small subunit

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>OS39533967 protein: transcription factor IIA small subunit

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>OS37780093 DNA: transcription factor IIA small subunit

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agaagagtaa

>OS37780093 protein: transcription factor IIA small subunit

matfelyrrstigmcltetldemvssgalspelaivlvqfdkamtalehqvkaakvtvkgghlhtyrfcdnvwfildtaifkne
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Homologs to YIR022W (ORF1761), SEQ. ID No. 101

>OS32522056 putative signal peptidase subunit

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>OS35055381 putative signal peptidase subunit

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>OS32522056 putative signal peptidase subunit

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 lglivitske*

>OS35055381 putative signal peptidase subunit

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Homologs to YHR113W (ORF1827), SEQ. ID No. 107

>OS32522056 putative signal peptidase subunit

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>OS35055381 putative signal peptidase subunit

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>OS32522056 putative signal peptidase subunit

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lgllvitske*

>OS35055381 putative signal peptidase subunit
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Homologs to YJL024C (ORF1962), SEQ. ID No. 113

>BN42103630 clathrin assembly protein AP17-like protein
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>BN45474405 clathrin assembly protein AP19 homolog
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>BN45690401 clathrin coat assembly protein AP17
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>OS33843933 clathrin assembly protein AP19-like protein
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>OS32894796 putative clathrin assembly protein

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>OS34902237 AP-1 Golgi-related complex component, clathrin assembly protein
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>GM53036028 putative clathrin coat assembly protein
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>BN45474405 clathrin assembly protein AP19 homolog

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>BN45690401 clathrin coat assembly protein AP17

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>OS33843933 clathrin assembly protein AP19-like protein

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>OS32824796 putative clathrin assembly protein

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>OS34902237 AP-1 Golgi-related complex component, clathrin assembly protein

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>OS32634329 clathrin assembly protein AP17-like protein

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>OS35146523 clathrin assembly small subunit protein AP19

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>GM53036028 putative clathrin coat assembly protein

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Homologs to YGR180c (ORF1964), SEQ. ID No. 115

>BN43093876

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7240762

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>BN51295293 20S proteasome beta subunit PBB1

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>BN51425457 multicatalytic endopeptidase complex, proteasome precursor, beta subunit

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>OS32503906 beta 1 subunit of 20S proteasome

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>OS34674802 multicatalytic endopeptidase complex, proteasome precursor, beta subunit

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>OS41132118 beta 5 subunit of 20S proteasome

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>OS34752809 20S proteasome beta subunit PBB2

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>BN46801388 20S proteasome beta subunit PBB1

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>BN51295293 20S proteasome beta subunit PBB1

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>BN51425457 multicatalytic endopeptidase complex, proteasome precursor, beta subunit

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>OS32503906 beta 1 subunit of 20S proteasome

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>OS31674802 multicatalytic endopeptidase complex, proteasome precursor, beta subunit

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Homologs to YLR441C (ORF2138), SEQ. ID No. 129

>OS30932534 S-phase-specific ribosomal protein

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>OS32589884 S-phase-specific ribosomal protein

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>BN41966449 Putative S-phase-specific ribosomal protein

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>BN43154133 Putative S-phase-specific ribosomal protein

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>GI450096495 ribosomal protein S3a

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>OS34661717 ribosomal protein S3a

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>BN46971595 Putative S-phase-specific ribosomal protein

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>OS30932534 S-phase-specific ribosomal protein

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>OS32589864 S-phase-specific ribosomal protein

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>BN41266449 Putative S-phase-specific ribosomal protein

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>BN43154133 Putative S-phase-specific ribosomal protein

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>GM50096495 ribosomal protein S3a

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>OS34661717 ribosomal protein S3a

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>BN46971595 Putative S-phase-specific ribosomal protein

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Homologs to YLR029C (ORF2328), SEQ. ID No. 135

>OS34946702 ribosomal L15 (YL10) protein homologue

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>OS34946702 ribosomal L15 (YL10) protein homologue

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>GM59696919

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>GM59696919

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Homologs to YNL224C (ORF3561), SEQ. ID No. 173

>OS32586448 translational initiation factor eIF1

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>GM59605347 translational initiation factor eIF1

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>OS34684287 translational initiation factor eIF1

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>OS34073720 translation initiation factor

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>GM59676621 translational initiation factor eIF1

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>GM59822253 translation initiation factor

atgtctgaattagaagatcaaatccctactgccttcgacccctttgctgatgcaaatgctgatgactcgggtgctgggtcaaag
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>GM52851017 translation initiation factor-like protein

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>GM52699053 translation initiation factor

atgtctgaattcgacacaaacatcccactgcttttgatcccttgctgatgcaaatgctgaggactcagggtctgggaaga
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>BN44219936 translation initiation factor

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>CM53877384 translation initiation factor-like protein

atgggtgaagtggttattatcagatccctacgagcacttccgaccatttgcggaggcaaaagaacagatgctccogg
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>OS40418529 translational initiation factor eIF1

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>OS32566448 translational initiation factor eIF1

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>GM59605347 translational initiation factor eIF1

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- >OS34684287 translational initiation factor eIF1
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- >OS34073720 translation initiation factor
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- >GM59676621 translational initiation factor eIF1
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- >GM52851017 translation initiation factor-like protein
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- >GM52699053 translation initiation factor
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- >BN44219936 translation initiation factor
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- >Qin53877364 translation initiation factor-like protein
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qlqgdqqrknvshflharhrkdqikihgf*
- >OS40418529 translational initiation factor eIF1
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- >GM59622253 translation initiation factor
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Homologs to YNL334C (ORF3578), SEQ. ID No. 175

- >OS32595690 imidazoleglycerol-phosphate synthase subunit H-like

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>GM49669448 imidazoleglycerol-phosphate synthase subunit H-like

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>OS32585690 imidazoleglycerol-phosphate synthase subunit H-like

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>GM49669448 imidazoleglycerol-phosphate synthase subunit H-like

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 plyr*

Homologs to YOR020C (ORF3687), SEQ. ID No. 185

>GM52366459 cp10-like protein

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>OS32631203 chaparonin

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>BN51277798 chaperonin CPN10

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>BN42676671 10 kDa chaperonin

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>GIM50703949 putative 10kd chaperonin

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>GM52366459 cp10-like protein

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ails*

>OS32631203 chaperonin

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vlfrehdkatlvd*

>BN51277798 chaperonin CPN10

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>BN42676671 10 kDa chaperonin

mmkrlvptfnrlivqrviqpaktesgillpekasslnsgkviavgpgsrdkdgklipvsvkegdtvllpeygggtqvkdgekey
hlfrdedvlgthhed*

>GM50703949 putative 10kd chaperonin

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Homologs to YOL103W (ORF4303), SEQ. ID No. 203

>BN51360974 DNA: putative sugar transporter

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>BN51360974 protein: putative sugar transporter

mqsstyaaavkgnaaafqrrsfslvrsatgtgtrfslgysyfaqlhssaskamgaktaraenglhslsvkarsvraqass
gggdeeeaiplrsegkisgtvlpfvgaclgailfyhlgvvngaleyakdlqiadnavlqgwivsallagatvgsftggala
dkfgrtrtqldaipiaigaficataqswqtrniivrllagvgigissaivplyiseispteirgalgsvnqlfioigilaaliaglpaan
plwwrtmfgvavipsvllaigmfgespsprwlvqqgktdqaokaiktygkekvvvelrdlansgggtsepeagwdfdfssr
ywkvvsvgaalfiqqlaginavvyystsvfrsagiqsdvaasaivgaavvlgavasslmdkmgrkslltsfggmalsml

ggggcaccttggagcttccatccagatggcaacatgccttggtctaattgggagccttatttaltggaatccctgtcaagaaa
 ttctggatggtggcgggttggtttgggtatccattccagctgctatcttgccgcagctatggctctctgcgcagagagt
 ccgcattggttatacaagcaagggaagaactgctgaagcagaagctgagtttgagagactcttgggtgatcagaagcaa
 aatttgcaatgtcggagttatccaaggtagatagaagtgatgatactgatactgtaaagctgctgggaallgcllcaiggctgt
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 ggtccagttccagggtcctctaccagaaatcttcttagtogaataagagccaaagccatggcagctgtgtatgtcagtg
 attgggtgataaattcttgggtgactactgttcttgcgttgcctggagaaacttggtccacagctgcttactccatgtttgtac
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 actcttctcaagactag

>GM59730390 protein: sugar transporter

mwwghssmykrtpsrdnsnmedmeensdigldkgtstnpslmislpvlvatisfflgyhlgvnpelesisvdlgrgn
 taeglvvsiclggaligcllsgwiadgvgrrrafqlcalpmiigasmsaatnrlgmlygrifvgtglglgppvaslyvtevspa
 fvrgtfgafiqiatclglnqalfigipvkeisgwwrvctvwstipaailaaamvfcaesphwlykqgrtacacaefellgvse
 akfamselskvdrddtdtvlksellhgrhskvvtfigstfalcqlsginagfyfctvksagvpsdianvcigianlgsivs
 mglmdklgrkvllfwffgmalamllqatgatslvsnvgaqyfsvvgmllvlftalgagpvpqllpeifpsnrakamavc
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Homologs to YPL079W (ORF4425), SEQ. ID No. 207

>BN44798833 60S ribosomal protein L21

atgcggcggggtcaggagtgagggcgagaaccaggatctgttcgctagaggggtcaggaaagaagggtgttatccca
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 taacagaatcatlagaagaggttgcatgttctgttgagcacgtgcagcagtcgaaggtgtgtcagggaglttaactaa
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 caeggglygclactaa

>BN44798833 60S ribosomal protein L21

mpaghgvrantrdlfargfrkkgviplestytrfkvgdydvdlvngaihkgmiphklyhgrtgrvwnvtkravgvvknqign
 riirkrlhvrvehvqqsrcaeeffdrkknndvlkaaakargetistkrqpkpkpgfmvegmtictvtpipydvndlkgyt*

Homologs to YPR052C (ORF4130), SEQ. ID No. 221

>GM59623606 high mobility group protein 2-related

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>OS36010716 unknown protein

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>OS34825203 HMG protein

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>BN51295208 putative HMG protein

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cagaagggtggaagtgaagagggaaggaagatgatgattag

>GM59623606 high mobility group protein 2-related

mknakgkgaaraskesikpvdcirkvgrkasgkpgrrsapkkekakkdpnkpkppsaiffvleef/ktfkaenpnv
kavsvvgkaggekwwkslssaaekapyeakaakrkaeyeklikeydkkqassaddeeedkseksevnededdasgecc
eeddeeeddeddd*

>OS36010716 unknown protein

msevrtsvmrtpasasarsasslasagrhtlssvpptprlp/ptrsatrtprpttlkw/ptivmsqfyddlp/

>OS34825203 HMG protein

mknakgkgaaraskeslkpvddrkvgkrkasgkpgrrsapkkekakkdpnkpkrppsaffvfllefkrftkaenpnv
kavsvvgkaggekwkslssackapyeakaakraeyeklikayckkqassaddeesdksksevndeddasgeec
eeddeeeeddeddd*

>BN51295209 putative HMG protein

mkggeikaqskstderiktrgkagkkaakdpnkpkrppsaffvflgfrkefnlanpdnksvgavgkaagakwksmt
dedkapyvakaeskkteytklmqkynmklangtstagddsdksksevndeaaeggseeeeddd

Homologs to YLR275W (ORF2923), SEQ. ID No. 225

>BN42537749 small nuclear ribonucleo protein D2 -related

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ccaagtaa

>OS37525380 small nuclear ribonucleo protein D2 -related

atggcgagggaagccactcaggggaagaaggaggaggaggaaticagtaacggggcccgctgtccgtgtcgtatgatga
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ga

>BN42537749 small nuclear ribonucleo protein D2 -related

msrpmneedtngkleeeefntgplsvlmmssvknntqvlincnnkdlgrvrafdrhcnmvlenvremwtevpktgkgkk
kalpvnrdfriskmfrgdsvlvlmpk*

>OS37525380 small nuclear ribonucleo protein D2 -related

maeeatgkdkeseeefstgplsvlmmssvknntqvlincnnkdlgrvrafdrhcnmvlenvremwtevpktgkgkkkal
pvnkdrfiskmfrgdsvlvlmpk*

Homologs to YGL106W (ORF 293) SEQ. ID No. 239

>BN42003647 calmodulin-3

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cgactcggagggaagagctcaaggaagcggttcagggtcttcgacaaggatcagaacgggttcaictcagctgctgagctc
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>BN45450720 calmodulin 2

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>BN42308806 putative calmodulin protein

atggggcaaggacggcctgagcgacgaccagggtgtcatogataagggaggccctcaogctcttcgacaccaacgggga
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tgaggcatalcttgacaagtatcgggggagaagctggagcctaacgagtttgatgagtgatcaaggaggtggatgtggg
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>OS34266853 calmodulin

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>OS34824439 calmodulin

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>OS41802485 calmodulin

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>GM47065673 calmodulin

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>OS34028983 calmodulin

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>BN45407352 calmodulin-3

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aa

>BN42003647 calmodulin-3

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>BN45450720 calmodulin 2

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seeelkeafvfdkdqngfisaaelrhvmtnlgekitdeevdemireadvdgdgqinyeefvkvmak*

>BN42308806 putative calmodulin protein

mgkdglddqvssmkeafitfdtngdglkaptelgilmrslgnpteaellqdminevdadgngtidtpeflnlmarkmkdtd
lrdafkvldkegtgfvavadlrhltsigeklepnefdewikeadvdgdgkikyedfiarmvak*

>OS34266856 calmodulin

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>OS31824439 calmodulin

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>OS41802485 calmodulin

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>GM47065673 calmodulin

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>OS34028983 calmodulin

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>BN45407352 calmodulin-3

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Homologs to YIL023c (ORF1717), SEQ. No. 243

>BN45773929 metal transporter family

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>OS32877780 metal transporter family

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> BN51401271

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Homologs to YKL103c (ORF1583), SEQ. No. 283

>BN51473779

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>BN51473779

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Homologs to YNL090W (ORF3165), SEQ. ID No. 285

>OS32558796 small GTP-binding protein RAB5B

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>OS33960403 putative Rop family GTPase ROP4

maasasrllkcvvgdgavgktcmllisytsntfptdyvptvfdnfsanvvvdgntvnlglwdtaggedynrlrplsyrgadvfla
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>BN42135991 GTP-binding protein

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daaikwvlqppkskkkkknknrevll*

>BN45412825 Rho1Ps homolog/ Rac-like protein

msasrllkcvlvgdgavgktollisytsntfptdyvptvfdnfsanvvvdgntvnlglwdtaggedynrlrplsyrgadvflafsl
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>GM47124407 Rac-like gtp binding protein ARAC2

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>GM47172047 Rac-like GTP binding protein

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>GM48914288 small G protein

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>GM50693528 small G-protein ROP9

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>GM52260563 rac-type small GTP-binding protein

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>GM50189916 rac-type small GTP-binding protein

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>GM43741326 putative rac protein

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>BN43381801 putative GTP binding protein Arac10

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>BN12385898 putative ROP family GTPase

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>BN44062474 putative GTP binding protein Arac10

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>BN42519337 Rac-like protein

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>BN42557868 putative GTP-binding protein

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>BN44504217 GTP-binding protein

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>BN41992996 putative ROP family GTPase

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>OS37307380 small GTP-binding protein

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>OS30848846 small GTP-binding protein

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>OS35505384 GTP-binding protein RAB21

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>OS32558796 small GTP-binding protein RAB5B

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>OS33860403 putative Rop family GTPase ROP4

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>BN42135991 GTP-binding protein

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>BN45412625 Rho1Ps homolog/ Rac-like protein

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>GM47124407 Rac-like gtp binding protein ARAC2

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>GM47172047 Rac-like GTP binding protein

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>GM48914268 small G protein

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>GM50693528 small G-protein ROP9

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>GM52260563 rac-type small GTP-binding protein

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>BN42385898 putative ROP family GTPase

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>BN44062474 putative GTP binding protein Arac10

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>BN42519337 Rac-like protein

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>BN42557868 putative GTP-binding protein

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>BN44504217 GTP-binding protein

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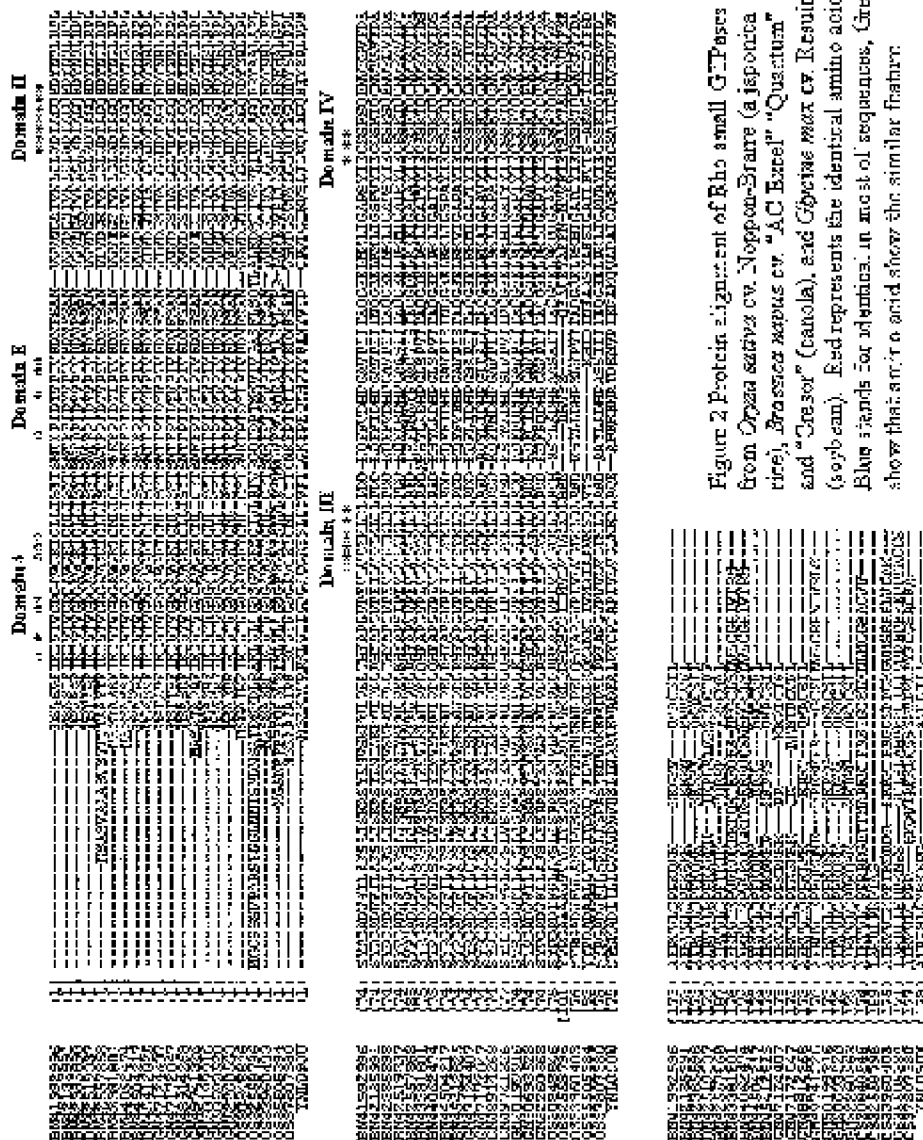


Figure 2 Protein alignment of Rho small GTPases from *Opiza sativa* cv. Nopon-Brave (a spontaneous rice), *Brassica napus* cv. 'AC Excel' 'Quantum' and 'Cresor' (canola), and *Glycine max* cv. Resnick (soybean). Red represents the identical amino acid. Blue stands for identical in most of sequences. Green show that an amino acid show the similar feature.

Figure 2.1

